

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3166	8663	A	3426	2	311	FHSCYPGWSAMVRSQLTATSASQF K*FSCLS/LPSSWDYKCAPPHPANFL FLVEMRFHHVLVRLVLNS*TQVIHL PRPPKVLGITGVRLGAQPCTFFFFYC SSV
3167	8664	A	3427	7	534	TSDFIYKALKLQQEVPKAKSHLVQN YRFFFFFFLRLWSLAPVAQTGVQWH DLSSLQPPPPGFKRFCLSLPSSWDY RCPPRPANF*FLVETGFHHVDQAG LKHLTSDDPASASPSAGITGVHPRP GQENQDLPLGLCVDQLYTENSRRFSK NYYQTPNFTSRKRDLSVFFFA
3168	8665	A	3428	368	688	LTVEFLNLLNILSLVCFIHQTN*IICY FNT/SSSHQNA*YI*EPHVPS*GQRGK ASRQRG*TPPRSGTAASWPRVEK*R EARPQNPAQQTYYVRESPTDASPSS PKMAA
3169	8666	A	3429	1	90	FFFVLSHQRNLCLRRYSRDMAAIK SKFFL/WPGRVAYAYNPSTLGGRGG QIT*AQEFKCS*AAIKSKFFL
3170	8667	A	3430	259	331	RNE*LLTRFSPLSLSH*VLGVSMF
3171	8668	A	3431	1	639	LGKFHTFQMSPGGGVGLLSL*SYRN SCLAG/GGCDHMSVHVCIRARGVK VRSKNSNHTETRK\VLGGMRLSLT RESSISDSMWLARKQTLHTPVMMQ TPHLTPTI*EEPQRIRPEADTFMSV/Y YPMQTEHHQTPLDYNRRGTSLED DEEPIVEDVMMSSSEGRIEDLNEGM DFDTMDIDLPPSKNR\RETELKAD FFDPASIMDESVLGVSMF
3172	8669	A	3432	1	354	LETSPLMFTMLDRDMSG/TMGFNEF KELWAVLNGWRQHLSSFDTRSGT VDPQELQKALTMMGFRLSPQAVNSI AKRYSTNGKITFDDYIACCVKLRL TDSFRRRDTAQQFIQCVMSV
3173	8670	A	3433	1	788	MAYPGHPGAGGGYYPGGPSVVKEE NLIRQNDVYVFPVSQYGGAPGGPA FPGQTQESLAYGYFAAVAGQDQGID ADELQRCLTQSGIAGVGYKPFNL\ET CRLMVSM\DRDMSGTMGF\SIEFK ELLGLLLEWAGR\QHFIS\STDREW EQ*DPQELPEGP*QTMGF*V*VPPGC *ISFAKRYSTNGKITFDDYIACCVQ T*GVFTDSFSKTGILAQCGCLLNFPI WIDFHFNVCVHG\VKSLGSCMNVIN DSNWSSPLLVLFAFG
3174	8671	A	3434	6222	7046	RTVTTFLSKDSHG\YCAQGGKIPDH QNPQCNRKQHPVSTILMLDKASFC QLRKRKHNLVNCINRNPMSLKN TSWHSSLSVTQRHQQSKLHFQGS LLH*PSQNIL/SNI*KCINYC*HCSSV LLSYLFITESYSVAQAGVQWHDLG LLQLPLRFKQFSCFSLPSSWDYRS APSPANFCILVEMGFCHVGQAGL KLLASSDPPALASQSAGITGVSHYT QPCSPFLKSTGLFSC\KVLNPNYHKG RIYLGRMCFLNSTWHLVKSTLFCPL FI

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3175	8672	A	3435	3	287	SRSVAQAGVRWRDLSSLQPPPPRFK QFSCLNFPSSWDYRCAPPRPANF*I LAEMRFRHVGQVGLELLTSGDPPA SASQSAGITDTSCHAWPFTF
3176	8673	C	3436	88	303	MTFLESSAVPPHWTGQDGRVCWTG WIPQCQAGSAPEVLECLSTQQVKSL QTLGGAAVSHKTNICLPFTKLW*
3177	8674	C	3437	354	416	MKESPGGELPQTGKKPVFLF*
3178	8675	A	3438	274	460	TLKNLRSAAASLTGPNPASPAHSSILS CPMRGHCRTL*KCHDWSFRAKMPS PFPQVGIIYPPPN
3179	8676	A	3439	480	613	LSFRAKMPSFPQVGIIYPPPN*GPIC LLCFSFLCECVFYRNHLD
3180	8677	A	3440	1	864	YPTTPYQHHPISPPPIPTHNHQKP PTPSHRPQPTQRYTYHHNHTALTPI APTRQSNPPHNTHHHTPS/TPRTNSS PPH\HHTLPQRIPPYPPTG*HTPQAHS HPAG*RASSQPRRAPSPASRPSPTDP ALRANPLRSYGSGLPTFPYLHCSN MPKACSPWRPAADMCTAR\PRFRPF KPDFQGPARRHRTTPETRRFPRHGPI SRGEPI\PGQPCPSQRKENSTPEFPPA SSGIGRVTDTGRLAAAPSPPLRIRGS EPDSPFESAEGHRRSPRPRTALAQ SLRNE
3181	8678	A	3441	23	266	EMESHSVTRLECSGAISAHCTLRLP GSSDSPASAS*EAGITGMCTT/ARLIF GFHHVQGAGLKL/NIVILLRPPKV LGLQA
3182	8679	A	3442	840	887	
3183	8680	A	3443	127	593	DKATKLTFRSYAAVILKIHVLTW VILFRRKIIRDETLKLLDLISLSVGKG QCYRVVFFWFFFFFEMKSHSV\TR LECSGAISAHCNLCPLGSSDSPASAS LVAGVTGM*HHTQPIFVFLVATGFH HVGQGSRTDIRVIRPPWPPKVLG LQA
3184	8681	A	3444	2	514	FFFFLRLQSL/DSVAHTGGQ/WGGS/ LQPPPPRFEGFLGLKLLGS*HYK/PP RMANFIFSRDGVFAMLARLVNSS ASSDLPGLASHSAGITG\VSHHARPI FSYKEHQSY\GLRACPAPV*PHLSYL QPQPQYFQIRSHTEAPGST/WNFG DTIQPSTFSFYLT*KIIPILYRVKK
3185	8682	A	3445	2	147	FFFCRD/RSLTMLPRLVLYSWAQVIL PSWPPKMLG*QAQATVPSPPKSIN
3186	8683	A	3446	2	328	TITYRGAKIRITSDSSSETMQAREE* SEIF*VLK/ESSSPH*PKILYSGKLSFK SKGEIK/YF*GKQN/LKEFVSSRPVL QGMLKVVLQREGKLYRSETQTYKK KEKASEKE
3187	8684	A	3447	1	357	GDRVLLCCPG*SADHSSLQS*PSGL KRYFCLGLLSNWKHRCMPPCANF FNFYFCRDK/SLPMLPRLVSNWSAQ GIFLSQPPVSGDYRCGAYHALTLFI YGRMGVFAMLAQAGPQTGGL
3188	8685	A	3448	2	84	GLTLLPRLVSNWPPQEILLPW/PPKV

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						LKL* <u>AQAGLKLLASGNPPALAPKVL</u> KL
3189	8686	A	3449	1	439	
3190	8687	A	3450	1	552	GNEFSILKSPGSVVFRNGNWPIGER IPDVAALSMGFSVKEDLSWPGLAV GNLFHRPRGYPSWVMVKGSGTKL ALTPQAVVISYPLENRVYVMVGKAN SVFEDLSVTLRQLRNRLFQENSVLS SLPLNSLSRNNEVDLLFSELQVLH DISSLLSRHKHLAKDHSPDLYSLEL AGLDEIGKRY
3191	8688	A	3451	3	1111	ILKSPAGSVVFRNGNWPIPRE\RDPP DVAALSHGLPL*KKDLSWPGLAVG NLFHRPRATVMVNVNGVNKLDLP P\GSGIS\YPLENAVPFSLDSVANS\IH SLF\SEETPVVLQLAPSEERVY\VK GRANSVFEDLS\VTLRHSRNRLVFK KTLFLSFTPPQILLSRNNEVDLLFLS ELQV\HDISSLSRPKHL\ARDHSPD LYFTGSWAGL\DEIG\KALLGEDSEQ FRDASKILVD\ALQKFADHDVVPVFM VGNPVVELVHCPSHLNTSPPLGKTR DLPLRPKQAQEPQQVPYNLA\YKYN FEYS\VVFNMVLWIM\ALALA\VIIT SYNIWNMDP\GYDSIIYRMTNQKISE WIECYLWPRIRKRGFGNWLFC
3192	8689	A	3452	3	371	MLPLARCSSSCLAPLSTYQTQVKTQ VHTETCI*MFIAALFIIVRR*KQPKCP SENK\WNKIWHIHTMK*YSATKKN KVLTYATI*MTENMLSQRSY*QKT T*YLFLLMYMKIQNREMYRYKVD
3193	8690	A	3453	2	318	ETESRSVAQAGVQ*RNLSLQ/PLPP GFK*FFSLSLRSSWDYRCMHDA*LI FLFLVETGFCHASQAGLELLTSSDPP ASASQSAKITSMSHHALPLFSNKVT FWDSW
3194	8691	A	3454	33	504	GLHNFLTYKATIISAVWYAVRVEN RSTEQNRVQK*TYMYVVKDAR*VN GNRILF*YC/WNN*IITWRKMNLNL DLTLHRKVYLKWVIDLNVKAKTVS PLGQNITESLHNFGVGKYFLDT*SI/ MPHKFFFNKLDIIRKIFCS*KDAINK MKKWPGVVAH
3195	8692	A	3455	16	1011	WPVRAQAGQRPVLHTQVASLFAGV PCVLSHPKKGLLVPPFPSPKKGHLG KPHCLPSAGRGAAGLGPLAQQPVS PAPASPMAPCKPKGLPPLPMGVEPE ILATMPVLTSHPP/SPEPMQSGNMPP S/PPSLCAFVPRWSHPPVPGWARWS CP/ALPAAPPSL*HWTRMQPPFCVPL RVPWVPSSGARGMKESGLDGQGFL GPTPSASPWGPWFDIRLPGCKQGIL AFKVTGPPTGFDFEGKRFKKENKP PG*LESKAPDTVK*NPPSTNPPPAPA FLTWDCGAYRGPAGFLLVCQPSLLS LILKNIDDTLKCVERFEKLTASKQP KATVVLARRS
3196	8693	A	3456	1	348	PQQLRCFSFWRKDTKVDWLLNRRG

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						ARWLEKKTRLHRGPWARPRLMRA QREEALRREGGNPPPRGPGGEEAPL LRSSSGRPAR/HQT*KKSGASPSDPR SASR*ALRREGGNPPPRGPGGEEAP LLRSSSGRPARLRPSRSPERHPPTLA PPPARPSCPALPRLSMSAG
3197	8694	A	3457	2	247	PGCTILAHCNLCLSGSSDSPASAS*V TGNNRHAQPCPLI*RTGFCHVG/R MNMLVFNSLTSSDPLEVST*GPQPP KVLGLQA
3198	8695	A	3458	1	515	GLGSLGPPAAVPTCPPRSPPP/GSPE GALQCGTLPAGTATPDGHVGVAVP FPPTVAPTRRSRSPQSC*WGLQH QLCPGSMEEHMPHGLALPGASHIV PPTLCAPGGSEGARGI*PPA*AGYAL SLPTQFQTLILHPSCCRPGVP/PINLA AQLPPQVPHAPHAWQLPSAPK
3199	8696	A	3459	2	223	IYISPKALKFCREVGPIPPPK/KGSF PKIPR*QIFPPRC*KTGKGQGIKRP IRGKVLRCCKPGLNLGPPRVL
3200	8697	A	3460	2362	2696	
3201	8698	A	3461	1586	2325	SPQRSGAARARPAPHRALLGRVPA RDAGSGRRTRSSRTRCGGCARRWS SISRRRSSETSAGSWRRLSKPSGPG RWRHCARNTGRRCPWWQISVVP RPSSRP/WLALEAELKDSGEKPGK GASRPEDLQLIGRLQTRLKERDIIK QLTKKKVEDVPSRVVSVPNLASA KNFLSGDLSSRINAPPITTSPLDPSP SCGRITYKPNQSTDAKTATRPDGET AQAKEVQKQGSPPHWEFTKYFSF
3202	8699	A	3462	125	489	YYLFFFFFFLRLQSLTLVAQAGGQW RNLSSLQPLPPGFKRFPCLSLSSWD YKCPPP/RPG*FFVFLVETGFHHVAQ AGLELLTLGDPPTSISQSAGITGVSH QARPD*ETLEFQGDVRNLEE
3203	8700	A	3463	1503	1511	LFPVPFACPSLNCPSPPPIGVHLPIG*I QRLETPP*EEGRWIPRRTCGPARPGP PPGAPSVTLPPRTVHFGHPAKGIHFR KP/RHPG*CVFILTD\CVHLH*KIND FIDTNFAMKSGYPNIRVRSFCLHIT
3204	8701	A	3464	54	593	RTALPAQHVASTWPGRPSRLLLRG GPGAPRSMQTGDSVGRGASKEPN*\n PHSGLPKHPLARSPPQRPSHRAMGQ GSPMPAGPT*TCAQALPPSQDGLD LGNRAGWGCSPECLSKAPGGGPA QAHPGPNPHTYRKQWCWKLSPGH ALAPSPPRREVALLNLYSFIVPRDSP RPCIISL
3205	8702	A	3465	2	324	FFFFFLKWSLA/SFAQAGVQWCDLG SLQALPPGFTPFSCLSLLSSWDYRRP PPHLA/NFFVFLVDMGFTVLARMV SIS*PHDPPALASQSAGITGVSHACP AYNVFKDDG
3206	8703	A	3466	142	413	AQEFKTS LGNMAKPCLYKKYKKM SWDYRRPSRPANFSC\FLVETGFCH VAPAGLELLGSSNSPT*ASQSAGITG

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						VSHHTRPQIFLLPLSN
3207	8704	A	3467	241	523	NISGSFCMPILTAPLFTVAKRWKQY VPISG*MINKMWYIHTVEYYSASKR KIR*/PCAATWMNLEDMMLSEVSQS LEDKYSMLPFM*SIYVKYLEQSNA
3208	8705	A	3468	137	382	NSAVHQKFISIPNTSLPHSLAILKPOI NSLEEET*PFWCKSSPVPKMRGER NDDNFHKVLLNVTNVDKPGQLRSP KWFCWG
3209	8706	A	3469	2	363	FFFDTESYSVAQAGVQWHDLCSLQ PPPAGFKQFFCLSLPSSQDYRHLP WLANF*FLVETGFHHVGQAGLKL TSSDLPASGSQSAGITGMSQRTLQQ LSLKTTELNRNFRCPYCIINA
3210	8707	A	3470	135	466	GIDTILTLNQ*SLKTRQ*FTLIIF/IFF FFLRWSL/DSVAQAGVQWRDLGSL QAPPRGFTPFSCSLPSSWDYRRPLP RPANFFYF**RRGFTMLARMVISIS*P RDLPAEFL
3211	8708	B	3471	27	21189	MKVSAARLAVILIATLALCAPASASP YSSDTPCCFAYIARPLPRAHIKEYF YTSGKCSNPVVVTRKNRQVCAN PEKKWVREYINSLEMSMICSGHHV YPNLPTDSFPGLDQFRGNYLHSRDY KNPEAFKGRVLVIGLGNSGSDIAV ELSRLATQVHDVKVLGNPKPKVIIST RSASWVMSRVWDDGYPWDMMYV TRFASFLRNVLPSFISDWLYVQKMN TWFKHENYGLMPLNGSLRKEPVFN DELPRLCGTSLSIKPSVKEFTETSAV FEDGTMFEAIDSVIFATGYDYSYPFL DETIMKSRNNEVTLFKGIFPPLMEK PTLAVIGLVQSLGAAIPTADLQAW WAAKVFANSCTLPTTNEMMDDTD EKMGGKLLKCPYQFRLMGPWKWDG ARNAILTQWNRTVKPTRTRVVSEV QRPHFPYNLLKMLSFPLLLAVTLT FY*
3212	8709	A	3472	9	339	ITLSLSSFFNLRPSFALLAQAGVHW RDLDSLQPPPLRFK*FSYLKSP\RSW DYGHAPPRPANSVLLVETGSLHVSQ GGLILPTSGDPPASASQSAGITGVN CARPPSLFS
3213	8710	A	3473	1	50	
3214	8711	A	3474	1	1256	MAAAAAQGGGGGEPRTTEGVGPG VPGEVEMVKGQPFVGPRTYQLQY IGEGAYGMVSSAYDHVRKTRVAIK KISPFEHQTYCQRTLRENQILLRFRH ENVIGIRD\LRASLEAMRDVYVVQ DLMETDLCKLREKPSKLSNDHILLT FLLPDSLAPSSYIHASANVLHLRS* SPPTWLIQHHLADLKVCGFGLAGIC RSWRHDHTGFLTE\YVATRWWYRAP EIMLNSKGYTKSIDIWSVG\CILGE MLSTRAIFP\GKHYLDQLNHILGILG SPSQEDLNCIINMKARNYLQSLPSK TKVAWAKLFPKSDFKAL\DLLDRM L\TFNPNKRITVEEALAHPLYEQYY

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						DPTDEPVGEGSPSPFGMEL\DDLPEKRLKELIF\QETARFQPGSAGRPPSPRQTSLHPGGWTCPPARPLSRRDC
3215	8712	A	3475	877	1463	LPFTAWP*E/QLQQA\HAGLPQQA\KILFDGGSEIGKILPAFQSGNLSCQLH**IGQRAGRGGRLRIGRQGGFSFHQ*DGQQLIALH/QPGPERVAASGPRWFAPAGENPV*W\WFRNRQNPLIALRSLPAFQSGNLSCQLH**IGQRAGRGGRLRIGRQGGFSFHQ*DGQQLIALHRLALRELQQA\HAGLPQQA\KILFDGGSEIGKIPV*GLLRWPPLPRDVQWDSAPLLRARWGL*GER*PREVPAALQGE*PQALLPGGGEPGWQPAEPHPAGGVHRAGPPGGGCWARAGGHQKHLRPAAGVPPDRGCLLQLGQIPH*AGEQVQAGPGTGQPAGEQAQRGLSGNAGPHQVPAEGDTGHLCD
3216	8713	A	3476	29	1076	EQRDPQDIFSQRKSSAFPPSPEIILS GGKSLSLQLHTPSG/QQGETPRGGQSQH/PCQPGGGVPRYACAGGV PVTERGAQGWVHPALRRARYPDA GVQSHMKPAGDWGPGSNKPAGTD ADAVSGRR*LPKTLPSLGLGKKSPGVPGHPEYPE/HGGSEALLHEFLLPVSRLL\HGPLYPQMSNGTLHHYFVP DGDYEENDDPEKCQL/PLQGE*PQALLPGGGEPGWKPAEPHPAGGSSPCWAARWEDAGRVLGGHQKHLRPRRGRELWQVPAAGVPPDRGCLLQLGQIPH*AGEQVQAGPGTGQPAGEQAQRGLSGNAGPHQGAEGDTGHLGGAQGLIRAAGPHH
3217	8714	A	3477	3	591	ERNYLFFLRWSLTLSSRLRGQWRNLG*\MQPPPP\GFKA\FSCSLPSSWDYRRMPPCPANFCILVEIGFHCLAKLVLSNRPHDPPTSASQSAGITGVSHRAQT*KGIHLNELCTALAKEGRAWSGR*RAGAATPAP/PAPFTL*PGCIPESWSPMPPPHLPLTALCKATHAGTKHPHLTKTVSSCGAVLQPTPQRKD
3218	8715	A	3478	1	235	RDHPGQH/GETPSLRKIEILAGHGVRHL*SQLLGRLRQENCLNSGGRGCSEPRSCHPTLA\WAIEQGSVSRKEGHFRLA
3219	8716	A	3479	2	928	RPPRPGTERALPSRLRSRPRVRTETPSPSSSGPPPSRSNTGMAPLRR*RV*R GTVPRSG*KGR*PCSRRRRSVPSGRTPALRGTRAPSDQKGKARPPEPAPSRPCPGSRFCRASRSRTSPRPPTPARESGNPGRSP\DGGEKAAAQGS*KESAACSNRAWS*WAA\SPPWITVTRQKRRGTLDQPPNQEDKPGARTLKS EPKGQAKVPERGQEPVKQADFVRSKSFLITPVKPAVDRKQGA\KLNFKELQRGISLSHQNLAAQSA\MMMEKELHQLKRASYASTDQPSWME\ARKKSQA\WSDMPQIIK

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3220	8717	A	3480	1	435	EKINKIRWLPQQNAAHFLLGTNDK AIKLWKISERDKKAEGYNLKDEDG RLRDPFRITALRVPILKPMDLMVEA SPRRIFANAHTYHINSISVNSDHETP NIVDIKPANMEELTEVITAAEFHPH QCNV\FVYSSSKGTIRLCDMR
3221	8718	A	3481	204	397	VPILKPMGSYG*EASPR\IFANAHT YH\NS\SVNSDH\ETYLSADDLRNL WHLEITDRSFNIV
3222	8719	A	3482	1	1462	PLRSWLPRLPDSQADIISTVEFNYS DLLAT/GDKGGRVVIFQREQEVLAQ PRRPALP*SVSSFLSTSCREWQGC FSLPFRERIK/GRPHSRGEYNVYS/TA FQSHGTGGFDYLSLEIEEKINKIRW LPQQNAAHFLLSTNDKTIKLWKISE RDKRAEGYNLKDEDGRLRDPFRIT ALRVPILKPMDLMVEASPRRIFANA HTYHINSISVNSDH\ETYLSAR*PGGI NLWHLGNHR*EAFNIVDIKPANME ELTEVITAAEFHPHQC\NV\FVYSSS KGTIRLCDMR\SSALCDRHS/KSFFE EPEDPK/SSRSFFS\EISSISDVKF\SH SG\RYM\MTRGLPVRWKVWGPSTW EEAGPVGGPTRVHEYLARTKL\CSL YENDCIF\DKFECCWNG\SDSAIMT GSYNNFFRMFDRDTRRDVTL\EASR ESSKPRASLKPRKVCTGGKRRKDEI SVDSLDFN\KKILHTAWHPVGQCYL PWLATN\NLYIFQDKIN
3223	8720	A	3483	603	659	MCGFFFVFFFWRRSL/DSVTQAGVQ WRDLGSLQPLPPGFKRFSCLSLPSS WDYRRPPPCLANFLFLVEMGF/TTV LARLVSNS*PRDLPTSASPSAGITGV S*HASSRL
3224	8721	A	3484	84	202	
3225	8722	A	3485	3	577	ILGFPPFVRWGSHTVAQAGVQWCD HGSLOQRSPGVK*SSHL SLLGSWNH RHATTTPG*FCFFSRIRSHCVAQAGL *LLTSNHPPALASQT\VGITGVSHWT WPNTGFSVLTA TNKNLKFHYAISK CLVRAKLSSRLKIEERNKALSAPV VVSIFDRVLRLLLGYSASDWQPEFV ETAVSNFVIYGIFRGQ
3226	8723	A	3486	3	248	SLYIEIPGGALPEGSKDSFAVLLEFA EEQLRADHVFCFHKNFSLGFIEIV RPGHPLVPKRPDACFMAYTFERESS GEEEE
3227	8724	C	3487	185	340	MDNFCSSLCD FCHQNKNLRLVXXX XXXGGRFKGPLEGPKFTRACNELV FSL*
3228	8725	A	3488	1	546	NDRLN*TRELTSHERRRFRPSSRLT DAQ\RNWRQVLSAGS\LYIEIPGRR AAEGGARN SFAVLLEFAEG\QLRAD HVL\ICFHKNREGQKPLLRTFSFFG LED FEDRGNPLVPKETPDACFHGLT TFERE\SSG\EEEEVGARLRGLGQFP RPGAHP\LVKPGWGKEPVDSPHLAL GLSPML

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3229	8726	A	3489	1	526	FFFLERDPCSVTQAGMQWHDLGSL QPPPPGFKWFSCLSPSSWDYRCPPP HPANFCIFSRD/MGFTILARLVNS*P HDPPTSASQSAGTTGVSHSAWPVC/ LFEIEFHSVAQAGVQWRDLGSLQP LPPEFK*FSCSLSPSSRDHRHLPSLPA KFHIFSRDRVSPCWPGWS*TPDLR
3230	8727	A	3490	276	735	FFFFFFLRQSFSLVSQAGVQWHNLG SLQPPPPGFRQFSCSLSPSSWDYRHP PPCANFCIFNRELIIVYLIKTF/THV GQAGLELLTSGDPPALASQSAGIPG MSHCAQSTH*FLLAQQLFCSIYPSFH AQGVIPRIVTHKRETGSQTLYSIV
3231	8728	A	3491	2	344	FIFIF/NFLRWSL/DSVAQAGAQRD LGSLQGPPTGTPVSCSLSPSSWDY RCLPPRPANFFAFLVETGFTVLARM VSIS*PRDPPASAYQSAGITGVTTAP GLLF*INICLAIFYFV
3232	8729	A	3492	109	559	QFLHRLVHDSGEVWMKLVE**NTL LAKMVSISWPRDLPASASQSAGITG LIGALVLSVGIYAEVER/HEI*NP*KC LPGSSHHPPGRRHVHGLLHWCA GVPP*QPGKH
3233	8730	A	3493	1	593	ETESRSIVQAGVQGRELGSLQTLPP GFTPFSCPSLSDYRHPQHSAFL AFLVETGFTVLARIVSIS*PHDPPAS ASQSAGITGVSHHARPQTGRFLLFL FFFETESCSVTQIGVCSGHDLGSL QLRPPGITPFSCSLSPSSWDYRRPRL RPANFFFFVFFSRDGVSLC*PGWSRS PDLVICPPRPPKVLGLQA
3234	8731	A	3494	3	484	RFFFFFFLRRSFT/SVAQAGV*WHDL GSLQPPPPWFR*YLCLGPLNSWDYR RGPPRLVNLCIF/M*R*SFTVLARLV SNSWPQ/CDLPP/SASQGAGNTGVS HCARPDEIFYQC*Y*ETEMVRRST TQDRAGSTTVLKLGLQRPEREIVN LALGALVYRNITPN
3235	8732	A	3495	104	288	GEVICGRRRSEVSRCNLVDLEPKGP WGHWQGG*GDRRAGGTP*GE/GHL RKKAI*GLQVQPGRPRTEGPLGA/PG KGD*TPTEGPRGDARNCDACPRPR ARPVLVW
3236	8733	A	3496	3	641	RPPFFFFFFFRRSL/NSVTQAR LQWHYLGSLQAPPPGFTLFSCLSLP SSWDHRRPP/RMPG*LFFAFLVETGF QRVSQGWVSIS*PQ/CDPPASGLSKC WGLQGVSHLRPSHLSFLAFSFFSFET GSFSAQAGLQWANHSSLQAPSP GFTPFCHSLPSSWDCRHPPRPANF /CCIFSRDGVSPC*SGWSRSPVLVIRP PRPPTVLGSQG
3237	8734	A	3497	1	296	VSRRFKQSIPP*AS*GWDHRCVPP/S LANFFFLLEMGFMPRLVLNSWA QVILPSQPSQSAVITGMSHCACLYW LLKTKQIKIKQTGMSKVIKLFPL
3238	8735	A	3498	1	347	KKTGRRKRNMIDYEKKKNKEQEER

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						RKKRKKRKSSSSSSSPEEKKEEKKK KREEEENRKKEEEEE*DK/KEED RRKHESRRRLRAVGDEVINKVCQE LKRTIPVGRDYRPLDPSS
3239	8736	A	3499	2	286	PQPCSLAPNPPRMPPGSF/TPCSPPPR SNITL*KQRPPSPPPSPEPPRIAQQRV AQNLTSPRPAAAKPPGWLSTNLSK ALPETPTVAQSPVLFTHF
3240	8737	A	3500	3	954	RPRAGAAGGGGGGSRPSGAHPSRS AC/GCPAGTRPGRAPPAASARPSRS KRGGEERVLEKEEEEDDR*R*R*RR SMCQRRSEVAPSSDRPGRCAPPSP TASGDLRVPRGRSGPPGTAPGPG *RAGASPGQRHPPGCSPWQP*TRKG EQVFFSPASVATGPDSPSPVPLPPG KPALPGADGTPFGCPPGRKEKPFDP RSSWNVMGFRSNILLEA*FPEQATA FPRAGN*WQIFAAHAAHRCASPACP S\PRASPENLRAPHQGASARPL*GM MDPDGFL/ALSAQHPCKPIAPISP KIPQSPGSWTGDTLSPH
3241	8738	C	3501	68	199	MPIIPALWEAQAGGLLRPGVCDQPG QYSKTSSLINKLKNPPSL*
3242	8739	A	3502	11	520	IRVDDFVAHRSRCCVAFSSFTPRSR RRPKRRRRRRRENDPAASSLPAPHL CSVSQSAAGARLVLRPRACGAQAQ RP*LASGLRTSALRRRGHPRAELRS GPQRRQASE/PSPRGVAGARWRRR EDG/RPSKRSRMAQREAAQRTSPQR GNRPKTSEKCPPEEKAVCRTPG
3243	8740	A	3504	78	595	NQNRLKEAGWRLKLADETSSSSHQ QVCGTHHVSACYS\GSPYS*KHPD SPSPATSRKQNLSTQSCISPMWPCSQ RSICQFGHGGTESGQGILLGLLRKAI GSPGKRSAPVQPNWEGGNG*EAAW ASSSSPCKVTAPLAPSELFPSKFL RNKKAQRKISHLLEVTVGHLLC
3244	8741	A	3505	2	267	ADLSAEAL*TRREWDDIFKVLKTSS/ LGQPKILYPSKLSLINEASSSSSSSS SS/REFTTRLVL*EMLKGILHMEAQ QYLPS*KHTKV
3245	8742	A	3506	1	323	IAGEVNTPRSVTDRSS*Q/IIQEGIVQ LNSAIH/QTGCTNINRILPLTTAEYTF FSLYRTFT/KIAHILGHMTHLNKG KRIEIIQSMLSDHNGIQEISNRKIAG KSPNT
3246	8743	A	3507	3	814	SSGLAGTPFPSEGAVCRSQPG*GSG \SPPLVPACWYLP CGP*DQRCPPG SLGPSAEPGS*NLSCGRPMCSPAGT SCPAPV/PDSVTPVLRARGTACLPSP TFPAWSVPRFQPGAAPSSADLVHFFH AASGPSASLSSSLSTKAPSLPLGACL PAGGVT*LFGPPSG/RLWRPP*GLTG GGLVWAAGVHWACLWPGQASGG SIRHVCVAVGVQGAPAQKEGGAGL GKGLGSFACGRPHLPAYFACGRPH LPPAYFVLDLPFAKVLNRINI

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3247	8744	C	3508	112	252	MFRSMYNXXXXXXXXXXXXXXXXX XXXXLGMSEXXXXXXXXXXXXXX LGF*
3248	8745	A	3509	448	715	FFIISIKIIEFFFFETESCSSVTQTRVQ WFDLGS\LQPPPGFKQFSCLSLSIS WHYTHVPPHLANYRIFSRDGV*PC WPGWSQTHDLE
3249	8746	A	3510	55	295	SQYAYTKEMESIVNNLPKKKTPGL HSFTGEFYQTFKNEMIL/YIL*FLPEI* SRG/IYPSSSSSSSL*LPKLDKDIIRK EN
3250	8747	A	3511	2	853	DLMCKKMKHLWFLLLVAAPRCV LSQLSSSSSSSSSSSSSSSSSSSS DSVRHNSYYWGVRQPSGKELEW IGSLYFTGTTTHYSPSLKSRVTISAD SENQFSLTLTSVTAADTAVYYC ARNIVGSSSSSSSSSSSSSSSPSTKGPS GFPLAPSSKSTSGGTAALGCLVKDY FPEPVTV\SWNSGALTSGVHTFPA/V LQSSGLYSLSSVGTVP\SSSFGHPRT Y\NCGKSQSPATTKVDKGELSPK\N CDKNSTHAPPGPQHLETPWGGPVS LFFFPKKT
3251	8748	A	3512	3	2310	QLLTMDWTWNILFLVAAATGAHSQ VQLVQSGAEVKKPGASVKVSKAS GYTFTNNGLAWVRQAPGGLEWM GWTIASNGKTNYAQKFQGRVTMTT DTSTNTAYMELRSLRSDDTAVYYC AREKDNYATGAWFAYWGQGLVT VSSGES*AWYPGIQCISMLEL*ISAF WGRPGLTLAGGREGAKVTQVAPA RCTPNAHEPRHWTLHGPRIDKNR GASAPWAQLCPTPRSHGTTSLAAS T KGPSVFPLAPCSRSTSESTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVTVPSSSLGK TYTCNVDPKPSNTKVDKR/VW*EA STGREGVCWKPGSALLPGRTPAVQ PQPRAARHAPS VSSPGGL*PPHSCSG RGSSGFFHQAPGRHRLDAPTPGPAH KGAGAGLRPAKSHIREDPAPDLSPP QRPNSPLPQLGHLSSQIPVTPNLLS AEPKSCDKTHTCPPCPGKPAQASPS SSRRDRCPRVACIQGQAPAGC*HVVH LHLFL\APELLGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGGRGV RGPHGQRPAPRLCPESDRCTNLCP YR\QPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFFLYSRLTVD KSRWQEGNVFSCSVMEALHNHY TQKSLSLSLGK
3252	8749	A	3513	1	1677	AEVQLVESGGGLVQPGGSLRLS CA ASGFSFSKAYMNWVRQAPGKGLE WVGRIKTKKDAGTTDYAAPVKGRF

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						TISRDN SKNTLYLQLNSLRAEDTAV YYCAKDEFSSSTRKNFLTGQSKTFAA YYGMDVWGGGTLTVTVSSASTKGPS VFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVL QYSGLYSLSSVTVPSSSLGTQITYT CNVNHKPSNTKV DKTVELKTPLGD TTHTCPPCPTP*LALGGPSVFLFPPKP KDTLMISRTPR\VTVCVVVDVDPKRT PEGQVPTWYV\VDGLAEVHKCQDKSR GKEQYNSY\YRVV\SVLTVV\HQDW \LNGK\EYK\CRVSHKSPQAPIETH LPKPKGSPQNPQVYTLPPSRDELTK N\QVSLTCLVKGFYP\SDIAVELESN GQPGNNFK\TTPPVLDSDGSFFLYSK LTVD\KSRWQQG\NVF\SCSVMEVA LHNPYTQKSLSLSPGKMIPTADKPP LPGSLAGRTKDAWHGTPVYILPRAP KHGNKAPTWPWAKKKKKKKKKK KGGRSRVSLGPKLRTQLS
3253	8750	A	3514	1	164	TRVNENQIESKAA YALFYKRQDVA RRLSPAGS/SGAPASPACSSPPSSEF MDVN
3254	8751	A	3515	1	712	EILIIHLKRFSYTKFSREKLDTLVEFP IRSGARERMAGGRQGKEGVYQY*P SPHPQ\DLDFSEFVIQPNESNPELY KYDLIAVSNHYGGMRDGHCMCQA VGGACPGGSGQGQDQDLPE*LGM *ASGEGSSVVGRK*TRSEIWTLSEEA RKGRRG*LSFPFR\TTFACNKDSGQ WHYFDDNSVSPVNENQIESKAA YV LFYQRQDVARRLLSPAGSSGAPASP ACSSPPSSEFMDVN
3255	8752	A	3516	3	3090	IPLLQLLRLRRLWRRHGRWTEPREPQ HEELPGLDSQWRQIENGESGRERPL RAGESWFLVEKHWWYKQWEAYVQG GDQDSSTFPGCINNATL FQDEINWR LKEGLVEGEDYVLLPARAWHYLVS WYGLEHGGPPIERKVIELPNIQKVE VYPVELLLVRHNDLGKSHTVQFSH TDSIGLVLR TARERFLVEPQEDTRL WAKNSEGSLDRLYDTHITVLDAAL ETGQLIIMETRKKDGTWPSAQLHV MNNNMSEDEDFKGQPGICGLTNL GNTCFMNSALQCLSNVPQLTEYFL NNCYLEELNFRNPLGMKGIEAEAY ADLVKQAWSGHRSIVPHVFKNKV GHFASQFLGYQQHDSQELLSFLLDG LHEDLNRVKKKEYVELCDAAGRPD QEVAQEA WQNHKRRNDSVIVDTFH GLFKSTLVCPDCGNVSVTFDPFCYL SVPLPISHKRVLVFFIPMDPRRKPE QHRLVVPKKGKISDLCVALS KHTGI SPERMMVADVFSHRFYKLYQLEEP LSSILDRDDIFVYEVSGRIEAIEGSRE DIVVPVYLRERTPARDYNNSYYGL MLFGHPLLVS VPRDRFTWEGLYNV LMYRLSRVYVTKPNSDDEDDGDEKE

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						DDEEDKDDVPGPSTGGSLRDPEPEQ AGPSSGVNTRCPFLLDNCLGTSQWP PRRRRKQLVQLQTVNSNGHNRLH HSPCTKSNAKPVHCYSTWKPEMK KIRYYDE*EGEGLREGNAFRRGYV* RKAPVRLQECIELFTTVEPPFPFGGK\ EREKPW\YCP\SCQHQHQLATKKLD LWMLPEILIIHLKTFFPYTQVLPEKK LEHPSWKFPYPGTLD\FS*/EFVIAH QNEVEIRELYK\YDLIAVSNH\YGG MRDGTLTQHLACNKDSGQWHLILI DNSVFPLFN*GIQIRVPRAAYVL\FY QRQ/DTLARRLLSPCRAHLAPSVLP CLHAPSPQLVSSCDVILRALGPAPPE KKKKKALSALSLLVSAPLLLFLVGA PARHCRLSRGYCSPVPLNRSPLPGKN RSCLLAVRAPPCVCPSSSDPPF
3256	8753	A	3518	1	271	PLPPGFK*FSYLRLPSSWDYRCPPPH PTNF*FLVAMWFCHVGQAGFELLT SGDPPTSASQSAGITGVSHRSRPIVD FLNYLLRKSYPFT
3257	8754	A	3519	3	633	FFFI*DRVSLIAQAGVQWRNCGSLQ PPPTGFKQFSCLSLWRSWHYRCRH HAQLIFVFLVKTGF\TMSVKADLEL LTSGDPTASASQSAGITGVNHQCPA SKQF*FHCKSW/CLF*MQSL\SF\FLG GGQSR\SVGQAGVQWHDLSLQPLS PGLKQFSSLSLPSSWDYRGVPLRLA NFCIFSRDGVSLCWP\GWS*TPDLKA NPTRLGLPKGWGL
3258	8755	A	3520	2	430	CLKNMVGAGEVDEDLEVETKEECE KYGKVGKCVIFEIPGAPDDEAVRIF LEFERVESAIKG*WYS*ILKNKKVEF TALIFTSKAYCLIKVKPLSYRIPALF CLLFAFQRLTLN\GRYFGGR\VVKA CFYNLDKFRVLDLAEQV
3259	8756	A	3521	3	1076	HEERQRQRELERQKEIEEREK\RRK DRHEASGFARRPD\PD\DEDEDYER\ ERRKRS\MGGAIA\PTSLVEKDKE PRDFPYEEDSRPRSQSSKAAIPPPVY VEQDRP\RSPT\GP\SNSFLANMGGT VAHKIMQK\YGLPGGPRVLGKHEQ GLSTALSVEKT\NKRGGKIIVGDATE KDASKKSDSNPLTEILKCP\TKVLL RNMVGAGEVDEDLEVETREECEK\ YGKVGKCV\FEIPGCPLMMEASTG YFLEI*EELNSAIKAVVALN\GRYFW CTGW*KAMFLQIWAKFRVLDLARN QVWIFKEPRARVISGDPLNELQAVE KKEKGPQPPWLFAYPRLLEGLLRY MLIDPFFYFVVF
3260	8757	A	3522	1381	1787	LEYVAHPLHQLLILNNFYSLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCLSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
3261	8758	A	3523	1147	1553	LEYVAHPLHQLLILNNFYSLNEKY

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						LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH
3262	8759	A	3524	1456	1862	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH
3263	8760	A	3525	889	1295	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH
3264	8761	A	3526	743	1149	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH
3265	8762	A	3527	2583	3580	DRVSLLLPRLECNGAILAHCNLCLS GSSDSPASASQVTGITGKCHHTQLIF VFLVEMGFHHIAQAGLELLTSDSPT LASQSAGITGVNHHAWLFFFC/SD TVSLCYPGWSRVA*SRITATSA/PGL K*FACFSLPSSRDYRHVPPHPGNFCI FGRDEVSPCWPGWF*TPDLRYPPA SASQSAEIIIVSHHTWPQEVFLFLNL FIYLRWSL/DSVAQARVQRRDLGSL QAPPPRFKPFSCSLPSSWDYRRPPP HPANFFVFLVETGFTVLARRVLIS* PRDLPASASQSAGITGVSHHTR/LIF/ NFFETGTHSVTWAAVQWYTI/GSLQ PRTPELK*SSHLILTSNWDYRCTPPC PPNLFYFLFYFHRDEGSLCCPGWS* TPELK
3266	8763	A	3528	1966	2372	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH
3267	8764	A	3529	10304	11097	FAFSPK*HSCLRPCI*FSSGLLHEVL *LLPLCWP*THGWDPGSREANKSPK LHAIRCVWVLEENLWLSSNSQSLQ TVKN*ESHIN*SCRSNLI/HH*FWNQ VK*K*LLNISGNCFEFLRWSL/DSVA QAGVYWRDLGSLQPPPGFKRFSCL SLPSSWDYWHLPCLAKFCIFSRDG/ GFTIWARLVLS*SCDLPASGSQSA GITGVSHHTWLQVTFYFLKEMRSCY FSQVGWPTPLKQCSHLKLLSSW DYRHMSPHLAISGS
3268	8765	A	3530	87	411	ARLVQNTVAQLKEVQYKLFQGLF FE*/QSHSVAQAGYSAVIIAHCNLSL

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						LGSSDPFFSAS*VAGTTGMCQHA W LIFDR*WR*GLAMLPRLEM*IFLISH LRLIWSAWS
3269	8766	A	3531	31	403	THLNGLQIRGSPLFFF/FELESSVA\ RLQCSGVISSHCNLRPGSSNSPASA S*IAGITGAHHNPG*FF\VFSSRGRFH HVGQAGLELLTSSDPPRPSTLPQSG WGFTRHGAIA PQWGQVPFHRS
3270	8767	A	3532	7	1047	
3271	8768	A	3533	3	53	
3272	8769	A	3534	7	960	
3273	8770	A	3535	1538	2287	WWSSSKLRLIYYYSLFFFFFFFFFG M*SYSVTQARVQWHHLGSLQPLPP GFKQFSCSLPSSWDYRHPPLANF LYF**RWGFTMLARLISNS*PQ/CDL PASASQSAGTTGLSHCAQ/LLFAFLT DNSVLIETALT*LQSCAS*KLN*IPL ESSDFYTFEFETESHVS/TQAGVQCR NLGSLQPPPPRFKQFSCSLPSSWDY KCTLPRPANFCIFTRQGFTMLARIVS PGSLGLMISLPRPPKVLGLQV
3274	8771	A	3536	3	263	LGVGDRVSLCHPVWSASSL*SQTPG LK*SSHLSLPSRWDNRHAPPCLA/SL KNFCRDRGLTMLPRLVSNWSAQAI LPPQLPEVLGLQV
3275	8772	A	3537	33	295	AGMQWCSLGSLQPPPPVLRSSHLS LPSSWEYSHTCNFCIFCRDGFVLP RLLG*SNRPASS*NTGITGVSHRAQ PSLFLSYSFFF
3276	8773	A	3538	3	33	
3277	8774	A	3539	1	375	
3278	8775	A	3540	3	340	HEVVAA*YY\G*PSIAQEVAGTLAE LDVTLQLEDKFLQNKVFLTGPDIS LADLVAITELMHPAGAGCHVF*GLP TLATWRQLVEASPGEDLFQEVHEVI LKATDFPPADHTI
3279	8776	A	3541	30	284	YSVSTPLRDSPPNHLSSLGHCPASS QTEPQAPQALGQPATKLLPHPPPP /MPQPSSKP*VSATSLCTSPPLPLCP AGGSSGTT
3280	8777	C	3542	127	435	MAASXNPEVLDITEETLHSRFLEGV RNVASVCLQIGYPTXASVPHSIINGY KRVLALSVDYTFPLAEKVKAFLA DPSAFVAAAXLGCCHHSCSXCCCSP S*
3281	8778	A	3543	3	417	
3282	8779	A	3544	2	881	RGKLCAYGRPPMMRRSIEGN/LENN PASEELLPH*RGHLGFCFTRED\LT E\RDMLLA\NKVPTAARCWCQLPP CEVTVP\A\QNTGLG\PEKTSFFPGL* VSPTKNLPGGTH*KS*SYVQLIKTG DKMGSQTKAKAAEKMLKNLPPSPF GAGQPKQGV\RKNGKHPTNPESA*I STRGKLCHSRFLGGCPANVAKCLS CKIGYP\TVASSTPII\NGYKRVPGP CLWTPDYTFPLAEKVKAFLADPSC LCVLLPPVGAATTACFALLQPPA

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						KVEAKEESESEDEDMGFG\LF
3283	8780	A	3545	2	311	DGVSLLLSPRLQWHNLGLLQPPPP* FKGFSCSLPGSWDYRHV/PPCLAN FVFLVETGFRHVGQTGLELLTSGDP PASASQRAGITGVSHRTWQKMYFL SQKYF
3284	8781	A	3546	1	290	KTFFFF*DRVLFCCPG*SAVAQSW LTAALTSWAQGSS*DHRLKP/HMLS FFYFCRQGLTMLPKVVLNSWAQAI LPPQPPM*PGLQACTYAWSLRAL
3285	8782	A	3547	229	486	IKIKINQAWVCACLSLPSSWDYRHG PPHPANFVFFLVETGF\TMRARLA SNS*PCDPPTSASQSAGITGVSHRAG CSEAFRSQV
3286	8783	A	3548	2	431	ARGSIYQNDTTI*NMVLDNRASECT VREL VKQK/R*MEKPTIIFGDFNNPV SLIEGSSK*KISGTMENLKNANFT* LIFIKCSAQHQNAHSFPV/PHRTF/S KIDHFLWCKRGLNCKMKIQI\QNVV CDHTALNKKPMPERSLEK
3287	8784	A	3549	2	194	VDFFFFFLRWSI/NSVTQAGVQWRN LGSLQALPLGFMPFSCSLSPSSWDY RCPPPAHPANFFLHF**RRGFTVLAR MVSIS*SHDPPASDSQSAGITGLSHR AR/LKGHYDF*EMAC/HCLICKRGRQ VP*LFFFFFEMEYHSVTQAGVQWR NLGSLQALPLGFMPFSCSLSPSSWD YRCPPPAHPANFFLHF
3288	8785	A	3550	2	489	ARGTQALMMMT/GTACHASPH*GG RLTS*PGAICFTHGDMAA*WREESC LLVT/WDLVMSEGLGMRYAFIGPLE TMHLNAEGML\SYCDRYSEGIKHV VQTFGPIPEFSRA\TAEKVNQDMCM KVP**PGSTLAAR\RHWRDE\CLM\R LAQV*RSSSCSPQLNFLC
3289	8786	B	3551	13	441	MEGVEEKKKEVPAVPETLKKKRRN FAELKIKRLRKKAQKMLRKARRK LIYEKAKHYHKEYRQMYRTEIRMA RMARKAGNFYVPAEPKLA\FVIRXR GINGVSPKVRKVLQLLRLRQIFNGT FVKLNKASINMLRDCRAIYCMG*
3290	8787	A	3552	1	775	RRVPA\VPETLKKKRRNFAELKIKR LARKKFAQQMLARKAR\RKLIYEKAK HYHKEYRQMYRT*NFEWARMGK KKLANFYVPAEPQIWR\FVIRGIN GVSPKGSERFFQLRLRQ\FNGNLL *KLNQGFRFNMAEDF*SPYIAMGGT PNLKVSKMN*SYKRWLWAKSNKK R\IAL\TDNAL\IARSLGKIRHILawe DLIHEIYTV\GKRFK\EANNFLWP\FK LSFSTKVEMKKKTTHFVEGGDAGN RIEDQINRLIRRMN
3291	8788	A	3553	1	356	SHHVQLLEFFVEMGSPCVSQA\VL* LLGSDPPVLAENVGIK/GPPHPA* S*F*IIACVFVYIYFLEMGSCSFAQA GVLWYNHSSLQR*TPGL*QISLLSPL SSWDYRHVPPCLVIYF

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3292	8789	A	3554	3	352	HEGFTMLVRLVSNS*HRDPQASASQ SAGITGVSHHANP/CFFLTESNWVA QAGVQWRVLS*LQPPA*FKGFSC SILSSLS/WGYRCLPP/HPANFFFF*K GFFWFPSWNAMGKKWFN
3293	8790	C	3555	55	201	MPKNYPRLWWQHVCNPQPTWEAE VGELLEPQAEVAVSQDHATALQP G*
3294	8791	A	3556	3	212	QEFFFFFEM*SRCVTRLEGSGAISA HCKLCLPGSCHSPASASQDSIFNTQ HLNVGRNSTSKSKPIDYF
3295	8792	A	3557	2	265	EKESRSVTRLECRGAISAH*NLHLP GSSHSPPSASHVAGTTGACTT/AQLI FFVFLVETGIIHVGQDGLNHL/NLVI RLPQPPKVLGLQA
3296	8793	A	3558	354	675	HFISYFPDGAELTSSIRVPFFYSNVLF FF/CRQESRCHQAGVQWHDGLSLQP PPPGFKRFSCLSL*SS*DYRQAPPRP ANFCIFNRGPVSPCWPGWSQSPDFV LVPNS
3297	8794	A	3559	1	1203	
3298	8795	A	3560	2	634	VNTEKLTAFVNTLNGKNGTGSHLV TVPPGPS*ADALISSPILAGESGAML GLGASDFEFGVDPSADPELALALRV SMEYQRQRQEEYARRAAAASAAE AGIATTGTEGERDSDDALLKMTISQ QE\FGRT\GLPDL\SSMTEEEQIAYA MQMSLQGA\EFGQAESADIDASSA MDTS*PAKEEDDYDVMQDPEFLQS VLENLPGVDPNNEAI
3299	8796	A	3561	506	930	IRTTQIGLCLSQVYFVFDLHAQYEH KATNITTPTLSKIIIRPRRFIFPVT*L LNMFAFSSPMVPVLSQRIGTI*FLF RFFNT*IFSDGLTNRLTCSRANCKV NPVIGSISKYVLCSSSFNFPSIGSET SGLAYRK
3300	8797	A	3563	3	271	FFLET*SCSVGRLECSGVILAHCKL RFPGSSDSPASAGVVGTTGAHHHT RLFCIFSRDGFHHVGQDGLDLL/NL VIHPPWPPKVLRLQA
3301	8798	A	3564	1	218	ETGSPSVTRLECSSIQAHCNLDLP GSSDPPVSAPOVAGTTGTCHNTQLI FVFFVEMGFCHLSQAVLQLLG*TIH PLWPPKVLGL*AQVILLSQTPQVAG TTGTCHNTQLIFVFFVEMGFCHLSQ AVLQLLG
3302	8799	A	3565	1	294	ASTFFFFFFGDRVSLFLPRLEYNGAIS AHRNLC/LPGFSSDSPASAS*VAQD YRHAPPHLANFVFLVETGFLHVGQ AGLKLPELSVIHPPWPPKVLGLQA
3303	8800	A	3566	3	292	FFETKFSSVTQAGVQWHNLGSLQPP PPAFKRFSCLSLPSSWDYRHLPPRPA NF*FLVEMGFHHVDHADLELPTSS DPPTLASQSAGIIGVSHRARP
3304	8801	A	3567	3	389	
3305	8802	A	3568	1	672	
3306	8803	A	3569	1	2018	MSDNGVRTGAPSTDQRTGMSVRAE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						WRRGEFLVTGRRPLVGGGAGEEGE LGGDARSSRDPELQSYAAFVAVVT RIWLPAPRPCALGGLASGPGKAEQF SRSLYLPDHLGEGNGLLGKSLEPY RSACMSAAGLKITGSKETKRLLLLI SIDWSRDLMNLCIYFRVYCQEKQEE RRELPRITGPPPEAAVVAFEWLKTS TLTGLHPQLPLSLPQPECALPYLVR AFSRGDYMGRIQEVGWVVTAGLVIW AGTCYYIYKFTKGRAQSVRTLARN GSTVKMETVVGVSQTLAINEAEIK TKPQVEIGAETGARS GPRAEVETKA TAIAIHRANSQAKAMVGAEPETQSE SKVVAGTLVMTEAVTLTEVKAKAR EVAMKEAVTQDAEAGKIVKKEAV TQTKAKAWALVAKTEAKREAMTQ TKAETHILAEKETEINRVMVTQSET LAVPREVAKMGATNKTGIVDETKT RALEETVSVAKTQSEARPGATVDA RGPNPNGMSREVAGVDMKSCAQSQ AVTKIQGDDMPGTGVEDMGNCKT MSRAESGADTRASAQPQIFAKTQTE AIPGAKIDAGGNTNAMCKVAGAD VRACIQPQTVAKKQAEVTSGARVD GRGNTNVISKAITGADMRAAAQPQ AVASTHAEAMSDAKVKNRGNPNA MTKAGAKANLRANSQVEALPDAR DKSRGNPNVMAKVGDTMLSCT QPQLVASVQADTLSDGKIKVRGNV NTMPKEGAGVDMKAQGMAQSQGE ALPNTRGKARGKAKAKCKTGPGM DMKTCTQPQAGVKTPAEALLDSRV DGRGNPNATSKAGTKADQRCGQP LVVANPQGEALPGAKNKVKGNPHT VLKVGAGEGTTDSAQPEAVVSFQG EALLGTKNKVKGNPNVVLKAEVGE GAMGTAQLQIMASSKGEALLDSKN KVKGNSNAVSKAGAGTDTTGSVQP QIVANSQGEVLPGAKNKIRGNPTTV PNSGVGPYTTDSARLQAVANSQGE VLPGAKNKVKANLNAVSKAEAGM GATGSVQPQAVANSHCETLPGAKN KVRGNWNAVSKAGAGMDTRGSAQ PQAVANSQGEVLPGAKNKVKGNPN VVS KAGAREDTVGSTQPQVLASSQ RETLPGARNKVKGNSNVVSKAGAR EDTMGSAQPQVVANSQRETLPGAR NKVKGNSNAISKA EAGAGIMGSVQ VQVVASFQGEVLPGAKNKVRGNSN AVPKAEAGADTVGSAQPQAVANSQ SETLLGARNKVKGN TIAVPKAGTG AGTRHSAQPQIVAGSQGETLPGARD KSMSTSEAEATAEDEAYAKPEAEA MPTSEEGSGTQACRKTPQNIHDY YWNGIGVEDWIAAERWIKFRFQTM DGDWENS VSWADDENEASIGSWSG ASDKAGIIRSWAVACDETSVKSWA GARAENVVGIGTWARAGEQASGGL

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						WAGGQTSEGTWAGDKASGGAWT GAENQASGGSWALAGNQAIGELW AAGQASDGSWPGGQASGVSWVGE EAIGGSWTGAENQASEGSWAGAGA GNMSSVSYWAGVVDQAGGGSWA GTSDQSGGGSKPRFEDQASGEGSW AGAGGQASGGSM LGPEDQSSGRSW ADTADQASGG SRLGHVDQSSGGA WAGTLDQSGGGSKPRFENQTTEEG SWAGAGGQAGGGSKVGPEDQSSG RSWANS GDQISGGFLVGIVDQANG GSWTGAGHPASVGP KPIFEDQVSGR GSWADAREQVVGDSRLGLRDQSSG DSWAGTGDQASGWFCVCPGSQTN GGSWGGASGQDVGGSRPGPTNQSS AGSWDSPGSQVSGSCWTGAGAVD QAGGCSKPGFEDQAIGGGFWPGAG DQTGGGSRPGSEDQSSGIGSWGVA GGQVLGGARPGPADQSSGGSWAGT GNQSSGRSWIGPGDQAVDCSKPEFE DQACGGGSWAGAGSQASGESWAG SRPGNEAIGGSRMGSEDQATGGSW ARSEDQASGRFQVSFEVEANEGFW FGPGA EAVIGSWCWTEEKADIVSRP DDKDEATTASRSGAGEEAGVESWTLAR AENKAKSRLGAGEEAGVESWTLAR NVGEDELSRESSPDIEEISLRLFWA ESENSNTFRSKSGK DASFESGAGDN TSIKDKFEAAGGVDIGSWFCAGNEN TSEDKSAPKAKAKKSSESRIYPYM VPGAGMGSWD GAMIWSETKFAHQ SEASFPVEDES RKQTRTGEKTRPWS CRCKHEANMDPRDLEKLCMIEMT EDPSVHEIANNALYNSADYSYSHEV VRNVGGISVIESLLNNPYPSVRQKA LNALNNISVAAENHRKV KTYLNQV CEDTVTYPLNSNVQLAGLRLIRHLT ITSEYQHMTNYISEFLRLLT VGSGE TKDHVLG*EQRQSQCHD*SRGQ GK LEGQFPG
3307	8804	A	3570	1	611	YAALGADVTRVSLPTPRCPALGAL ASGPGESGPTLLQDCGAKCPG/GPQ PRGENREKEETTRIGPGVMESKEKR AVNSLSMENANQENEEKEQVANK GEPLALPLDAGEYCVPRGKS*GGSA FRAAHP EYRWDM MHRPW RTHRP DEEK RIMEKD WGGGETADGKKLE GEKPVGVISLRGESGTDPPSPMTHH D*VFALLPLNP
3308	8805	A	3571	1	379	EMESHSVTRLECS/GTILVHCNLC LGSSDSPASAFQVAGITGVHYNA*V IFVFLVETGFCYVGQAGLEFLTSTD PPASGFQNCWNYRDEKPHPAETVS KTTTTKNYICVSTINYKKKNLGLSNI L
3309	8806	A	3572	6	222	DRVSRSA AQAGV/QWC/NLSSLQPL PPRFK*FSCLSLPSTWDYRHTPPRPA NFCIFSRDRVSPCWAGWSQSLDLK

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3310	8807	A	3573	1	445	
3311	8808	A	3574	1	3212	DSINNLAELNKFALRKQLEQDVL SYQNLKRTLEEQISEIRREEESFSL YSDQTSYLSICLENNRFQVEHFSQ EELKKKVSDLIQLVKELYTDNQHL KKTIFDLSCMGFQNGFPDRLASTE QTEIMKDLKGGCKNGYL RHTESKI SDCDGAHAPGCLEEGAFINLLAPLF NEKATLLLESRPDLLKVRELLGQ LFLTEQEVSGEHLDGKTEKTPKQKG ELVHFVQTNFSKPHDELKLSCEAQ LVKAGEVPKVGLKDASVQTVATEG DLLRFKHEATREAWEEKPINTALSA EHRPENLHGVPGWQAALLSLPGITN REAKKSRLPILIKPSRSLGNMYRLPA TQEVVTQLQSQILELQGELKEFKTC NKQLHQKLILAEAVMEGRPTDKT LLNAQPPVGAAYQDSPGEQKGIKT SSVWRDKEMDSQQRSYEIDSEICP PDDLASLPCKENPEDVLSPTSVAT YLSSKSQPSAKVSVMGTDQSESINT SNETEYLKQKIHDLETELEGYQNFIF QLQKHSQCSEAITVLCGTEGAQDG LSKPKNNGSDGEEMTFSSLHQVRYV KHVKILGLAPEMIDSRVLENLKQQ LEEQEYKLQKEQNLNMQLFSEIHNL QNKFRDLSPPRYDSLVSQARELSL QRQQIKDGHGICVISRQHMNTMIKA FEELLQASDV DYCVAEGFQEQLNQ CAELLEKLEKLFLNGKSVGVEMNT QNELMERIEEDNLTYQHLLPESPEPS ASHALSDYETSEKSFSDQKQDNE TEKTSVMVNSFSQDLLMEHIQEIRT LRKRLEESIKTNEKLRKQLERQGSE FVQGSTSIFASGSELHSSLTSEIHFLR KONQALNAMLIGSRDKQKENDKL RESLSRKTVSLEHLQREYASVKEEN ERLQKECSEKERHNQQLIQEVRC GQELSRVQEELKLRQQLSQNDKL LQSLRVELKAYEKLDEEHRLREAS GEGWKGD PFRDLHSLLEIQLR LQLERSIETSSTLQSRLEQLARGA EKAQEGALTLAVQAVSIPEVPLQPD KHDGDKYPMESDNSFDLFDSSQAV TPKSVSETPPLSGNDTDSLSCDSGSS ATSTPCVSRLVTGHHLWASKNGRH VLGLIEDYEALLKQISQGRLLAEM DIQTQEAPSSTSQELGVTKGPHAP LSKFVSSVSTAKLTLAEAYR/RGLK LLWRVSLPEDGQLPLHCEQIWRNE RQRVPKLHKKLFEQEKKFAKTP*RF LQLSKRQEKVIFDQLVVTHKILRK ARGNLELRPGGAHSRTCSPSRPGS ALATRKEHRNQQHSAEQASRNSWQ GGQRRHRKEPSLWLSKPCPSLRCPF SLTNTMVTNIPWKVIIHLICLIPPRQ
3312	8809	A	3575	1	1362	SGNIKVLERFLYIDTKFSQNRCQKA LPMASAYQSNLPHNYTMTVHNN

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						QLAQUALRVYSQHAIGAVLYKYSMQ VHEDCYKFWNSNGMQLCEERSLTD QHCVHKFHSPLPKSGEKPEADRNPPV LYHNSRARSTGACNCGRKQAPRDD PFDIKAANYDFYQFWEEKCCGKIG SYSISQYLEPSTPGSWLLA*KWNP/ RPAPPDSADKLKEKEPQTQGESTS LSLALSLGQSTDLSLGTYPADPQ/DRR R*SRSSWSSRSEN/SRRDQTSIDRH/ LTVEYLPGLHSNCPKGLLPFSSW VFVKLGPG*SYNFHTRFR/NQQGFIP GNKLSYALGTLSSRARSWR*RRLR HKLLACSK*SYSWKEKCGCNGKRK TAR*H\TRAFVGFYEYDSRGRRFMC SGALTK**K*WGSGA/IRDSAFKSP*I VDMPLY\RHPLKVEGLKTLITLQL MRLFVVVPDASFAR
3313	8810	A	3576	1	673	EGGWMEYDYVHLQKKEEFEMTH IELLDKGSITRQMSQL*LEQLKLFV RLEQEVSRPIDHDLAIWTPAQPLAP GRSGG\LGPSDRQLLLFYLEQCEAN LTTLTNAVDAAFTAVATNQQPKILV GASKVLL\SAHKL\FIGDTLSRQA K\AADVR\SQVTHYSNLL\CDLL\QGI VATTK\AAALQYPIAFPQPKDMV/E KRVKELGHSTQ\QFPPRS*QQLGSP EGW
3314	8811	A	3577	3	531	FFLLQSL/DSAGQARVQWCDLGSQ PLPPRFMRVSCSLSSWDYRHLPP RLAMIFVFLVE\QGFTVLARLFSNS* PQ/CDPPTSASQSAGITGMSHHA\RL FLFFETGSGSIAQGGVQ*CNLGSLOP LPPRLKPSSHLSS*DYRRVPTCP SNFCIFGRDGVSPCCPDWSGTPGLK
3315	8812	A	3578	1	223	GSGGIHRLPLSSRPEQPIVWLWAPG CFSHLSRLQVTV*/GEIKQRCRELHH SLAQHPRHQAGNHISHPILHLKIL
3316	8813	A	3579	3	341	FFETESCSVSQAGVQWRDLGSLQA LPPGFTPFSCSLSPSSWDYRHLPPHP ANF/SVFLVETGFHRVSHDGLDLLT RDPPTSASQSAGITGVSHRARPIVAI FMFCEYPLFSSH
3317	8814	C	3580	168	347	MTYGLLLFLGNNPHLNLYXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXSTIV*
3318	8815	A	3581	852	1216	GFLINGNTDFFFETESRSVAQGGV QWRDLGSLQPLPPGFKRFSCLSPSS WDYRHLPPQYPS*IFVFLVETGCSSY STIL**RPHVGQAGLELLTPGDPPAS TSQNAGITGLSHRTWSAI
3319	8816	A	3582	2	238	
3320	8817	A	3583	680	891	
3321	8818	A	3584	697	979	IFGVSQGYKILWKMNSLPGVSFES KRSF*QK*LQILSS*FAKKIFYWHEN NRCKWRPNIPKCIYSITSQKLFYPS LLFFPLLPTFLGVGGAR
3322	8819	A	3585	2	518	GRGYQNPGRQCTSDRLSEHVSEGES

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						PPDSQEDSFQGRQKSKDKAATPRK DGPKRSVLSKSVPGYKPKVIPNAIC GICLKGRESNKKRG*IHFIHCSQCE NSG\HPSCLDMTNGACFYD*DLTPW QCMECKTCHICG\NPHHEEEMMFC\ DMCDRGYHTFCGGPGSNPTRPLNL
3323	8820	A	3586	1	165	SLEDRVLLCHPGTAYCSLELLGSISP PALTLTSEAS\LPGRDYREIPGSPCQL FL
3324	8821	A	3587	1	249	LVDRVLLCHPGTA/VLQP*TPGINQS SCLSLPSS*DYRYVPPCLVYCFIFLA EMGLTVLPRLISNSWPQAILPSQPPK VLGLQT
3325	8822	A	3588	3	282	NSWDYRHLPLSCLANFCIFSRDGGFT ILTKLVLNS*PRDPAASASQSVGITG VSTHGLASWN\FNKLKNSYTQVD*L GSQEWPLKVCLAKPRTAS
3326	8823	A	3589	1	714	
3327	8824	A	3590	1	726	MAEGETESPGPKKCGPYISSVTSQS VNLMIKGVVLFFIGVFLALVLNLLQI QRNVTLFPDPVIASIFSSAWVPPC CGTASAVIGLLYPCIDRHLGEPHKF K\REWSSVMRCVAVFVGINHASAK VDFDNNIQLSLTLAALSIGLWWTFD RSRSGFGLGVGMLF/LATVVTHL*V YNGVYQYTSPDFLYV\RSWLP\CIFF AGGITMGNIGR\QLAMYECKVIAEK I/LIRNEEGKK\YLLYRKAR
3328	8825	A	3591	469	537	PGLARRAMASGRSHGWP*IPPLRST FQGGRTLDAAFTRINCHGKTYLFKG SQHWRFEDGVLDPDYPRNISDGF GIPDNVDAGLALPAHIYSGRERVYF FKGKQYWEYQFQHQPNEEREGSS LSAVFEHFAMMQRDSWEDIFELLF WGKTSAGTRQPQFINLDWHGEPWQ ADAAMAGRIYISG
3329	8826	A	3592	193	384	
3330	8827	A	3593	96	1635	ARSPAMAPLRPLLILALLAWVALA DQESCKGRCTEGFNVDKCKQRDEL CS\YYQSCCTDYTAECKPQVTRGDV FTMPEDYTVYERLGEEKNNATVH EQVGGPSLTSDLQAQSKG\NPEQTP VLKPEEEAPAPEVGASKPEGIDSRPE TLHPG\RPQPPAEELCSGKPFDAFT DLKNGSLFAFRGQYCYELDEKAVR PG\YPKL\IRDVWGIEGPIDAAFTRI NLFRGRPYLFKG*QYW/RAFEDGV\ LGPWIYPRNISWTAFDGHSPGQTW D\AALGLPCPLAYSGRERV\YFFQRG KQYW/ESYQFPGTSPVQEECEGSS\ SAVFEHFAMMQRDSWEDIFELLF \WGAERSGWVTR\QPQFHLAGEWH GVPG\QVD\AAMG\GRILHLQGMAT RPLLWPKKK\RFH\RNK\KGYRSQ R\AHSRGR*PETPRRPISRA\MWLSF VLPSEESNLGA\NNY\DDYRMD\WL VA\ATCEPIQECFFSFQDKYYRVNL RTRRVDTVDPYPYRSIAQYWLGC

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						APGHL
3331	8828	A	3594	44	166	
3332	8829	A	3595	3	1173	SSAPEAAKKPTPCHRCRGLVDKFN QGMVDTAKKNFGGGNTAWEEKTL SKYESSEIRLLEILEGLCESSDFECNQ MLEAQEEHLEAWWLQKSEYPDLF EWFCVKTLKVCCVPGTYGPDCLA CQGGSQRP\CSGNHCS\GDGSRQG DGSCRCHMGYQGPLC\DCMDRLL QLRSRNETHSI\CTAVRTGLSDSYPP CCLSLGCWRGVGHAWIRGRNTHQT PGYSSRVWIAAFSPACDESKTCSG LTNRDCGECEVGWVRTRAPCVDV EKCAAQT\PPCSAAQFCKNANGSYT CE\ECSSCVGCTGEGPGNCKQCIS GYAREHGQ\CADVERVPH*PEKTL EEKTKTCYNTPG\SYVCVCPDGFE T\RRCLCAAGRRLKPQKGESPTQLP LP
3333	8830	C	3596	1	300	MRSFGQLTLCPRNGTVTGKWRGSH VVGLLTTLNFGDGPDRNKTRTFQA TVLGSQMGLKGGAGSVWLQAAGL GLLPASLLWPSLLCHCYVLPPAPGV PLV*
3334	8831	A	3597	359	1229	MPQPPTLGQEMTGPSQPWTGKGG LPGP*QLRAKAQEVDSHLGRKKIKQ QNRSKSC
3335	8832	A	3598	2	311	VRWNSAAPLVTSRGAPASARPRGQ ALPGGSAPSAPHGQLPGRAQPAPVS GPPPTSGLCHFDPAAPWPPGLGLG MLPPHPQDWPAQP*HPPGLGLFFEIF SAS
3336	8833	A	3599	1	426	
3337	8834	A	3600	18	738	
3338	8835	A	3601	65	425	RLPQPPGAAVGGSTRPCPSWKAVR VDLVVAPVSQFPFALLGWTGSKLF QRELRRFSRKEKGLWLNHGLFD/R GAGKQQWQDS*VTEVLLLQKTFF QAASEEDIFRHLGLEYLPEQRNA
3339	8836	A	3602	3	233	FFFFFKTLQIPLLSPPPPGPCRVQSL LPNPFPEKGA\PPQTDERGQDFRLD PPLGSPSPRV*SLNCYVPVPPKEK
3340	8837	A	3603	7	510	THAPAPSPRAQAP*PLFIHCP*APRV TPPPQPVKCVPAEVI/SPPPPGPCR VQSLIPLTRFPEKGAYLLSRQMKRG QDFKAGIQPLGLSLPQPGSTGRGRV TAGD
3341	8838	C	3604	846	989	MKSYNGMREMGDQASRRKLIKWN TDSKFLDMENGEQKKITPRPGVKI*
3342	8839	A	3605	3	232	KSLREGLESAMLVLKSLLPFSYFV SSMSSGNWSALHNHLGPEDTGTAS PYNRCS*RGRDHLGKRSSSTRGTTLG PN
3343	8840	A	3606	303	400	
3344	8841	A	3607	3	404	LRQRLTVTQAGVQ*HRLSSLQPLPP RLKRFSLSLPSSWDYRRVPPHMA NFLY/FLVETGFHHVGQAGLKLLISS

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						DLPALASQSAGTTGMRHRAQPKSF QLEQKWKTEPHKLIYVVTLNKRM YKLKTYHIPYYF
3345	8842	A	3608	2838	3122	FFFFFFETKSCSVA\RLECSGTISAHC NLHLPGSSDSPASAS*AAGITGACH HTRLVFLYF**RRGFHHVSQAGLEL LT*VIHPPQPPKVLGLQA
3346	8843	A	3609	1	325	RLFFFETVSHSVT\RECT*AILAHC NLCFPRSSNSLASASQVAEITGACY YTQLIFVFSVETGFHHVGGAGLELL T*VIHPPPPKVLGLQVSATVPGLII GTFSL
3347	8844	A	3610	3	398	GSLQPPPPRLK*FSCLSIPSSWDYKR LPPCPANFCIF\TELGFHQVGQAGLE LLTSGDPPASTSQTVGITGISHHAWP PEILSKGTMGKQMVNMLLLASSCR EMGHSAPAHLGQCLPMILPKDLAVI IINPV
3348	8845	A	3611	3	311	AQTGMQW\DLCSVKPPPPRFRFSC LSLLSC*DYKRTPPCANFC/DFVVE TEFHHVQAGLELLTSSDLPASASE NPQITGMNYCIWPEWYYYIHSLTNT IHK
3349	8846	A	3612	310	415	SQYFGTLRRVDHLRSGVRDQPGQL GKTPS*PQVIHPPQCPKVLGLQYYH FLFFLRSL/DSVAQAGVQWRDLGS LQRPPPGFTPFSCSLPSSWDYRRPP PRLANFFVFSVETGF\TVSARMVSIS *PRDPPASASQSAGDTGVSQAPV
3350	8847	A	3613	1	114	ARAEMLIVQYILPRLTHCAIFTILFIF SLLT*VMLLSS
3351	8848	A	3614	335	477	TPASLKIPVE**NTLLAKMVSIS*PR DLPASASQSAGITGVSHRARC
3352	8849	A	3615	135	804	GIDTILTLNQN*SLKTRQ*FTLIIF/IFF FFLRWSLALSPRDCGLQWRDLGSL QAPLPGFTPFSCSLPSSWDYRCPPP RPANFFCNFFSRDGGFTVLARMVS IS*PQ/CDPPTLASQRAGITGLSHCT RLFFF*WMESPSVTQAGIQWHDLG LQPMPPQFR*FSWLSLPSSQDYRCM PPCQANF/CIFSRDEVSPC*PGWSGS PDLVIHLPWPPKVLGLHA
3353	8850	A	3616	3	285	HEIIVLRVRVSPCCPGWSA\TVD*SW FIAASYS*VKRLSCLSLRLRIWGCRQ VPPWLSFKLFWRQGLAVLPKLVSN SWPKMTLLPQLRLGLQE
3354	8851	A	3617	3	575	PSLRHASHEAGWQCPHLGQPLPGY TELRTLPQ*GDGYGRPGVSAASQR R/GLAGQCVEGRDWVEGKAG*CSG GHGGEKGGLD*GALLPGPQNR/S GAGDPC*AVESVGCQ*PGECHFQR DPPGSGAAPGAPPAVP*LHRQDA AAGGTAGPSLPHLPPPLPGLRVERS KPGGAAEEQGHPHLEHGP GD
3355	8852	A	3618	3	379	FFETESCSFTQAGVQWHDLT*SP PPGFK*FSLSLSSWDYRRPPRTA/ NYIYIVFLVETGFPYVGQAGQKLLT

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						SCNLPALVSQSARITGVSHCAQLCN FLLTVKHFKPLTLRLEARTPQSFL
3356	8853	A	3622	1	214	ETESRSV/SQAGVQWRDLGSL*PPPP PGFQRFSCSLSPSSWDYRRAPPLPH NF\CIFSRDGVSPCWPGWSQIS
3357	8854	A	3623	2	309	WCVFFETETHSAAQAGVQWCNLS LQPPPPGVKQFSCSLSPSSWDYRCA SPCLASFCIFSRA*GFTMLTCLLELT SGNPPTSASQSAGIQGVSHHTWPSI F
3358	8855	A	3624	1	294	FFFFFFLRQGLTSLARLECSGMISAH CSLDLPGSGDPPTSAS*VAGTTGTC HHAWLIFLFLVETGFHHVAQAGTLS KHRNHIQPVQVRATCSKDGQ
3359	8856	A	3625	23	282	ASTGKPLSPQVQSES/CLALQLP*RS WN*TRVMSTTPWPNFFGIFVEMGF RHIGQAGLELLTSSNPILASQSAGI TGLSHRVQPTSS
3360	8857	A	3626	37	289	QWHDLGSLQPLPPGFRRLSCLSLTS SWDCR/QPALRPANFFCIFK*RWGF TVLAQDGLDLLTSSDLPASAS*SAGI TGVSHRAWA
3361	8858	A	3627	70	362	KLHFKAIEGISSLGEQMKPSMWML LCPQIKIKLTLPIQIKQAKTCRQIPKV QGSQ*KNVGPSSFPVPW/EHSGSMI EAPWALNPYLGLGPVQILETQK
3362	8859	A	3628	60	303	KLKNHHHHHHQQQQQKQQQQQK QMDPRVSFSFFKKKKSSTPKPSQ*FP *SSRNS/HPR*ISESDLRPTAIPIGL KMKLPL
3363	8860	C	3629	193	285	MLLVSYPRNSNRCQIQYHEAFCPHIF LRVL*
3364	8861	A	3630	159	483	DPTSFGHGYLVFPTPCFKGFYFF*DR VSFCCSGML/IGSLQAQPSGFKPKPS SHLRLSSEDCRHTPPRLANLFFYFF L*RWDLTMLPRLVSNS*AQVILPSW PPIMLG
3365	8862	A	3631	6	244	DRVLLVTQAGVQWHDLGSLKPPPP GFK*VSCLSLPSSWNYRRLPPRPAN F*FLVETGFLHVCQAGLKLPTSGDP PASA
3366	8863	A	3632	2	262	NDLGSLK\PPPPGFK*VSCLSLP/RVS WNYRRLPPRPSLIFVLVETGFL\HV CQAGLKLPTSGDPPPSASQSTWITG VNHRRARPQIGF
3367	8864	A	3633	1	1149	
3368	8865	A	3634	280	602	TDFFFFFFLRWSFTLVAQAGV*LHD PE*LQPPPPGFKRFSCSLSPSSWDYR HPPWPANF*FLVETGFHHVQAG LELLTSGDPPASASQSVGITGVSHR ARPELNF
3369	8866	A	3635	3	679	SLHQSGRSNPTCCFPSSKGTGTNGH PTPSQSPPGTRDGPLFFPHSASTPP PTGASQPLTGTGPPSPVEPVSHAC ASL*FSEGLRSEHPAVACGKTLQSP TGSKEACSGEQGNCVLAIEIVLGT QDPSAH*GGAGARGGGALWVTEG

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						VKGPGPVSGQCRKSQPHACGEIPCR APPTMGTSGLP\GLPKLCPHFHCSR ASPAPSNSPFCFWSPTSGGPNPFPC
3370	8867	A	3636	1	334	EMESRSVAQAGVQWHDLGSLQPLP PGFKRFSCSLSPSSWDYMRAP/PRP G*FFVFLVEMGFHLVGQAGLKLLTS /S/DLPTSASQSAGITGMSHRTRPNSL LVIQSGRFNTKITR
3371	8868	A	3637	2	309	FFFETRFRFVAQAGV*WHAYGSPQ PRPPGPKPSSQLSLPS*DYRHTLLCL ANF\DFLVETGFYHVAQTGLELLSV RDPPALASQSAGIAGVSHRARPGCI F
3372	8869	A	3640	19	458	KHLFYSSNLYFRSTFRHTRRRSPCEP SLALR/WCVLEPGSSRV**RLHPNTV GFQDASAKPRERTTSFHAFANF*K QYIFQC*LPPLTWLEIFSPFSRETGST KRCRLQDPGPSHFWRVVLGCLLWG QDRAPSWAPLQMQCLCHCLYL
3373	8870	A	3641	1	322	FLRRSLALVTQARVQWHDPGSLQP SPSGFKRFSCSLSPSTRDYRHPPRL ANFF/VFFLYL**GFATLAWLVLNH L/CDPPASASQSARTTGASHHAQPP VSFFKTRI
3374	8871	A	3642	333	438	
3375	8872	A	3643	391	492	
3376	8873	A	3644	598	699	
3377	8874	C	3645	176	319	MCSAQPAFSVDIIKSRHLGILGFYK PRILCQKHMLRLLHSFQNFQR*
3378	8875	A	3646	2	50	QLLGTGMHHYA*LIF
3379	8876	A	3647	3147	3308	FFKKNLCASAHYY/TWCVPLPFFFF LRQGL/NSIGQAGVQWCNHSSLQPC PPQDLE
3380	8877	A	3648	1554	3041	GTRERRAPDPCAGKCRNHVAGGRL KLSLHLSLPSSWDHRHAPL/PHD*FF KYLR/RSPCVTQAGLKLLGSSDPPI LASQSIGITDMSHCT/WPSSPTCHF LRDSFAPSPRPGMQ*CDHSSL*PQTL GLKQFSHQPPFYFFVQMGFAMLPK LVLNWPQ/DNPSALAPQSAGIVGM SCCAQPPCFNINSHS*IQE
3381	8878	A	3649	280	444	
3382	8879	C	3650	135	377	MAGSWGAGVQVWLMSVIPILWEA KMGGSLPRSLRPAWVTQGDVPSN RLFHSSASVLWLQATLTGTPKSLEYI TLAFRAK*
3383	8880	A	3651	1791	6596	CPKDTQILIFQKNNFSIRRFTHLAD FLKEFCLTFKKKGRSOLL*FCCFVYI IF*KKFVCFCSSLHWCVPLPFFFFLR Q/RHSIGQAGVQWCNHSSLQPCPP RLK\HPCTSASQVAGTTGMHHYA*L IF*IFETGSPCVTQAGLK/PPGLK*SS HLGLPEYWDYRHEPLHLPSSPTPCH FLRDSFAPSPRPGMQ*CDHSSL*PQT LGLKQFSHQPPFYFFVQMGSCYVA QAGLK/PPGLKQSFCLGPPKCWDCG HELLCPASMF*YQHPPHMYTLKTTV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: In USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						TFSTQNYIRYSLNCRKIKTIPKSDCR VDFFLQNT
3384	8881	A	3652	3	332	ETESHSAQDGVQWRHLSSLQPPLL GFK*FSCSLPSSWDYSCPSPT/P*LI CFFFFLIEPGFHHFGLAGLELQTS DLPASAFQDAGITGMSH*TRPELLS LDHTPFT
3385	8882	A	3653	3	272	FETESHVSPRLECSGVIFAHCSECL PGSSDSPASAS*VSGMIGTRNHAQLI FVFLVEVRFHVVGAGLELLA*VI HPPQPPKVLGLHV
3386	8883	A	3654	1	272	ETGSRSTIRLECSGAITAHCSLDLPG RSNPPTSAS*/RIAGASGECRHTQL/I* KFIFFVNTGCRYVVQAGLKLLASGA KQSSCLGLSKCWD
3387	8884	A	3655	249	906	RIHFPRVSGPSQSNPKFAVASRGFFS LSLSSAQPDPLPPPLGEALALSLHPV PRRSTETVAGDSSELQLGLRSPQQP LAGLAFLARLFLFPPP*RCKSKPN* NDRRRSSVDSQIHLVGRESAHLPLAG LRVCVSLPLLARCFGQVLOQVPGL WIPSPGGS/AGVSGRRREERHMGVV VMRVRVEARVSS*ESKI/SRALR*ST HLGLPKCWDYRREPPCPAH
3388	8885	A	3656	1	514	FFFFSRSL/NSVIQAGAQWRDLGSLQ P/LLPPGLKQFSCSLSSWDYRCPP PRLANFYIF/M*RRGFTILARLVLS* TQ/CDPPTSASQSAGITGVSHPTQ/LL FSF/CLKESGSSLMVSATLRFHK*RH SGPSRAALSSSP*LEPRKLKFGTASL QNKWAMQQTRQHWAAQRGSKPM
3389	8886	A	3657	2	307	FFFFFFETESYSVTQAGVQWHDGL LQPLPPGLKQFSSLSLPE*L/DVTGSP PPCPVNFCTFGKGLGFTMVGQAGS GTSCLKVICPPGLPKVLGITGCEPRR L
3390	8887	A	3658	79	91	NTFW*RRGFTVLARMVLIS*PHDLM TC/PASASQSARITGMSHCARLVLYF SRDGVSLCWPGWSQTADLR*STCL GLPKCWDYRYEPPCPASLHHFLIYA TSIIKYL
3391	8888	A	3659	162	493	DGSSPPVAQAGVQWRDLGSLQAPP PGFTPFSCLSLS\RSWDYRRPPRPA NF/SCIFIVETGFHRVSQDGLDLLTS* S/VPASASQSAGITGVSHRARPRSCIS FDSTVTLAQ
3392	8889	A	3660	3	251	GGALRLHQVPPALPLRGAVSGAAA VQGMSDCTPCCEVHLLQD*VPAGE ARVQWHDGLGSLQPPPPRFKRFSCLI LPSSWDYRH
3393	8890	A	3661	3	251	GGALRLHQVPPALPLRGAVSGAAA VQGMSDCTPCCEVHLLQD*VPAGE ARVQWHDGLGSLQPPPPRFKRFSCLI LPSSWDYRH
3394	8891	A	3662	17	287	KYHRIQCPNSG\CEAVYSSVSGLKA HLGCTLGNFVAGKYKCLLCQKEF VSESGVKYHINSVHAEVRLL*SCGP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DM*ATREVDVFPIVMD
3395	8892	A	3663	3	567	DRKLKYTRPGLPTFSQEV LHKWKT DIKKYHRIQCPNQGCEAVYSSVSGL KAHLGSCTLGNFVAGKYKCLLCQK EFVSESGVKYHINSVHAEDWFFVN PTTTKSFEKLMKIKQPAARRRKAEE AAQEQKVSKGGSSLGIELPETEPS LRVGKDQRRNEDW*CQPPCKEP/ GAGASASTVPESKAPKD
3396	8893	A	3664	1	184	SSRDILLCTDIASRGDSTGV L VVN YDFPPTLQDVELAARRRRSLPGLASS VKEPLPQAT
3397	8894	A	3665	2	1748	HEARTKGNMALSARLRL LFPFVN SVCFLAPRRGLTVRSPDEPLPVVR IPVASTSGKLEQRQSRRRNLPEGR LVRPGPLLVSARRPELNRPARTLG RWERAPLASQGWKSRRARRDHFSV ERAQQEAPAVRKLSSKGSFADLGA WKPRVLHALQEAAPVVQPTTVQ SSTIPSLRGRHVVC AETGSGKTL YLLPLLQRL LGQPSLDSLPIAPRGL VLVPSRELAQQVRAVAQPLGRSLG LLVRDLEGGHGMRRIRLQLSRQPSA DVLVATPGALWKALKSRLISLEQLS FLVLDEADTLLDESFLVVDYILEK KDLAVFLYHLRLEAEVEVVEMLGP HGQPCPQHNSDISAYTYERTLMME QRSQMLRQMRLTKTEREREAQLVK DRHSALRLESLSDEEDES AVGAD KIQMTWTRDKYMTETWDP SHAPD NFREL VHIKPDQSNVRRMHTAVKL NEVIVTRSHDARLVLLNMPGPPRNS WCTTSSRTEKRQWNC PAVRTEKNA QTRQTIIAETKTQKKDTEPRIPEADL AVQYDNHYTNTKYCLCQMLREQ ESPOGRLLHAAQSSREIW
3398	8895	A	3666	1	1704	MALTRPVRLFSLVTR LLLAPRRGLT VRSPDEPLPVVRIPVALQRQLEQRQ SRRRNLPRPVLVRPGPLLVSARRPE LNQPARLTLGRWERAPLASQGWKS RRARRDHFSIERAQQEAPAVRKLSS KGSFADLGLPRVLHALQEAAPV VQPTTVQSSTIPSLRGRHVVC AAE TGSGKTL SYLLPLLQRL LGHPSLDS LPIAPRGLVLVPSREFFQHLRAVA QPLGRSLG LVRDLAEGGHGMRRIR LQLSRQPSADVLVATPGALWKAL KSRLISLAEELSFLVLDEGDTLLG*K ASWELVDYILAEKSHVAEGPADLED PFNPKAQLVLVGATFPEGVGQLLN KVASPDVTTITSSKLHCIMPHVKQ TFLRLKGADKVAELVHILKHSR AEKGLGPSGTGFVFCNSSTVNWL GYILDDHKIQHLRLQGQMPALMRV GIFQSFQKSSRDILLCTDIASRGD STGV L VVN YDFPPTLARLTFHRA GESGPVWGAEGPGTVISFVTHPW DVNPWFKKD*SLAARPKEEVL PGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3399	8896	A	3667	2	222	AIPR*KKPFAPQSNPDFEQNLIKM RWSLTLFQAGMQWPNLSSLQPPPP RFKQF*CLSLPSSWDYWYTPPRLAN FCIFSRDGVSPCWGWSRTPDLR
3400	8897	A	3668	1	29	
3401	8898	A	3669	2	206	VTQAGVQWLALSSLQPLPPG/LK*F YCLSLPSSWEYRHTPPHPTKFCIFFL VEGVSPYWPGWSQTPGLR
3402	8899	A	3670	3	139	TSHMWWCRHVVSATREAEVGEPL EPRQSRLQ*AMTAP/CTPAWATK
3403	8900	A	3671	86	384	
3404	8901	A	3672	3	746	RQEEGLPPVVDAIDDASVEEDLAVA VAGGRLEEVSFLOPYPARRRALLR ASGVRRIDREEKRELQALRQSREDC GCHCDRICDPETCSCSLAGIKCQMD HTAFPCGCCREGCENPMGRVEFNQ ARVQTHFIHTLTRLQLEQEAESF/QG AGGPCPGQPTQPW*GGPGPYFPTGQ APHEQ*AGRQQLQQRHD\YSSTASS SASGTSEAPDCPTHPGLPGPGFQPG VDDDSLARILSFSDSDFGEEEEED
3405	8902	A	3673	72	332	LPALETPRAQSKCSPQPSWVSRDY RCVPHTALANF*IFGEMGS/LLCCPR LISNS\WPQGILPPPPKVLGLQGSYS AKITTGFFLK
3406	8903	A	3674	33	396	RVWYLHRVTGRPASCLREVGPGRS LETASLREIWSRRCRAT/ECSQQL NHRLARQREHEARLRQREQNSRY FTDV*HLRSKQAEWSSKTYQSRM HAYHREKMKEEKRRSLWARLEKL M
3407	8904	A	3675	217	935	QRQREKEDQIRQQWEQNSRYFRMS DICSSKQAEWSSKTSYQRSMHAYQ REKMKEEKRRSLEARREKLRLMQ EEQDLLARELEELR/REHELAGKKN PGAAREAEISQRAEETDC*TTFVR TLEKEQPETSRDGAGPSPEACRKL GNAE/MKKKKQQEASAEQGNKRYE NEYERARREALERMKAEEERRQLE DKLQAEALLQMEELKLKEVEVGT SPSQP*PPPQLLVSMRWALERLP
3408	8905	A	3676	1	382	EMEPCFVS*TGV*WHDLSSLQPLP KFKRFSLKIPE\SWDYRRTP/PMP/V LTGFHHVDQAGFELLTSSDPPTSAS QSVGITGMDHTWPTLHTLTKPCE VDENAVMRELKLTGQGPLRWQF EHLNPA
3409	8906	A	3677	1	2456	MPTYPKLEKTDQSTS YTKFNDLSPD SSRERYTSLEIKSVCYTALPEQGQK QLQLWYNCVKTQCKTTQECSLKWI FTMNETSDREDGLPKGHHVTDSEN DEPLNLNASDSESEELHRQKDSSE SEERAEPASDSENEEDVNQHGSSE SEETRLKPGSDSENEELLNGHASDS ENEDVGKHPASDSEIEELQKSPASD SETEDALKPQISDSESEEPHRHQASD SENEEPPKPRMSDSESEELPKPVSD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SESEPPRRHQASDSENEELPKPRISD SESEDPPRRHQASDSENEELPKPRISD SESEDPPRNQASDSENEELPKPRVS DSESEGPQKGPASDSETEDASRHKQ KPESDDSDRENKGEDTEMQNSF HSDSHMDRKKFHSSDSEEEHKKQ KMDSDEDEKEGEEKVAKRKA LSDSEDEEKASAKKSRVVSADDDSD DSDAVSDKSGK\KRRTIASDSEEEA GKELSDKKNEEKDLFGSDSESGNEE ENLIAD\NLENLVMKRK*NLQVLTK KIWEEKGETQVKEAEDSDSDDNK RGKHMDFLSDFEMMLQRKKSMSG KRRNRDGGTFISDADDVVSAMIV KMNEAAEDLKETFIDSGVMSAIKE WLSPLPDRSLPALKIREG\VLKILQE LPSVSQETLKHSGIGR\AVMYLYKH PKESRSNKDMAGKLINEWSRPIFGL TSNYKGMTREEREQRDLEQMPQRR RMNS/DLVVRHPPERDLEKVLTGEEK ALRPGDPGF\VPRARVPMPSNKDYV VRPKWNVEMESSRPGILKKGLSRLE KHKRRFAEQRLSKVHRAVKFSIEG NRMPL
3410	8907	A	3678	1	564	TLKQVGLTEHVMYLYNDPKESRSN KDMAGKLINEWSRPIFGLTSNYKG MTREEREQRDLEQMPQRRRN\DIST GGQTPRRDLEKVLTGKEKALRPGD SLNLV\PRARVPMPSNKDYGVPRK MKCGNGVIQVSGDPPQKGIQSDWI NQMRKFHRY*GKKADLAHAVENP AIEGNKMPIGDPCPGMCPPILL
3411	8908	A	3679	63	361	
3412	8909	A	3680	151	384	
3413	8910	B	3681	385	479	MAGAFRRRFASEVRAQGLESLEH GLRCAGSLRGGQSLPTTMWSPVKV GFE*
3414	8911	A	3682	3	698	VFFFFSGCTRGPLFESDFHRAPHRC GQGLAAP*AAGAPQPRAPGETRGPE PAPHWRSASGDKPPGQAA\PPALVP GEGPSWSDPRGHRCSQATLPRVL AGPLQP*LS*LSL*DPPELRL*PPL* LRL**SLEPP*PPLDSNRFP*PRSP PPLENPRPRPRPRKKPRPPAEP PTESVSDDLPAWSTRISVHLQTS WPSWASLASSMFFKVTKPNSRELW SS
3415	8912	A	3683	138	550	FCCCFSTSEHSLAYGSCSPRRTEVL CAQQNPSETQAAPLAS\YMWK*PC NSRLKGPGLGEGWPES\RM TSGV TVPGGTSPGTRAGGS\PCPGGLS PEALRQ*GAGSGPRVSPGA/PGCGAPAA YGAASPCPQRCGAL
3416	8913	A	3684	2	555	FFFFFLGAHVALYSNPTFTGLHIVV GKDWPPP*AAGAPQPRAPGETRGPE PAPHWRSASGDKPPGASGCLQLLF QGEVPPGDS*PQRSSLALRPPFPRVL GPGPFQPAKAKQRYRQRPQGSQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						APP/GPPRKQPQPLRKVSG*SGGCDL RLRHRPACPGRVCTLAQLEPATRM GWSYVGQCGL
3417	8914	B	3685	95	371	MASDEGKLFVGGLSFDTNEQSLEQ VFSKYGQISEVVVVKDRETQSRGF GFVTFENIDDAKDAMMAMNGKSV DGRQIRVDQAGKSSDNPIPW*
3418	8915	A	3686	314	1055	SKCFHLHQVWKQKGEEYRVGTGYG GWSWISKTHVYRFVPKLHGNTNVN YRKSLEGTKNNMDENMDESDKRK CSRSPKKIKIEPDSEKDEVKGSAA KGADQNEMDISKITEKKDQDVKEL LDSDSDKPCCKERTNGSRR*HENRVT CKLSGEFSSRCGQC**GFSSKD*LQK ENKIIQTRWTS*KEN*TVYTGRKTA TRKNQVGGWN*GYRKD\STNSSKN LSESPVITKAKEGCQSDSDETRTEPK CK
3419	8916	A	3687	11	345	DSLTVASQGVQWHNLISLQPLPGV K*LFCLSLPSS*DYRRAPHPANFSF LVEMGFYHVGQAGLELLISSDLTSL ASQSAGITSVSHWAWPENVYLNQ QTEKSLMVSG
3420	8917	A	3688	1	521	NPTKSCMLEG*NPHVHCK\REGAQA ITGMPI*KATKYLKYFLLQKLCVPF QS/YESGVGRCTQDRHWGWTTHQ WPRKGTEICLQVQSYAELKGIDVDS LVIEHIQ/V\NKAPIMYHLTYRTHGQ MNP/YHKLPCHIQMMLSEKKHLVP KAEKEDARKKKIPQKKHKLKRQTN SAKRKCK
3421	8918	A	3689	1	281	ETGSHSDAQAGVQWHDLGPMQPLP PGFKRFSHLSSLSSWDYRHAP/PRPG LFL*RWGFHQVGQVDLELLNSSDPP ASTSQSAGITSASHRAWPN
3422	8919	A	3690	3	314	HAEHEITELTATFTKFDNRDGNRILDE KEQEKMRQDLEER\LTRVLQLET VLERVVAQIDALSSKLEMLEKKG VLSLFTSFNIRAFKSLFSHYSSVT PINYL
3423	8920	A	3691	61	400	LVTGIWSATCLWVLLLLLFEKGCP S VQPRQLQCS\NVITACCSLNLARG SND PPTSASRVPGDHRCCHYTWAN FLIF LWEMRSHCVGFRLGLGTPVL KLQT ILQPQPPKVLGLQA
3424	8921	A	3692	33	436	REQEL/CKGKQKDGTSFGEGGWY KACKVDSPTVTTTLKNLGALYRRQ GKFEAAETLEEAAMRSRKQGLDNV HKQRVAEVLNDPENMEKRRSRESL NVDVVKYESGPDGGEGVSGRAS FCGKRQQQWPGRHR
3425	8922	A	3693	37	355	NSEYGGWYKACKVDSPTVTTTLK NLGALYRRQGKFEAAETLEEAAMR SRKQGLDNVHKQRVAEVLNDPEN MEKRRSRESLNVDVVKYESGPDGG EEDGTGSLKRS
3426	8923	A	3694	229	2000	QRERARPSGARRMYDTMSTMVYIK

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						EDKLEKLTQDEIISKTKQVIQGLEAL KNEHNSILOSLLETCLKLKKDDSEN LVEEKSNMIRKSLEMLELGLSEAQV MMALSNHLNAVESEKQKLRAQVR RLCQENQWLRDELANTQQKLQKSE QSVAQLEEEKKHLEFMNQLKKYDD DISPSEDKDTDSTKEPLDDLFPNDED DPGQGIQQQHSSAAAAAQGGYEI PARLRTLHNLVIQYASQGRYEVAVP LCKQALEDEKTSBGHDHPDVATML NILALVYRDQNKYKDAANLLNDAL AIREKTLGKDHPAVAATLNNLAVL YGKRGKYKEAEPLCKRALEIREKV LGKDHPDVAKQLNNLALLCQNGG KYEEVEYYYQRFLEIFQTKLGPDDP NVGKTKNNLASCYLKQGKFKQAE LYKEILTRAHEREFGSVDDENKPI WMHAEERECKGQKDGTSFAGEY GGWYK\ACTVDSPTVTTLINLGAL YRRQKFEAAETLEEAAMRSRKQG LDNVHKQ\VAEVLN*PLRTLEKPQ EPVESL\NV\DVVKYESGPDG\GEEV SMSVEWNGGVSGRASFCGKRQQQ QWPGRRRH
3427	8924	A	3695	1	314	KVDSPTVTTTLKNLGALYRRQKGF EAAETLE\EAAMRSRKQGLDNFTKQ RLPEVLNDP\ENMEKRRSRESL\NV V\KYESGPDGGEEVSMVKWNGM RKMMLGAG
3428	8925	A	3696	2	450	VNKAGGLIYQLDSYAP/RAEAEKTF SYPLDLLLKLHDERVLVAFGQRDGI RVGHAVLAINGMDVNGRYTADGK EVLEYLGNPANYPVSIRFGRPRLTS NEKLMLASMFHS\KFFVLADP\RQ AGIDSLLRKIYEIYSDFALKNPFYSL EMP
3429	8926	A	3697	2	823	FGTRGKAAMAFSVYVVKAGGLI YQLDSYAPRAEAEKTFSYPLDLLL KLHDERVLVAFGQRDGI RVGHAVLA INGMDVNGRYTADGKEVLEYLGNP ANYPVSIRFGRPRLTSNEKLMLAS MFHSLFAIG\SQLSPE\QGSSGIGCLE TDPFQFH\CSRTL\TGIF\VLADP\R QAGIDSLLRKDFMEILLQTLPLKNPI PIPLEMP\IRCEPL*PQNPEA*SLEVA\ EKAG\TFGPRVHRLNPVMGPPQNPE SSLQOEYCLLTLPVEIPAALVSAP
3430	8927	A	3698	165	354	ENFGGKITNFAKLFYILPYSHYFW CLEKNRNR/SLTLLPRLVSNWSAQ ALLWPPKVLRQA
3431	8928	A	3699	3	166	SETGFCHVAQAGLELLVSRSPASV SQS\TGISHQARPSISYFYDHSAPITH TDH
3432	8929	A	3700	1	421	ETKSHSVTKTEVEWRDPSSLQPLSP GFKQFSCRSPLN\SWDYR/PSPANFV FLVETGFYLVGQAGLELLTSNDPPA SASQSAGITGVSHCAQPRITNSLT TASFIQPRKHSEFPVMTCPSSNATESK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VGGRGPHGAIARLM
3433	8930	A	3701	2	205	APVTSW/IQPKVGSCPFSESTKTISLY ISSEQQFHLPRPSESDDFIEDTADMLA VSFSGYSSAPKNQEQ
3434	8931	A	3702	2	205	APVTSW/IQPKVGSCPFSESTKTISLY ISSEQQFHLPRPSESDDFIEDTADMLA VSFSGYSSAPKNQEQ
3435	8932	C	3703	282	445	MISAHCNLLPPEAGELLEPGGRRFS EPLHSSLMTQDSVSKINKNNKTSIS NPE*
3436	8933	A	3704	170	607	WPSG*FQR*SMRLKYKIHLNVSRR PQLAPGKELYFSF*LLFYFYFYFIHIII FEMESHSVTRLECSGTISAHCNHL PGSSDSPASASPVAGTLIDACHHTW LIFYNF*VEMGFHHVGVQAGLKLTL *VTHPPRPSKVLGLQA
3437	8934	A	3705	3	231	FETESLFRLECSGTISAHCNLRSLG SSNFWLIFCNLVEMGFHHVGVQTSLE LLTSSHPPTSAFQSARITGVSHRTW
3438	8935	A	3706	4	144	
3439	8936	A	3707	333	416	FTGLPCLFSPQNNVSLQSCIDLK NN
3440	8937	A	3708	1	1219	MAAVPELLQQEEDRSKLRSVSVD LNVDPQLQIDIPDALSERDKVKFTV HTKTTLPTFQSPEFSVTRQHEDFVW LHDTLIETTDYAGLIIPPAPTKPDFD GPREKMQKLGEGECSMTKEEFAK MKQELEAEYLAVFKKTVSSHEVFL QRLSSHPVLSKDRNFHVLFLEYDQDL SVRRKNTKEMFGGFFKSVMKSADE VLFTGVKEVDFFEQEKNFLINYNN RIKDSCVKADKMTRSHKNVADDYI HTAACLHSLALEEPTVHKYLLKVA ELFEKLRKVEGRVSSDEDLKLTLL RYYMLNNEAAKDLLYRRTQS/ALI DYENSNAKLDKARLKSVDKLAEA HQQECCQKFEQLSESAKEELINFK VRKRVA\AFRKNLIEMSELEIKHARN NVSLQSCIDLFEE
3441	8938	A	3709	527	724	TMKIGLGFSLVSNIFSFPVELINFKR KRVA\AFRKNLIEMSELEIKHARNN VSLQSCIDLKNN
3442	8939	A	3710	1	1220	QEGGSAGSAGSGADGTGLRQSLAG HVGRPGRGQWGQRSGDLPGRPP PARSEHRCVAEG/NLSLYVFGGYNP DYDESGGPDNEDYPLFRELWRYHF ATGVWHQMGTDG\YMPR\ELASMS LVLHGNNLLVFGDTGIPFGESNGND VHVCNVKYKRWALLSCRGKKPSRI YGQAMAIINGSLYVFGGTTGYIYST DLHKLDLNTREWTQLKPNNLSCDL PEERYRHEIAHDGQRIYILGDGTSW TAYSLNKIHAYNLETNAWEEIATK PHEKIGFPAARRCHSCVQIKNDVFIC GGYNGEVILGDIWKLNLQTFQWVK LPATMPEPVYFHCAA\TTA\GCMYI HG\GVVNIH\ENKRTG\SLFKIWL\VV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PSLLELAWEKLLGAFF\NLANL\SR QLLHLGFTQGLIERLK
3443	8940	A	3711	2	266	FLMESRSVTRLECSSTITAHCNLC LPVSSDAVSASQVAGTTGMRHHAQ LIFVFLVETGFHHVGQDGLHLL\N IVIHLP RPPKVLGLQA
3444	8941	A	3712	1	453	FKRAMDLVQEEFLQRLDFSQHSW LPARALVEEALAQRQVDPSPGEIV ELAKGACPWKEHLYHLESGLSPPV AIFVVIYTDQ/RWTVANIAGCPLPE PWRGLRDEALDQVSGIPGCIFVHAS GFIGHRTREGALSMARATLAQRSF LPQIS
3445	8942	A	3713	20	891	RWNSRYDHHQRSFTETMSSLSPG KPWQTKLSSAGLIYLFHGAQVLAQ LGTSEEDSMVGTLYDKMYENFVEE VDADVNGISQWAEGERYALTTTL SARVARLNPTW\NHPDQDTEAGFK RAMDLVQKEVSCRD*IFYQHSWLP ARGLGGKSHLPQRIPRWNP SGK\I VELAKRCHVPWKEHLLPPGNLGLS PSKWPIFFVIYTD/SRL/EQWRIQC VAQ/VSPTHSQSRAA\LEPWRGLRG TRPWT*FSGIPGCIFVHASGFI\SA VNATREGALSMARATLAQRLIPPT NLLV
3446	8943	A	3714	176	450	
3447	8944	A	3715	1	472	
3448	8945	A	3716	418	1354	AAARRATCLGCRSCSGATARRASS WRTAPRVHSAWKLADGRRLASGS FDKTASRLA WRRTRFGQKKTIIGG HGG*C/VTSFCWHP SNPEPICYGV/Y GDKTIRIWECEDYKNALPLVNIKGE NINICWSPDWQTIAVGNKDDVVTFI *CQDTPFQSRRAVQVPRSTKSPWNH DHNMFLLTNGNGCINILSYPELKA\ VQSINAHPSN\CICNQV*PHGESTLP QASCKMLLVSLWDVG*VSVCFGAF SRLDWAC*EPFSFSDGKMLASASE DHFIDIAEVETGDKLW\EVQCESPT\ SQVAWAPQKASAGHLPR
3449	8946	A	3717	1	296	LWDV/EELVCVGAFLDWP/VRTSV SAHDGKMLASASEDHFIDIAEVKTG DKLW\EVQCESPTFTVAWHPKRPLL AFACDDQKTANMTSSREAGTVKPV GAS
3450	8947	A	3718	2	276	RSTFALVAPAGVQWHDNRSLOPLL PRFKQLSCLSLSSWDYRCPPPSPA NF/SLFLVETGFRHAGQAGLQLLTS GDLPTSASKSAGITGMGLQ
3451	8948	A	3719	3	613	GLRALRRGQGLPGL*CCSRPQPSR AQGHPSMGGPMQRTVTPRGMASV GPQSYGGGMRPPNSLAGPGLPAM NMGPVGRGPWASPSGNSIPYSSSSP GSYTGP PGGGGPPGTPI MPSPGDST NSENMYTIMNPIGQAGRANFPLG PGPEGPMAAMSAMEPHHVNGSLGS GDMDGLPKSSPGA VAGLSNAPGTP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RDDGEMAA
3452	8949	B	3720	134	471	MYAKGGKGS AVPSDSQAREKLALY VYEYLLHIGA QKSAQTFLSEIRWEK NIMPSPGDSTNSENMYTIMNPIGQ GAGRANFPLGPGPEGPMAAMSAME PHHVNGSLGSGDMDG*
3453	8950	B	3721	223	692	MEPSPRAQGHPSMGGXMQRVTPPR GMASVGPQSYGGGMRPPNSLAGP GLPAMNMGPGVRGPWASPSGNSIP YSSSSPGSYTGPPGGGGPPGTPIMPS PGDSTNSENMYTIMNPIGQGAGRA NFPLGPGPEGPMAAMSAMEPHHVN GSLGSGDMDG*
3454	8951	B	3722	228	292	XLARDDHERVMGRQPRASLRA*
3455	8952	A	3723	1	1753	MYAKGGKGS AVPSDSQARENLSAF QAATELTSLDRLALYVYEYLLHIGA QKSAQTFLSEIRWEKNITLGEPPGFL HSWWWYGLGCCGVFWDLYCAAP DRREACEHSGEAKAFQDYETPERP AHRHGNAGRAGSSSGMIDVGGSSD PQILRPTTPVCSLTNASSLSHGAGHL QRGGGTPQSAAAAPSPVMGSMAPG DTMAAGSMAAGFFQGPSPSPH NPANPMMGPHGQPFMSPRFPGGPR PTLRD\GSQPPAGPPWVPSPPG\A MEPSPRAQGHPEHGRPNARGVTPP RG/MGPAWGPRA YGGGMRPPNSL TRPRACLPMNMGPRKFVGPWAQPP VEYSIP\YSSSSPGSYTG\PPGGGGPP GTP\IMPSPGDS\TNSENMYTIMNPI GQGADRANFPLGPGPEGPMAA YG \GMEPHHVNGSLGSGDMDG\LPREF PQAPVAGLSNAPG\TPRDDGEMAA AGTFHAPSSQSE\NYSP\GMTMSRV NWAAAPGALCGPRLLRPCLRAK GLKVTPSGTLDLANQGLPMLGGP TRKTLTILLKTQGPRETFFSVWTLPA ICILVPERKALWGGPSSPGRQGGGA H
3456	8953	A	3725	65	210	ATRAGLIFDDSFEDVWQDASSFRL IFIVDGWHPELTPQQRRLPAI
3457	8954	A	3726	2548	3800	NSLILLFFFFRQRLTLECSGVISAH HNLHLPSSNS/P/ASAS*VAGITGM HRHAWPICIFLVETGFRHVGQAGLE LLTSGDPPAPTSQSM*ATTGLILL SKILFPFHSTKVFK*SCPS*KILKEEN CSVINEWFNNESSYTSKEKNNLVPN AC*ENTM*VATNCDF/SL*RSNY PKLFHNNETTSQIHLKIKISRPATS GQWILFSLVWWRARKG*GILMIHN GILY*TIC*IKLHRLP*GMDYPNQPD/ MKSGWDKRMSHTL*F*GKEIVDF QNQQNKLSTLYLSVQE**HEEFFFR DLKYNKPGSTIKSLVSF/HSLTLFFFF FFEARSHSASQAGVQWGNIGSLQPA PPGLKRSSYLSLLSSWDYRRVPPHP ANFCIFCR/GWGFVSPCCPGSSGTP VLKWRHLSLPNC

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3458	8955	A	3727	2	217	SSPSPPHPPASPPSSPSP/PASPPPSLP LPSPDFPPLSPCSSLSPFSSFSPPPSPP SPPFSRGPSPSDNFH
3459	8956	A	3728	25	396	ISGRSTFSLFSRQGLSALSPRLE/CSV AISAHCNLRPGSSN/GTTGA*HHTR LILYF/LAEMGFHHVGGAGFEVLT SNPPASASTSARITGMSNRT/GHLFN FHP*MCYKYRCGLAGRGGSRW
3460	8957	A	3729	80	460	YISLNVTTHLIFFFFLRQGL/CSVTO AGV\QWCNLGSLQPLPPRFK\NWDY RCVTPHLANFVFLVEMGF/LPASAS QSAGITGVSHCTQLGVFICICYGSSH GVRQSWHQFCSSKLLVKSGRVGVG LLG
3461	8958	A	3730	1	316	FFFFFETESHIVQAGVQWRDLSSL QPPPPRFKRFSSLSLPSSWDYRHVPP RPA\NFAFLVEMGFHHVGGAGLELL TPGDPSSASQSAGMTGVTHCAWP RCLMF
3462	8959	A	3731	3	1717	RPQTLKGHQEKIRQRQSILPPPGPA PIPASSTAAGIPRRPRIAWARR/WPLS EPGFRRRRESQEEPRAVLAQKIEKET QILNCALDDIEWFVARLQKAAEAF KQLNQKKGKKGKKAPEGVLT LRARPP/PEGEF\DCFKIKLAINLL AKLQKHQNPQRR/DVVHFLFGPLD LIVNTCSGPDIAHSVSCPLFSRDAVD FLRGHLVPKEMSLWESLGESWMRP RSEWPREPQVPLYVPKFHSGWEPPV DVLQEAPWEVEGLASAPIEEVSPVS RQSIRNSQKH/RPHFRAHPPGGCPY HQSAPHILTRGYQPTPAMAKYVKIL YDFTARNANELSVLKDEVLEVLED GRQWWKLRSRSGQAGYVP\GNILG EARPEDAGAPFEQAGQKYLGTQP DPQATPKLPGGT/IDELMQHMDEVN DELIRKINTTSRAQPQRHFRVERSQP VSQPLTYESG/PDEVRA/FLEAKAFS PRIVENLGILTGPFSLNKEELKKV CGEEGFRVYSLTMQK\AFLEKQQS GSELEELMNKFHSMNQRRGEDQLG PAALGWGLRRGSPPTMHGVFLYV YVFCIK
3463	8960	A	3732	1	324	
3464	8961	A	3733	1	581	MDKLLETYSLQRLSQEEIESLNRTI MSFKTKSVINTIPTKKSPGPDRLTAN FYQMCKEELADIIHGLCIRHEMTPV NPGVGQCCTSSYANRRPCFSSLVVD ETYVPPAFSDDKFIFHKDLCAQGV ALQTMKQEFNLNVKQKPQITEEQL EAVIADFSGLLEKCCQGQNVQVCF AEEGQKLISKTRALGV
3465	8962	A	3734	39	1935	LATMKWVESIFLIFLLNFTESRTLHR NEYGIASILDSYQCTAEISLADLATIF FAQFVQEATYKEVSKMVKDALTAI EKPTGDEQSSGCLENQLPAFLEELC HEKEILEKYGHSDCCSQSEGRHNC FLAHKKPTASIPLFQVPEPVTSCA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						YEEDRETFMKNKFIYEIARRHPFLYA PTILLWAARYDKIIPSCCKAENAVE CFQTKAATVTKELRESSLLNQHAC AVMKNFGTRTFQAITVTKLSQKFTK VNFTEIQKLVDVAHVHEHCCRGD VLDCLQDGEKIMSYICSQQDTLSNK ITECCKLTTLERGQCIIHAENDEKPE GLSPNLNRFLGDRDFNQFSSGEKNI FLASFVHEYSRRHPQLAVSVILRVA KGYQELLEKCFQTENPLECQDKGE EELQKYIRE\GQPWAKGSSGFSKK* GEYYLQTGSSLSLQQ*RPPQLTSSEL MAITRKMAATAATCCQLSEDKLLA\ CGEGAADIINGHLCIRHEMTPGKPL VFGQVPAPPSICPNRRPHASSTWVV DGNIWSPPCISLMTKFHFSP*RDPGG PSLQGW*ALAKPMKAKRFPSTLV KAKGPQIPGGNNSEAVIARFPQAWL EK\CCQ/GPQEQEVCFAQEGTK\LSK TRAALGV
3466	8963	A	3735	95	272	RALQPDTTWE*GSQRRPWLQVVTN KPVL*SKTSKS
3467	8964	B	3736	344	1420	MLLKTVLLLGHVAQVLMLDNGLL QTPPMGWLAWERFCNINCEDEPK NCISEQLFMEMADRMADQGWDRDM GYTYLNIDDCWIGGRDASGRLMPD PKRFPHGIPFLADYVHSLGLKLGIIY ADMGNFTCMGYPGTTLDKVVQDA QTFAEWKVDMLKLDGCFSTPEEAA QGYPKMAAGLNATGRPIAFSCSWP AYEGGLPPRVNYSLQADICNLWRN YDDIQDSWRSVLSILNWFVEHQDIL QPVAGPGHWNDPDMLLIGNFGLSL EQSRAQMALWTVLAAPLLMSTDLR TISAQNMDILQNPLMIKINQDPLGIQ GRRHKGSWMPKGSVPGCLRDPG TQDSQKGISHRSVHAASVQQG*
3468	8965	B	3737	49	2119	MALWTVLAAPLLMSTDLRTISAQN MDILQNPLMIKINQDPLGIQGRRIHK EKSLIEVYMRPLSNKASALVFFSCR TELCLIATTCLGQLNFTGSVIYEAQ DVLLS*
3469	8966	A	3738	139	536	QSLGFIPFRKRQRISISYTFYFETGS YSVAQAGVQWHNLGSLQPRPPGFK QSSCLSPPGSWDHWRAAPHQANFA LLVETGSPHAAQASLKLLSSSDPSA LASQSTGITGVSHHGQPYISHTLIIFI GKFY
3470	8967	A	3739	1	213	QFSCSLPSSRDYRHEQP/PLIFVFLV ETGFYHVQAGLELLTSGDPPALAS QSAEITGVSPRTRPNNLKS
3471	8968	B	3740	75	729	MEGTAGGERPSVVNGDSGKSGGVG DPREPLSCLQEGSGCHPTTESFEKSV REDASPLPHVCCCKQDALILQRLH HEDGSQHIGLLHPGDRGPDHEYLLV EEAERAMSEREARPNEESVQRNRLI CRTNPYRIFEYLPISLEEAFFLVYAL GCLSIYYEKEPLTIVKLWKAFTVVQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PTFRTTYMAYHYFRSKGWVPKVG KYGTDLLLYRKGPFFYHAX*
3472	8969	A	3741	1	2649	
3473	8970	A	3742	41	656	PVPRPCCGLRARSWPSSPRAARAAL PHGESALSRLRLALLAARASLDLCL FAFSSPQLGRAVQLLHQRGVVRV VTDCDYMALNGSQIGLLRKAGIQV RHDQDPGYMHKFAIVDRRVLITG SLNWTQTQAIQNNRENVLITEDDEYV RLFLEEFERIWEQFNPTKYTFPPKK SHGSCAPPVSRAGGRLLSWHRTCG TSSESQT
3474	8971	A	3743	3	267	FNMESQSLASLKCSGAVSAHCNLCF LGSSNSPASASRVSGITGVLYHTWLI FVFLVQTGFHHVQGAGLELL/NLVI HPPRPPKVLGLQA
3475	8972	A	3744	2	430	FFFETGGAFVTQAGVQWPNLSSLOP SPPGFKPSSHLSPSTWDYRYTPPCP ASFCIFVTDGTFCHVDQAGLELLASC NLPASASRSAGITGVSHHACPFLLFS FFKSGITSPNYPISHHEIESNVAPVF LFEDSTAIYVYYF
3476	8973	A	3745	2	316	EFLFFETEFCSVTRLECSGAISAHCK LCLLGSRRHSPASASRVARTTGTRHH AQRIFVFSVETGFHRVSRDGLDL/ NLVIHPPQPPKVLGIRGREPPCPACF FAF
3477	8974	A	3746	1	1053	
3478	8975	A	3747	1	3011	SLQRLPGLMHNLTQFLLDGNFLQSL PAELENMKQLSYLGLSFNEFTDIPE VLEKLTAVDKLCMSGNCVETRLRQ ALRKMPHIKHVDLRLNVIRKLIAD VDFLQHVTQLDLRDNKLGDLAMI FNNIEVLHCERNQLVTLDCGYFLK ALYASSNELVQLDVYPVPNYLSYM DVSRRNLAVPEWVVCESRKLGSF GILGHNVICELPARLFCNSSLRKL GQGHNVQLARLPERLERTSVEVLDV QHNQLELPPNLLMKADSLRFLNAS ANKLESPPATLSEETNSILQELYLT NNSLTDKCVPLLTGHPHLKILHMA YNRLQSFPASKMAKLEEEIDLSG NKLKAIPPTIMNCRRMHTVIAHSNC HRGPFPEVMQLPÆIKCVD\LSCNE\ LSEVTLPAENLSPNCRSLDLTGNPR PCPLITKPLELLNNIRCFKID\QPSTG DG\SGAPAVWSHG\YTEA\SGVKNK LCV\VALSVNNFCDNREALYGVFD GDRNVEVPYLLQCTMSDILAEELQ KKTKEEEYMVNTFIVMQRKLGTA GQKLGGAAVLCHIKHDPVDPGGSF TLTSANVGKCQTVLCRNGKPLPLSR SYIMSCEEELKRIKQHKAITEDGKV NGVTESTRILGYTFLHPSVVP RPHV QSVLLTPQDEFFILGSKGLWDSLSV EEAVEAVRNVPDALAAAKKLCTLA QSYGCHDSISAVVVQLSVTEDSFCC CELSAGGAVPPPSPGIFPPSVNMVIK

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						DRPSDGLGVPSSSSGMASEISSELST SEMSSEVGSTASDEPPPG\ALSENSP\ AYPSEQRCLHPIWLSNSFQRQLSS ATFSSAFSDNGLSDSDDEPIEGVFTN GRRVEVEVDIHCSRATEKEKQQHL LQVPSEASDEGIVISANEDEPGLPRK ADFSAVGTIGRRRANGSVAPQERSH NVIEVATDAPLRKPGGYFAAPAQPD PDDQFIIPPELEEEVKEIMKHHQEQQ QQQQPPPPQLQPQLPRHYQLDQLP DYYDTPL
3479	8976	A	3748	1	246	LPTLECSGMISAHCNLRPLGSSDSP\ ASASQVAGITSAHHYAWLVFVFSV EMGFHHVGQGWRSRLDLVIRPPQPP KMLGLQA
3480	8977	A	3749	153	527	LLVFYLP TSLKGGRLQDMSLLCQ LYSLYESIQEYKGACQAASSPNWTY ALENGFFDEEEYFPEQNSLHRRD RGPPRDLSLP\APPSPAATGFWSPSR GSWEGCDCWEALPTGHA VI CCFS
3481	8978	A	3750	2	377	IPAASTFFCFLRQSLTLWPHAGVQW CGLSSLHPPPGFMLFSCLSLPSSWD YRRPPRPAKFSVFLVETGFHRVSQ DGLDLMTS\DPALASQSAGITGVS HCTRPKEAYFYFLALDPRCKDGV R
3482	8979	A	3751	2	294	LFLHADRLEYSGMTISHLQPQTGA QGDPLTSSLPREVGLQ/CVCHHTQL FFF/CIFVETESHHLA\RAGLKLLGSS DPTASPSQSDGITGMSHHSCPSTF
3483	8980	A	3752	80	267	RQGLTILPRLVLNSC/RLKLSSHLSLP KYWDYRQEPPCLAISIIFFKKS LIYY LNLAILYFKCK
3484	8981	A	3753	1	972	
3485	8982	A	3754	1	283	PKPOEIELPEAKNR\PWIFNKILGTTV KLMELKPNTCYCLSVRAANTAGVG KWCKPYKVSPGKRGALGVERS PKP REPGLWRLGTPLCPHDSSG
3486	8983	B	3755	346	472	XRNMNILQYCPSSDMWTLFETCDV HIRKQQMVSVEETIYIVGG*
3487	8984	A	3756	1	1346	MSAEEMVQIRLEDRCYPVSKRKLIE QSDYFRALYRSGMREALSQEAGGP EVQQLRGLSAPGLRLVLD FINAGGA REGWLLGPRGEKGGGVDEDEEMD EVSLSELVEAASFLQVTSLLQLLLS QVRLNNCLEMYRLAQVYGLPDLQE ACLRFMVVHFHEVLCKPQFHLLGS PPQAPGDVSLKQRLREARMTGTPV LVALGDFLGGPLAPHYQGEPPSML RYEEMTERWFPLANNLPDLVNVR GYGSAILDNYLFIVGGYRITSQEISA AHFLQGP/RTNEWLQVASMNQKRS NFKLVAVNSKLYAIGGQAVSNVEC YNPEQDAWNFVAPLPNPLAEFSAC ECKGKIYVIGGYSTRDRNMNILQYC PSSDMWTLFETCDVHIRKQQMVS EETIYIVGGCLHEIRGPNRRSSQSED MLTVQSYNTVTRQWLYLKENTSKS

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						GLNFDLCAP
3488	8985	A	3757	3	358	TNSMPPMMSMSYRICAMLKGE/DV QALRRAHQRNVKHMQRLLMDRGL PCHPLPPANINPIRVR/DPHPCPIALS HPIYSWSLTLPNKPTSVAVFNILLS CLTIPFIASFVSLFEKLSAILD
3489	8986	A	3758	1	164	GSTTPAMEFASLFKKILLIDCRD/RG LALLPRLVLSSWPQVIFLPWPPKFL GLRT
3490	8987	A	3759	3	280	FFFETESHSA\RLRYRGTLAHCILC RQGSSNSPASDPQVAGTTGTRHRA QLTFVFLVQMGFHHFGQAGLELPN LGIHPTSASPKCWDLPA
3491	8988	A	3760	3	516	AQHQPMMNIFYPVGVHAPLMNIQR NPFNIHPQLPLHLHTGVPLMQVATP TSVSQGLPPPPPPPSQQVNYIASQ PRWKRNCTKLQIQEKAAQEVKLA KPFYQNKDITKEEYKEIVRKA VDKV CHSKSGEVNSTKVGNLVKAYVDQ YEYSRKGSRKLEWGPVSTGKN
3492	8989	A	3761	173	411	
3493	8990	A	3762	438	789	LTWSTPVLPAPTAAP\GKYGNFGQG PSSGNTSSSSHSQRPLMAAVKLAES KVSVAVEASADSSKTDKKLQIQEK AAQEVKLAIKPFYQNKDITKEEYKE IVRKA VDKCVLLECSIQKM
3494	8991	A	3763	1097	4669	ILLGTSCGYALAHTQEGEEKKQTS GTSNTRGSRKPAMTTPTRRSTRNT RAETASQSQRSPISDMSGCDAPGNS NPSLSVPSSAESEKQTRQAPKRKSV RRGRKPPLLKKKLRSVAAPKSSS NDSVDEETAESDTPVLEKEHQPDV DSSNICTVQTHVENQSANCLKSCNE QIEESEKHTANYDTEERVGSSSESC AQDLPLVLVGEEGEVKKLENTGIEA NVLCESEISENILEKGGDPLEKQDQ ISGLSQSEVKT D VCTVHLPNDFPTC LTSESKVYQPVSCPLSDLSENVESV VNEEKITESSLVEITEHKDFLKTTEE LIESPKLESSEGEIIQTVDRQSVKSPE VQLLGHVETEDVEIATCDTFGNED FNNIQDSENNLLKNNLLNTKLEKSL EEKNESL TEHPRSTELPKTHIEQIQK HFSEDNNEMIPMECDSDQNESE VEPSVNADLKQMNENSVTHCSENN MPSSDLADEKVETVSQPSSEPKDTI DKTKKPRTRRSRHFSPSTTWSPNKD TPQEKKRQSPSPRRETGKESRKSQ SPSPKNESARGRKKRSQSPKKDIA RERRQSQRSPKRD TTRESRRSELS PRRETSRENKRSQPRVKDSSPGEKS RSQSRERESDRDGQRRERERRTRK WSRSRSHSRSPSRCTKSKSSSFGRI DRDSYSPRWKGRWANDGWRCPRG NDRYRKNDPEKQENETRKEKNDIH LDADDPNSADKHRNDPCPNWITEKI NSGPDPRTRNPEKLKESHWEENRN ENSGNSWNKNFGSGWVSNRGRGR

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						GNRGRGTYRSSFAYKDQENNRWQ NRKPLSGNSNSSGSESKFVEQQSY KRKSEQEFSFDTPADRSGWTSASSW AVRKTLPAADVQNYYSRRGRNSSGP QSGWMKQEEETSGQDSSLKDQTNQ QVDGSQLPINMMQPMNVMQQQM NAQHQP MNIFYPVGVHAPLMNIQ RNPFNHQPQLPLHLHTGVPLMQVAT PTSVSQGLPPPPPPPPPSQQVNYIAS QPDGKQLQGIPSSSHVSNMSTPVL PAPTAAPGNTGMVQGPSSGNTSSSS HSKASNAACKNWQKGKVSVAVEA SA\YSSKTDKKFAKFQEKAAQVVKI WA\KPFYQNKDITKEEYKEIVRKA VDKVCHSKSGEVNSTKA\ANLVKA YVDKYKYSRKGLKKTLEPRVTE KDLG
3495	8992	A	3764	108	253	
3496	8993	A	3765	2	283	RRLFFFETESRSVSRLECSG\ISAHC NLH/LPGSSNSPGSASRVAGITGACH HAQLIF/VFLVETGFHHVQGAGLEL L/NLMICPPQPPKVLGLQA
3497	8994	A	3766	1	290	RSTFFFFLERVYCSVTRLECSGTMS AHCNRLPGSSGSHASVSQVAGITG AHHHTQPIFVFLVETGFHHIGQAGL ELL/NLMIHPPRPPKVLGLQV
3498	8995	A	3767	234	1449	EPGTHDPHLFLQGLFWQAGGGEG GDGTGPAGGRQICVPPAALAHVRV PGEFLAQVAAAA*AIHDEQRPGLKH HPPG/ELMQRGVASESYMIVAPPMP SSWSSSGTNGPPSPTNLT*PIVHFIFS AFTP/TKKTTTNTAMKTATHIPDVQ SAFCSPHSGTQRGDGLGKRKRGRG RTWERRRRVSIETSTCFRPGCERLG AAAGANLSQLASSQRPLRERWVLY TIIMAAAGAPDGMEEPGMDTEAET VATEAPARPVNCLAEAAAAGAAAE DSGAARGSLQAPAPQPPGDPAQA SVSNGEDAGGGAGRELVDLKIIWN KTKHDVKFPLDSTGSELKQKIHISIT GIPPDESPRRGGPAGPYQQSQRLEL YAQATEALLKTGAAYPCFCSPQRLE LLKKEALRNHQTPR
3499	8996	A	3768	1	8157	
3500	8997	A	3769	1126	1355	
3501	8998	A	3770	1	1611	MGSRCNPPPPAHSDTTGKDSFGNI RGAETGQGASACSVTSARVTCGAG SEPHSHRNPGISAQVGLAPSYGAAR GRRRPLALQQSPQERRHVGWNSTR GLLPASLPGTASSQSASATASAALP LKVTGPLARNPTPPWTAAAALATR GQRPEKGLFPGPAPFSLGKRKRGRG RTWERRRRVSIETSTCFRPGCERLG AAAGANLSQLASSQRPLRERWVLY TIIMAAAGAPDGMEEPGMDTEAET VATEAPARPVNCLAEAAAAGAAAE DSGAARGSLQAPAPQPPGDPAQA SVSNGEDAGGGAGRELVDLKIIWN

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						KTKHDKVFPDSTGSELKQKIHSIT GLPPAMQKVMYKGLVPEDKTLREI KVTSGAKIMVVGSTINDVLAVENTP KDAAQQDAKAEENKKEPLCRQKQ HRKVLDKGKPEDVMPSVKGAQERL PTVPLSGMYNKSGGKVRLTFKLEQ DQLWIGTKNGTEKLPMSIKNVVVS DPIEGHEDYHNDGRFQLAPTEA\SY YWVYWVPTQYVDAIK\DTVLGKW QYF
3502	8999	A	3771	482	631	AGGWGPQAPDTPWVGPAQAGRL HPLRSTKRS/MSVPATRTTVPLTVM Q*RRVCRWCWGPLGHWEAHGFLV SGDVNHFGGPAALLL
3503	9000	A	3772	1	1579	
3504	9001	A	3773	3	486	DRYMLTRDYLTVKVDNLNMEARP IETYQVHDYLRSLCSLYENDCIFD KFECWNGSDSVIMTGAYNNFFRM FDRNTKRDVTL\EASRESSKPRAVL K\PRRVCVGG\KRRRDDISVGQLGTF TKKIL\HTAWHPAE\NIHLPFAATNN LLHLSRGKVNDSMH
3505	9002	A	3774	72	1317	KLLPAPRQPPRPTNGSPRDPTPAQV* VEAPAGSSQ*TAP/ARRPLRAARTLP AAEAAGLTLRGCFHGDGRACAAL RRWPWRQLRGWGFVPAPPLLRTP AELVG/RSPEPRCPGKVSMAEFLTEF LEIPPFNKQYTESQLRAGAGYILED NEAQVDVLESQFSQLLHQINSTRDF ESIRLAHDHFLSNLLAQSFILLKPSP VEEKSEPQDFQEADSWGDTKRTPG VGKEDAAEETVKPGPEEGTLEKEE KVPPRSPQAQAPVNIDEGLTGCTI QLLPAQDKAIVFEIMEAGEPTGPILG AEALPGGLRTLPOEPGKPKDEVLR YPDRSLSPEDAESLSVLSVSPDTAN QEPTPKSPCGLTEQYLHKDRWPEVS PEDTQSLSLSEESPSKETSLDVSSKQ LSPKALAPFQLGN
3506	9003	A	3775	1	350	FGTRKPGAVGAGEFVSPCESGNT GEPSALEEQRGPLPLNKTFLGYAF LLTMATTSDKLASRSKLPDGPTGSS EEEEEFLEIPPFNKQYQESQLRAGA GYILKEFKEAQVRSFFV
3507	9004	A	3776	3	318	RRGLTLSSRLEYSGLIKTHWNHLHL GSSNPPTSASQVAGTTGTCHHAQLN FF/CLTFLVATRSHDIAQAGLELLDS SHPPASASHSAGTTGVNHHAHPAV ALLWIN
3508	9005	A	3777	4	378	ARNHHDLCFKKAILFFEMESCSVSQ AGVQWRVFGSLQAPPGFLPFS/CY RCQPPSPANFFLYFLVETGFLF**RQ GFTVLD RMVSI*PRDPPALASQSA GITGVSPRTRQEGHS*R*EENGIG
3509	9006	A	3778	19	418	VEMGFCQADQAGLELLTSGDPPAS VSQSTGITVLSLSFFFETESRSVAQA GVQWRDLGSLQRPPPGFTPFSCLSL PSSWDYRRPPRLANFFVFSVETGF

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						HRVSQDGLDLLT/S/GDPPASASQSA GDTGVSQAPV
3510	9007	A	3779	3	331	CFIFYFILFYFETESRSVAQAGVQWR HLDSLQAPPPGFTPFSCSLPSSWDY RRP/PPRPANFFVLLVQTGFHRVSQD GLDLLT/S/GDPLASASQSAGITGLSH RARPAQVS
3511	9008	A	3780	659	1092	AYNIFQFANRTNTGENLPKTLVIKYY SSTFRSFFFFFFLQRSSVAQAGVQ WRNLGSLQPPPPGFTPFSCSLPSSW DYGRPPRPANF/SVFLVETGFHRVS QDGLDLLT/S/GDPPTSASQSAGITG VSHCARPHSVLIKEITQT
3512	9009	A	3781	8	295	GRVSLRHQAGVQWRSLGSLQAPPP RFTPFSCSLLRSDWHRPPRPANL LYFLVETGFHRVRQDGLDLLT/S/GD PPALASQSAGITGVSHRAHPTY
3513	9010	A	3782	1474	1870	SARGITGVSHCTRPFSFFFFFFFETE SHSIAQAGVQWRYLGSLOPLPPGFK QFACLSLSSSWDCRHAPRPANFL/F LVEMGFHHL*LELLISSDPPASAFKS ARITGVSHRAWPIRFLLKNIFKFLN FC
3514	9011	A	3783	60	560	SDNYEKSHNIQEMTGLQSTLLVNN RVQLNFKWELNFFLSFLKQSSTLVA QAGVQWHDLGSLQPPPGVKRFSC LSLPSSWDYRHVPPCLANFVFLFFL VETGFLHVGQAGPELLTSGGPASA SQSAGITSVTHRPLPEDSAFYQCRL NLWQRSPLECRCSLVLKT
3515	9012	A	3784	3	230	FFFKTESRSVTRLECSGAVLAHCNL QLPGSSNSPASASRVAGITRHVPPH/ RLIFVFLVETGFHHVGQDGLDLLTL
3516	9013	A	3785	3	4117	
3517	9014	A	3786	1	457	FPVRNLDLSTYICIGQKEEQLPSEYEL YADINHYGGMIGGHYTACAPLPND RSSQRNDVGWRLFDDSTLTTRDQS QAVTRYAYVLFYRRRNSPVERPPK AGHSEHHPDLGPAEAAASQ/ATRP WPGPRGG/APRGQPLNASPPLWIGQ TPPLKQT
3518	9015	A	3787	1	298	NNQESCSVTEAGVQWHDLGSLQPP PSGFKQFS/CAQLLSSQDHRHMPPCP ANFYVFLIAEMGFYHVSQAGLELL TSSDLPALASQSAGIIGVSHRAWAK
3519	9016	A	3788	3	286	FFFFLFETQSHSHIRLECSGVISDYC NLCLPSSSDSLVLASGVAGTMGVR HNARLIFVFLVKMRFHVGPRLGP QIPWTGIWIPSHFGPPQSA
3520	9017	A	3789	1	1422	
3521	9018	A	3790	353	470	IPGVSLYSLFSLAQNPQSTEILKKL MTTNEIQSNIYT
3522	9019	A	3791	1328	1615	VSLFHAGVQWCDLSSLQPPPPGFKR FS/RLNLLSSWDYRRPLPHSTFCKF/ VEMGFHHIGQAGLKLLTSGDPPASA SQSARITGVSHRARNCFYVT
3523	9020	A	3792	2	114	CQPGFVMKGPPHVRVQCQALNKWE

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						TELPSCSR\VCLEPA
3524	9021	A	3794	1940	2062	
3525	9022	A	3795	785	892	
3526	9023	A	3796	1	2745	
3527	9024	A	3797	1	3297	
3528	9025	A	3798	1	2202	
3529	9026	A	3799	1	2868	
3530	9027	A	3800	1	3237	
3531	9028	A	3801	1	2001	
3532	9029	A	3802	1	2982	
3533	9030	A	3803	1169	3269	VHCRFWILALCQMSRLQKSPLLFNI VLEVLAKAIKQEKEIKGIQLGKEEV KLSLFADDMIVYLENPTVSAQNLLK LMSNFSKVSQYKINVQKSQAFLYT NNRQTESQIMSGLPFTITSKRITYLGI QLTRDVKDLFKENYKPLLKEIKEDT NKWKNIPCSWVGGRINLVKMAILP KVIYRFNAIPIKLPMTFFTELEKTTL KFIWNQKRALIAKSSLSQKNKTGGI TLPDFKLYYKATVTKTSWYQYQN RDIDQWNRTEPSEIMPHIYNYLIFDK PDKNKQWGKDSL FNKWCWENWL AICRKLKLDPFLTPYTKINSR WIKDL HVRPKTIKTLEENLGNTIQDIGMGK DFMSKTPKAMATKAKIDKWDLIK KSFCTAKETTIRVNRQPTWEKIFA TYSSDKGLISRIYNELKQIYKKKTN NPIKKWAKDMNRHFSEEDIYAACK HMKKCSSLAIREMQIKTTMRYHLT PVRMVIIKKSGNNRCWRGCEIGTL LHCWWDCKLVQPLWKS VWQFLRD LELEIPFDPAIPLLGIPEDYKPCCYK DTCTRMFIAALFTIAKTWNQPKCPT MIDGIKKMWHIYTM EYAAIKKDE FMSFAGTWMKLEIILRKLSQGQK TKHRMYSLIGGNLTMRFTGHSAGS HHTPGPIMRCGAGGGIALGEIPNVN DELMGTANQHGTCIPMQQNCTLCT CTLKLV
3534	9031	A	3804	2821	5793	
3535	9032	A	3805	2	256	KRSLSLPSRLECSGVILAHCKLRLLG SRHSPPSDSGAAGTAGARHHARLFF LYFLVFHRVCLDGLDLL/NLVIHLPR SPK VWGLQA
3536	9033	A	3806	1	2406	
3537	9034	A	3807	139	6503	
3538	9035	A	3808	1	3204	
3539	9036	A	3809	77	277	PHPTPCSCFPFWSASSPLT*THQALT EEDEW*QAKNSGQAAQGQTPALPL GNLGQVTAPLCPRFIC
3540	9037	B	3810	21	219	MMPRSSRTKSCRSSCVAWSSCMKE NKELRAEAERLGHELQQAGLKTK AEQTCRHLTAQVRS LGGT*
3541	9038	A	3811	1	6359	MTLHATRGAALLSWVNSLHVADP VEAVLQLQDCSIFIKIIDRIHGTEEGQ QILKQPVSERLDFVCSFLQKNRKHP SSPECLVSAQKVLEGSELELAKMT

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						MLLLYHSTMSSKSPRDWEQFEYKI QAELAVILKFVLDHEDGLNLNEDLE NFLQKAPVPSTCSSTFPEELSPPSHQ AKREIRFLELQKVASSSSGNNFLSGS PASPMGDILQTPQFQMRRLKKQLA DERSNRDELELELAENRKLLETEKDA QIAMMQQRIDRLALLNEKQAASPL EPKELEELRDKNESLTMRLHETLQK CQDLKTEKSQMDRKINQLSEENGD LSFKLREFASHLQQLQDALNELTEE HSKATQEWLEKQAQLEKELSAALQ DKKCLEEKNEILQGKLSQLEEHLSSQ LQDNPPQEKGEVLGDVQLQLETLKQ EAATLAANNNTQLQARVEMLETERG QQEAKLLAERGFEEEEKQQLSSLIT DLQSSISNLSQAKEELEQASQAHGA RLTAQVASLTSELTTLNATIQQQDQ ELAGLKQQAQEKQAQLAQTLQQQE QASQGLRHQVEQLSSSLKQKEQQL KEVAEKQEATRODHAQQLATAAEE REASLRERDAALKQLEALEKEKAA KLEILQQQLQVANEARDSAQTSVT QAQREKAELSRKVEELQACVETAR QEQHEAQAQVAEELQLRSEQQKA TEKERV AQEKDQLQEQLQALKESL KVTKGSLEEEKRRAADALEEQQRCI SELKAETRSLVEQHKRERKELEER AGRKGLEARLQQLGEAHQAETEVL RRELAEAMAAQHTAESECEQLVKE VAAWRERYEDSQQEEAQYGAMFQ EQLMTLKEECEKARQELQEAKEKV AGIESHSELQISRQNELAELHANL ARALQQVQEKEVRAQKLADDLSTL QEKMAATSKEVARLETIVRKAGEQ QETASRELVKEPARAGDRQPEWLE EQQGRQFCSTQAALQAMERAEQ MGNELERLRAALMESQGGQQEERG QQEREVARLTQERGRAQADLALEK AARAELEMRLQNALNEQRVEFATL QEALAHALTEKEGKDQELAKLRGL EAAQIKELEELRQTVKQLKEQLAK KEKEHASGSGAQSEAAGRTEPTGP KLEALRAEVSKLEQQCQKQEQEAD SLERSLEAERASRAERDSALETQOG QLEKAQELGHSQSALASARELA AFRTKVQDHSCAEDEWKAQVARG RQEAERKNSLISSLEEEVSILNRQVL EKEGESKELKRLVMAESEKSQKLEE RLRLLQAETASNSARAAERSSALR EEVQSLREEAEKQRVASENLRQELT SQAERAEELGQELKAWQEKFFQKE QALSTLQLEHTSTQALVSELLSAKH LCQQQLQAEQAAAEKRHREELEHSK QAAGGLRAELLRAQRELGELIPLRQ KVAEQERTAQQLRAEKASYAEQLS MLKKAHGLLAENRWLGERANLG RQFLEVELDQAREKYVQELAAVRA DADTRLAEVQREAQSTARELEVMT

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AKYEGAKVKVLEERQRFQEERQKL TAQVEQLEVFQREQTKQVEELSKK LADSDQASKVQQQKLKAVQAQGG ESQQEAQRLQAQLNELQAQLSQKE QAAEHYKLQMEKAKTHYDAKKQQ NQELQEQLRSLEQLQKENKELRAE AERLGHELQQA GLKTKEVAEQ\TCR HLYLPRLRSLEVAQ\VAHARPSSFRD LGKFQVATDALKSREPQAKPQLDL SIDLSDLSC EEGTPLSITSKLPRTPD GTSVPGEPASPIQRLPPKVESLESL YFTPIPARSQAPLESSLDSLGDVFD SGRKTRSARRRTTQIINITMTKKLD VEEPDSANSSFYSTRSAPASQASLR ATSTQSLARLGSPDYGNSALLSLP GYRPTTRSSARRSQAGVSSGAPPGR NSFYMGTCQDEPEQLDDWNRIAEL QQRNRVCPPHLKTCYPLESRPSLSL GTITDEEMKTGDPQETLRRASMQPI QIAEGTGITTRQQRKRVSLPHQGP GTPESKKATSCFPRPMTPRDRHEGR KQSTTEAQKKAAPASTKQADRRQS MAFSILNTPKKLGNSLLRRGASKKA LSKASPNTSRGTRRSPIATTTASAA TAAAGATPRAKGKAKH
3542	9039	A	3812	241	6884	LSGITKMTLHATRGAALLSWVNSL HVADPVEAVLQLQDCSIFIKIIDRIH GTEEGQILKQPVSERLDFVCSFLQ KNRKHPSSPECLVSAQKVLEGSELE LAKMTMLLLYHSTMSSKSPRDWEQ FEYKIQAEALAVILKFVLDHEDGLNL NEDLENFLQKAPVPSTCSSTFPEELS PPSHQAKREIRFLELQKVASSSSGN NFLSGSPASPMGDILQTPQFQMRRL KKQLADERSNRDELELELAENRKL LTEKDAQIAMMQQRIDRLALLNEK QAASPLEPKELEELRDKNESLTMRL HETLKQCQDLKTEKSQMDRKINQL SEENGDL SFKLREFASHLQQLQDAL NELTEEHSKATQEWLEKQAQLEKE LSAAALQDKKCLEEKNEILQGKLSQL EEHLSQLQDNPPQEKGEVLGDVLQ LETLKQEAATLAANNTQLQARVEM LETERGQQEAKLLAERGHFEEEEKQ QLSSLITDLQSSISNLSQAKEELEQA SQAHGARLTAQVASLTSELTTLNAT IQQQDQELAGLKQQAQKEKQAQLAQ TLQQQEASQGLRHQVEQLSSSLK QKEQQLKEVAEKQEATRQDHAQQ LATAAEEREASLRERDAALKQLEA LEKEKAAKLEILQQQLQVANEARD SAQTSVTQAQREKAELS R KVEELQ ACVETARQEQHEAQAQVAEELQL RSEQQKATEKERV AQEKDQLQEQL QALKESLKVTKGSLEEEKRRADA LEEQQR CISELKAETRSLVEQHKRE RKELEEEERAGRKGLEARLLQLGEA HQAETEVLRRLEAEAMAAQHTAES

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						<p> ECEQLVKEVAAWRDGYEDSQEE AQYGAMFQEQLMTLKEECEKARQ ELQEAKEKVAGIESHSELQISRQON KLAELHANLALALQQVQEKEVRAQ KLADDLSTLQEKMAATSKEVARLE TLVRKAGEQQETASRELVKEPARA GDRQPEWLEEQQGRQFCSTQAALQ AMEREAEQMGNELERLRAALMES QGQQQEERGQQEREVARLTQERGR AQADLALEKAARAELEMRLQNAL NEQRVEFATLQEALAHALTEKEGK DQELAKLRGLEAAQIKELEELRQTV KQLKEQLAKKEKEHASGSGAQSEA AGRTEPTGPKLEALRAEVSKLEQQC QKQQEQADSLERSLEAERASRAER DSALETLQGQLEEKAEQELGHSQSAL ASAQRELAAFRTKVQDHKAEDW KAQVARGRQEAERKNSLISSLEEV SILNRQVLEKEGESKELKRLVMAES EKSQKLEE/RLRLQAETASNSARA AERSALREEVQSLREVEAEKQ RVA SENLRQELTSQAERAEELGQELKA WQEKFFQKEQALSTLQLEHTSTQA LVSELLPAKHLCCQLQAEQAAAEK RHREELEQSKQAAGGLRAELLRAQ RELGELIPLRQKVAEQERTAQQRLA EKASYAEQLSMLKKAHGLLAEENR GLGERANLGRQFLEVELDQAREKY VQELAAVRADAETRLAEVQREAQS TARELEVMTAKYEGAKVKVLEERQ RFQEERQKLTAQVEELSKKLADSD QASKVQQQKLKAVQAQGGESQQE AQRFAQLNELQAQLSQKEQAAEH YKLQMEKAKTHYDAKKQQNQELQ EQLRSLEQLQKENKELRAEAERLG HELQQAAGLKTKEAEQTCRHLTAQV RSLEAQVAHADQQLRDLGKFQVAT DALKSREPQAK\PQLDLSIDSLDLSC EEG\TPL\SITSKLPRTQPDGTSVPGE PASPISQRLPPKVESLESYFTPIPAR SQAPLESSLDSLGDVFL\DSGRKTR SARRRTTQIINI\TMTKKLDV\EEPDI SAPNLSFYS\TRSAPASQASLRATSS TQSLARLGSPDYGNSALLSLPGYRP TTRSSARRSQAGVSSGAPPGRNSFY MGTCQDEPEQLDDWNRIAEQQRN RVCPPHLKTCYPLESRPSLSLGTITD EEMKTGDPQETLRRASMQPIQIAE GT\GITTRQQRKRVSLEPHQGPPTPE SKKATS\CFPRPMTPRDRHEGRKQS TTEAQK\KAAPASTKQA\DRRQSM\ AFSILNTPKKLGNSLLRTG*PQRKA LSK\ASPNTSRG\TRRSRPIATTTASA ATAAAAIGCHPSRPRGKGKALKGPV PVSGPHLCSPMVAVTWSSAYCPSQ CLLSAPRPTVAKPLETVMPARTLA WSLVLHWRLLGAGPGGLEHGQCG RSPYLASFLLKAKSLLHHNQI </p>

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3543	9040	A	3813	1	3466	EKEKAAKLEILQQQLQVANEARDS AQTSVTQAQREKAELSRKVEELQA CVETARQEQHEAQAQVAEELQLR SEQQKATEKERV AQEKDQLQEQQLQ ALKESLKVTKGSLEEEKRRAADAL EEQQRCSISELKAETRSLEQHKRER KELEEERAGRKGLEARLQQLGEAH QAETEVLRRELAEAMAAQHTAESE CEQLVKEVAAWRERYEDSQEEAQ YGAMFQEQMLTLKEECEKARQELQ EAKEKVAGIESHSELQISRQONELA ELHANLARALQQVQEKEVRAQKLA DDLSTLQEKMAATSKEVARLETLV RKAGEQQETASRELVKEPARAGDR QPEWLEEQQGRQFCSTQAALQAME REAEQMGNELERLRAALMESQGGQ QEERGQQEREVARLTQERGRAQAD LALEKAAAELEMRLQNALNEQRV EFATLQEALAHALTEKEGKDQELA KLRGLEAAQIKELEELRQTVKQLKE QLAKKEKEHASGSGAQSEAAGRTE PTGPKLEALRAEVSKLEQQCQKQQ EQADSLERSLEAERASRAERDSALE TLQGQLEEKAEQELGHSQSALASQ RELAAFRTKVQDHSTAEDWKAQV ARRRQEAERKNSLITILEEEVSILNR QVLEKEGESKELKRLVMAESEKSQ KLEERLRLQAEASNSARAAERSS ALREEVQSLREEAEKQRVASENLR QELTSQAERAELGQELKAWQEKF FQKEQALSTLQLEHTSTQALVSELL PAKHLCCQQLQAEQAAAERHREEL EQSKQAAGGLRAELLRAQRELGELI PLRQKVA\EQERTAQQRLAEKASYA EQLSMLKKAHGLLAEENRGLGERA NLGRQFLEVELDQAREKYVQELAA VRADAETRLAEVQREAQSTARELE VMTAKYEGAKVKVLEERQRFQEER QKLTAQVEQLEVFQREQTQVEEL SKKLADSDQASKVQQQKLKAVQA QGGESQQAQRLQAQLNELQAQLS QKEQAAEHYKLQMEKAK'THYDAK KQONQELQELRTLEQLQKENKEL RAEAERLGHELQQAGLKTKEAEQT CRHLTAQVRTLEAQVAHADQQLRD LGKFQVATDALKSREPQAKPQLDL SIDSLLDSCEEGLPLSITRSGGSLPPY VCLWSACCLSGCILVR
3544	9041	A	3814	35	266	
3545	9042	C	3815	383	628	MDPSAGVTIVTCLASLFSGRVLRFR CSHDWRNYTERVLLFQWVELKTKC WRHTEAGLKPSHYFLEKMKKTLRE SQATYDRI*
3546	9043	A	3816	2	513	DIYGGDYERFGLQGS AVASSFGNM MSKEKRDSISKEDLARATLVITITNNI GSTA\WLCALNENIDRVVFGNFLR INMVSMKLLAYAMDFWSKGQLKA LFF/VEHQGYLGAVGALLGTVQND

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						LMTSRRRGSGRETASQKGQRTKKL LLEKVKVALGRKPShLWQMNLGFC
3547	9044	A	3817	29	175	KSRPGTVAHACNPSTLGSRGGRIP AQEFKTSLGNTVSE\PCLYLRKNN
3548	9045	A	3818	171	419	KFFPFQSLWWERRAFPLKGEDMAA LLCQDEKKDQVERSSTAFHGEIFGT SVPENG\HHPKKQSDGMEEYKTFGL GLTNVKKNR
3549	9046	A	3819	2	1209	WPSKETAFNLTTQMPCLQSASTWS SYEHNSSESYLLREHVSELDSSFHSV LSLPSDVPLHFHFTLLKTEIKGNL AENKFVDEYIISPSVHSTLNQWRN GYSPICKPQIRSESSAQLLQGRKKRH LSETALGERTKL\KEFDHFHTESGSH SNFTAVSNVNVLSRIQNSSRNTARR RLRSESSYDINDNIV\IPMSL\VAPAK LEKLQYKEILTPSWRMVVLQPLDE YNLGKEEIEDLSDEVFSLRHKKYEE REQARWSLWEQSKWHRRNSRAYS KNVEGQDLLLKEYPNNFSSSQCA AASPPGLPSENQDLCAAYGLPSLNQS QETKSLWWERRAFPLKGEDMAALL CQDEKKDQVERSSTAFHGEIFGT PENGHHPKKQSDGMEEYKTFGLGL TNVKKNR
3550	9047	A	3820	7	447	
3551	9048	A	3821	1	373	EQQVLRSTCLGVGAKV/L\VEGMVL QYSTQKGILT/ENHIQEINAQ/TTGLR /KTMLLLDILPSRGPKAFDT/FLDSLQ EFPWVREKLKKAREEAMTDLPAGL EEKGRTGRRMGWGAGEEKGQKCQ TVGMRT
3552	9049	A	3822	1	708	TPVWWNSLWGRFPNSQDSGCSFSP PPQRYVVADGEMEARDKQVLRSLR LELGAEVLEGLVLQYLYQEGILTE NHIQEINAQTTGLRKTMLLLDILPSR GPKAFDTFLDSLQEFPPWVREKLKK AREEAMTRPCLAVDRLTGIP\SHILN SSPSDRQINQLAQR LGPEWEPVLS LGLSQTDIYRCKANHPHNVSQV EAFIRWRQRFQKQATFRTLDNGL\AR AVEVDPSLLHMLE
3553	9050	A	3823	791	1090	HFLHGPLAQEDKSERERWQ\HLAD\ LADFALA\MKD TLTNINNQSFNFM LRIGEHTPAGLPSRLPSHAGAWPP TRRDMRLRTTEAIRVGRFTHSQGKE T
3554	9051	C	3824	172	243	MRPSHGPSEQLCSTLSPPIKPRPT*
3555	9052	A	3825	1	615	
3556	9053	A	3826	1	596	PGWEKRMSRSSVVNTQEALPTAAIP RDAKGRVYYFNHITNASQWERPSG\ NS\SSGGKNGQGEPVVRCSHLLV KHSQSR\RPSSWRQ\EKITRTKGGGP GSLINGLHPEDSSSGEEDF\ESLASQF SDCK/SSAKARG\DLGAFQKQVRLQ KPFLKTPRFAL\RTGGDERGPCFTD\

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						SGIHILPHLSEGGEPRPGLGAGQGG
3557	9054	A	3827	1	295	ETVFHSVTQSGMQWHNLASLQRLP LRLKQTSHL SLLSSWDCRHMPNNL A/NF/CVLRDKISPCPGWASNPPG LKQCIGILKYPQALTPYELINIWEGI
3558	9055	A	3828	131	771	MGVILEPSGTTVPLVSSV*LLVWDH GPTRIVGLIIRLGPR/YPLVSSSSKSG RTMPNILDIIASA VENKIPPSKTSKI NVKPELKEEPEESIISAVDENNKLYS DIPHSWICDALQKAFTDKEELLKQQ ASNLHEQKKAGVIFEAEVITLLTS VLKTSSASRTSLSSRHQFAPGATVL YKGDKMVLNLD RSRVPTECIEKIEA ILKELEKPAP
3559	9056	A	3829	1	655	MPVNAGGKVQESQKPPTLIPEPKDS QANFKSSSEQSLTEMWRPNNNLSK EKTEWHVEKSSGKLQAAMASVIVR PSSSTKTDSMPAMQLASKDRVSERS SAGAHKTDCLKLA EAGETGRILPN VNSDSVHTKSEKNFQAVSQGSVPSS VMSAVNTMCNTKTDVITSAADTTS VSSWGGSEVISS/CIKYHFGLYIIRM CIFKKCQSASGSKTRMQGYLE
3560	9057	A	3830	1	515	LTLENQIKEEREQDNSESPNGRTSPL VSQNEQGSTLRDLLTTTAGKLRV GSTDAGIAFAPVYAMGAPSSKSGRT MPNILDIIASVVENKIPPSKTSKINV KPELKEEPEESIISAVDENNKLYSDIP HSWICEKHILWLRIIIIAVIGSF SKNV GNKDSLQWFLVCIRK
3561	9058	A	3831	6	226	RKGGFFVDLFVRVSNQVAVNMYK QLGYSVYRTVIEYYSASNGEPDEDA YGKLPSMAVSPRSRNSYILSTDCSI
3562	9059	A	3832	37	611	SGGGAMTTLRAFTCDDLFRV/FNNI NLDPLTETYGIPFYLQYLAHWPEYF IVAEAPGGELMGYIMGKAEGSVAR EEWHGHVTA LSVAPFRRGLAA KLMELLEISERKGGIFLVDLFVRV SNQVAVNMYK\QLGYSVYRTVIE YYFGPATGEP**GTLIDMRESTFPRD TGERNPIIPLPHPGGGLEDH
3563	9060	A	3833	1	191	MQK*ITAWAPAPMKIKIISPERKYS VWIGGSIWPQLST/FQQM WISKQEY DESGPSIVHRKCF
3564	9061	A	3834	2	1203	LSRRCQLSHSVLPPLRRRVSLPVAM EEEIAALVIDNGSGMCKAGFAGDD APRAVFPSIVGRPRHQGVMMVGMGQ KDSYVGDEA QSKRGILTLKYP IEHG IVTNWDDMEKIWHHTFYNELRVAP EEHPVLLTEAPLNPKANREKMTQIM FETFNTPAMYVAIQAVLSLYASGRT TGIVMDSGDGVTHTVPIYEGYALPH AILRLDLAGRDLTDYLMKILTERGY SFTTTAEREIVRDIKEKLCYVALDFE QEMATAASSSSLEKSYELPDGQVITI GNERFRCPEALFQPSFLGMESCGIH ETTFNSIMKCDVDIRKDL YANTVLS GGTTMYPGIADRMQKEITALAPST

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MKIKIAPPKYSVWIGGSILASLST FQQMWISKQEYDESGPSIVHRKCF
3565	9062	A	3835	3	412	SRFPEGLFQPFPG\MKSCGIHETTF HSH/IKFDVAIR\KDLYANTLLPGGN HQVSGALLTGMQKEIHAPAAQATL RFKIIAPPGSASTRW/VGSVGSILASL STFQ\QMWISKQEYDESGPLHSSTA KCFLNGLSQIA
3566	9063	A	3837	3	480	SHITVLTNLVNGLNAPVKRHLRAN WIKSQDPPVCFIQETHLTCRDTHRL KIKGWRKIYQANGK/QKKAGVAIL VSDKTDKPTKI/KRQGHYIMVKGS MQQEEQVLRDPQRDLDSHTMIMGD FNTLLSILDRSTRQKVNKDIQELKSA LHQADLIDIYRTLH
3567	9064	A	3838	1	834	MGDFNTPLSTLDRSTRQKVNKDIQE LNSALYQVDLIDIYRTLHPKSTEYTF FSAPHHTYSKIDHIVGSKALLSKCK RTEITNCLSDHSAIKLELTIKKLTQN RSTTWKLNLLNDYWYKQPSN KHL YANKLENLEEMDKFLDTYTL RLNQEEVESLNRPIRSEIEAITNSLP T/KKSPGPDGFTAIFYQMVLAR AIRQEKEIKGIQLVKEEVKLSLFADD MIVYLENPIVSAQNLLKLIGNFSKVS GYKI/NVQKSQAFLYTNNRQTESQI M
3568	9065	B	3839	1	543	MGDFNTPLSTLDRSTRQKVNKDIQE LNSALYQVDLIDIYRTLHPKSTEYTF FSAPHHTYSKIDHIVGSKALLSKCK RTEITNCLSDHSAIKLELTIKKLTQN RSTTWKLNLLNDYWYKQPSN KHL YANKLENLEEMDKFLDTYTL RLNQEEVESLNRPIRSEIEAITNSLP TKK*
3569	9066	A	3840	1	1470	MEQSWVENDFDELREEGFRRSNFS EVKEESRTQPEAKNLARRDTHRL KIKGWRKIYEENGKQKKAGVPILVS DKTDFKPTKIKRDKEGHYTMVKGSI QQEELTILNIYAPNTGAPRIKQVLR DLQRDLDSHTIIMEDFNTPLSTLDRS TRQKVNKDIQELNSALQQVDLIDIC RMLHPKSTEYTFFSAPHHTYSKIDH RVGSKALLSKCKRTEITNCLSDHSA IKLELRIKKLTENRSTAYNLNLL NDYGVHNEMKSEIKMFFETNENKD TTYQNLWDTFKAVEIQTIREYYKH LYRNKLENLEEMDKFLDTYTLPRV NQEEVESLNRPIRSEIEAITNSLP KSPGPDGFTAIFYQRYKEELVPFLL KLFQSIEKEGILPNSFYDASIILPKPG KDTTKKENFRPISLMNIDAKIMNKIL ANQIQQHIKKLIHHDQVGFIPGMQV WFNIGKSINVIQHINRTKDQK\NHRII SIDAEKAF
3570	9067	A	3841	2807	4148	
3571	9068	A	3842	2	1516	WRKIYQANGK/QKKAGVAILVSDK TDFKPIKIKRDKEGHYIMVKGSIQQ

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						EELTILNIHAPNTEAPRFIKQVLSDL QRDLDSHTIIMGDFNTPLSTLDRSTR RKVNKDTQELNSALHQVDLIDIYRT LHPKSTEYTFLSAPHHTYSKTDHIV GSKALLSKCKRSDIITNCLSDHSAIR LELRICKLTQNRSTTWKLNLLND YVWHNEMKAEIKMFFQTENKDT TYQNLWDTFKAEEVKSLNRPITGSE IVAIINSLPTKRSPGPDGFTVEFYQR CRKAFDKIQRPFLLKTLNKLADGM YLKIIIRAIYDKPTANVILNGQKLEVF PLKTGTRQGCPPLFNIVLEVLR AIRQEKEIKGIQLRKEKVKLSLFVD DMIVCLENPIISVQKLLKLISNFSKV SGYKINVQKSQAFLYINNRRQTESI MSELPFTIASKRIKYLGIQLTRDVKG LFKENYKPLLNKIKEGTNKWKNVP CSWIGKINIMKMAILPKETPSHMQR HT
3572	9069	A	3843	3	120	FIIDKKQKQLKSPSIDEWIKMWT HKIEYHSAIKGIF
3573	9070	A	3844	2	244	SRLSFPSSWDYICAPPHLANFCIFLV ERSVAMLRLVSSSWAQAILPPWP PKAQGFTGMGHHQAAGLYIFSG LGSNAI
3574	9071	A	3845	1	2616	
3575	9072	A	3846	1	773	QTSPMIPSIVVHCVNEIEQRGLTETG LYRISGCDRTVKELKEKFLRVKTPV LLSKVDDIHAICSLKDFLRNLKEPL LTFRLNRAFMEAAEITDEDNSIAAM YQAVGELPQANRDTLAFLMIHLQR VAQSPHTKMDVANLAKVFGPTIVA HAVPNPDPVTMLQGHQGVQPKVV E\RLFLGLWEYWEFSFMDGWEQG GTFDPLHVIENSNAFSTPQTPDIKAV PGGGLCVHFTAGEAEIQGPPSCGQ NKSTAAFNY
3576	9073	A	3847	1	422	CGRVRACGRVREPSSQIHNNMANL FIRKMNPNLLYLSRHTVKPRALSTF LFG\SIR\SAAPRGCGNPGA\AVR\SL SPGLPA/HHLPACGWGFKKQDCPLR KRCKDCYLVK\RRGRWYVYCKTH PRHKQKTRCRTLFPESRT
3577	9074	A	3848	1959	4060	RFFSFFFFFETESHVAQAGVQWCN LGSLQAPPPG\SRHSPASASRVAGTT GAHHHARLIFVFLVETGFHRISQDG LDLLTS*SARLGIPKCWDYRCEPPH LASI
3578	9075	A	3849	1	1320	
3579	9076	A	3850	1239	1733	ALFFSFFFFFETESRVAQAGVQW RDLGSLQAPP\PGSRRSPASASRVAG TTGARHRIFFVFLVEMGFHRDLDFP TS*SA\QGLQA*ATAPGPFLLLLL LRRSLTLLPRLECNAILARCNL LGSSNSPASASRVAGIAGMHHR LIFCILVEMGFHHL
3580	9077	A	3851	131	436	VTHLHQKKGSVFFFFFETESCPV

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						AQAGVQWRDLRSLQAPPPG\SRHSP ASASRVARTTGAHHYTRLIFVCLV ETGFHHVSQDGLDLQDQFPWSLFLF CPP
3581	9078	A	3852	56	192	KFLFSPKALNSVRKFFQYFPPPKKR/ CPSQNSQVG/CLKSPP*GEKF
3582	9079	A	3853	1	230	FQLHQHLLNPKHDYRGWAKWNR NSLYEKMKEGERRK\RRSAIPYLQG QRLDNVVAKKSVPQFFPLRVDPG VKSSC
3583	9080	A	3854	3	126	SCCGVGNQFKGPGGGGG/RGGG/RR NVSGGGAGGRGWKNERKER
3584	9081	A	3855	1	1021	MPRLEAFVNNQTCPKKECGAASEG DTIGKQSELSFGKAKMARETHWPK KVGKLRSTVVKQLPKTFQAISSTET KDQGPVVPAPVKGEGPVPAPVKDE GPMVSAPIKDQDPMVPEHPKDESA MATAPIKNQGS MVSEPVKNOGLSG\ PGPVKDQDVVVPEH*KGHDSALV APW*RIKGP\VVPRSPVKNQDPILPV LVKDQGPTVLQPPKNQGRIVPEPLK NQVPVVPVPLKDQDPLVPVPAKDQE P/TLPG/PLGSETAAPVPAHSHSPPPA GSSPAPPRAPGSGRLRLPCSLAPRDLG TRDRAGTVSGALRTMRHPTGGLCQ KGPCWVPPPPLLQIQHFQPP
3585	9082	A	3856	1	448	SSRKDQGLVVSGPVKDQDVVVPEH QRSRFSCQVVPVKNQGPVVPESV KNQDPILPVLVKDQGPTVLQPPKNQ GRIVPEPLKNQVPVVPVPLKDQDPL VPVPAKDQGPVPEPLKTQGP/KGT LSLPTVSPLPRVMIPTAPHTEYIESSP
3586	9083	A	3857	1	573	DPQFISGSPESPRLWCVGLGNTKVT FTNPKNPVRAVVIHPRHYTFASGSP DNIKQWKFPDGSFIQNLSGHNAINT LAVNFDGGLVFGAANGPMHLWDW ETWAPIFKRVHA\AVQPG\SLDSESG IFACAFDQSESRL\TAEADKPIKV YREDDTATEETHPVSWKPEIKRKR FLMNVEFFLSLFFSF
3587	9084	A	3858	1	589	EDLRKCTFIFIIGGPGSGKGTQCEKL VEKYGFTHLSTGELLREELASESER SKLIRDIMERGDLVPSGIVLELLKEA MVASLGDTRGFLIDGYPREVKQGE EFGRRIGDPQLVIGKE\CSPDT\MTN RL\QRSRSSLPVDDTTK\TMAKRLE AAYR\ASIPVIAYYETKTQLHKINAE GTPEDVFLQLCTAIDSIIF
3588	9085	A	3859	1	557	KLLSPKQPLLRAQLKTLVRLLCFSH AFVGLSKITTWYQYGFVQTQGPKA NILVSGNEIRQFARFMTEKLNVSHT GVPLGEEYILVFSRTQNRLLNEAEL LLALAHEFQMKTVTVPWRTTPLTD VVRLVSNASMLVSMHGAQLVTTLF LPRGATVVELFPYAVNPDHYTPYK TLAMLPGHGTSSM
3589	9086	A	3860	323	656	NEELMPKGRLYPPLANIQEV SINIAI

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						KVTEYLYANKMGFPDQTQEPEDKA KYVK/EKGTWAEWNMDSLLPDVY EWPEICNQAPPVNTIEALPLINTFV CSRGTPFFQTRKR
3590	9087	A	3861	1411	1799	GYLQFSFSFFLFFFFFFFLRWSLTLS PRLECSSVISTHCNLRPLGSSDSRAS ASQVAGTTGAHHHARLIVCVLVER VFHHVGQAGLEVL TSGGPPTSASQS ARITGMSHHTRPVICSFQFSDLPHEY F
3591	9088	A	3862	1	1007	MDGGHLFSNLTGKEEVIHKGAKLH PNGYRMAQGSETLVARGGPCRSVE PSAASPQELRGWWEAQALKRWGL MGGVWVMEVDPSWLGAIASIVSSS ASRLKSVWHIPCPHFLLLRPQLKE AQRKKQLEERCREEESIGNAVLT WNNEILPNWETMWCSRKVRDLWW QGIPPSVRGKVWSLAIGNELNITHEL FDICLARAKERWRSSTGGSEVENE GLCVAVCAQQGHVGVMGFGSDEP SAVSPCEKKGKSLAAWVLIFVDFRVG LQKSFQKRKERESTKLQQLWSWCL MLTYFAAFEVFFEEENLPKLFAHFKK NNLTPDIYLID/W*FRLLVGC
3592	9089	A	3863	1	1857	
3593	9090	A	3864	1	840	GIPAADRIEASLELIKLDISRTFPNLCI FQQGGPYHDMHLHSILGAYTCYRPD VGYVQGMSFIAAVLILNLDTADAFI AFSNLLNKPCQMAFFRVDHGLMLT YFAAFEVFFEEENLPKLFAHFKKNNL TPDIYLIDWIFTLYSKSLPLDLACRI WDVFCRDGEEFLFRTALGILKLFED ILTKMDFIHMAQFLTRLPELPAEE LFGPSIATIQMSRNKKWAQVLTAL QKDSREMREGKSVPTLRLQREFAL GTNQSPMPRLCCFRLTPGQPRRTD AL
3594	9091	A	3865	3	288	FFEMESLYVTRLNCSGTITISVHC NLCFPGSSDPASASQIAGITGRHH AQLILVFLVEMGFC/HISTKQMEVIH PPWPPKVLGLQVVTHDVL
3595	9092	A	3866	285	489	
3596	9093	A	3867	3	425	GSSDPPASAFQVAGSISVCHHTQLIF VFLVEVEFHVSQASLQL/RDLSLPS SWDYRRPPRPANFFVFLVEMGFH HLNKAIKSFACNEIQPLSAVSVARA GWGVFEYVSVYFLCSNSDYFSSNPS IANWMREWPLRLSLF
3597	9094	A	3868	1	156	APHPANFAFLVEMEFHDVGQGD QLLASSDLPASASQSAGITGVSHCN WI
3598	9095	A	3869	1	526	LAESGEGVLVSGGSLRLPACIASRFIF SSYYMSGVRQAPGKLEWVSFIR\A TSVRGRFTMSRDESKNITYLQMKSL RRGMFRGDLG\WPGGDGHWGAL RIWEPLWIFRCLWKMGLRLGASDG VTEPGGLGSHIWTRCLNKPGLVLM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AEECVSGAVSVGLQDRCTAANRAI FSLEL
3599	9096	A	3870	2	353	
3600	9097	A	3871	136	315	FKYVLSFLFLASGDGESLDEDESEFTL ARDFEIGHFFRERIVPRAVLYFTGE AIEDDDNV
3601	9098	A	3872	132	1552	GDKNIQMADHSFSDGVPDSVEAA KNASNTEKLTQVMQNPRLAALQ ERLDNVPHTPSSYIETLPKAVKRRIN ALKQLQVRCAHIEAKFYEEVHDLE RKYAALYQPLFDKRREFITGDVEPT DAESEWSENEEEEEKLAGDMKSKV VVTEKAAATAEPPDPKGIPEFWTIF RNVDMSELVQEYDEPILKHLQDIK VKFSDPGQPMFVLEFHFEPNDYFT NSVLTKTYKMKSEPKADPFSEFGP EIVDCDGCTIDWKKGKNVTVKTIK KKQKHKGRTVTRITKQVPNESFFN FFNPLKGKSVASGDGESLDEDESEFT LASDFEIGHFFRERIVPRAVLYFTGE AIEDDDNFEEGEEGEEEGDEEG EEDDAEFNPKVLIFVLLIHTFSRR DPSQPAECKQQYEAAGAWQTGCR DSRPVGGASVLAAAQSRGQSLHL TRFQVHDFHFHSFFLIILINLYSGN
3602	9099	A	3873	171	324	
3603	9100	A	3874	3	383	
3604	9101	A	3875	2	314	FFFFISALKALFAFLQILLFQVNVLR TAHIVISFINLLSVTPSKAFLLAFIF CREDYSFTAYATISYKIGPKANLL NNAEAYVITMQVTKSTQNSFRVNG Y
3605	9102	A	3876	3	319	TESRSVPQLGVQWRDLGSLQPPPPG FTRFSCSLPSSWDYRHTPPRANFL VFLVETGFRHVGQTGLELLTSGDPP ASASQSAGILCVLCTSTLGNHREHI YRMV
3606	9103	A	3877	118	1341	
3607	9104	A	3878	1	214	GFTSSLACMQMGEMFMGFTCQTH LLALGCALFTAYLGVGMANFMAE GTCERRIVGKKKASITKDHQORRI
3608	9105	A	3879	1	176	MRTFALLTAMLLVA/HAQAEPLQ ARADEAAAQEQPGADDQEMAHAF TWESAAALPLSA
3609	9106	A	3880	3	125	AASTFLFPNLKNSLRGSLRTFSSVT NVRKTALTWLSQDI
3610	9107	A	3881	1169	1512	YTQKNWHLFCFIFLRWSFVLVAQP GVQWCNLSSLQPLPRFR*FSCLSL SSWDYRCAPPRANF/SVFLVETGF HHVGQADLELLTSGDLPTSASQSAG ITGVSHCTWPDILYEI
3611	9108	A	3882	43	347	AGVQ*CDLG*LQLLPLGFK*FSCLSL PSSWDYRRLPPRANF*FLVETGFH HVGQADLELLTSGDSPASASQSAGI TGM SHRAGPI*KSFLKYSTNKLRTT
3612	9109	A	3883	10900	11295	KPWVNETGKLFQDSYSSSHIHLSGF SFPSFFSETESCSVTQAGVQWHDLS

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						SLKPLPPGFKQFSCSLPSSWDYRR VPTRPANF/SVFLLETFHRVSQDGL DRLT/S/GDPPSSASQSAGITGVSHRA RPHSPHF
3613	9110	A	3884	3	227	RFSCSLSSSSWDYRAPPPRLANFCI LVETGFHHAGQTGLELLTSGDPPAS ASEIAGITGMSHHTQPGQLLWECC
3614	9111	A	3885	2	296	KWSSALVAYAGVTWHHLGSLRSP PGFKRFCCLSLPSSWDYRHAPPPA/ NFFVFLVKTGFLHVGQAGLELPISG DPPALAPKQSAWIRGVSHRAQPQN
3615	9112	A	3886	1	162	LGGLVFPSEVCK/RKLDGMQLIKV HLDKAQQNNVENKAETFSGVCKK HRDLMA
3616	9113	A	3887	2	474	
3617	9114	A	3888	2	592	STGKFSQEKAMFSSSAKIVKPNGEK PDEFESGISQALLEMNSDLKAQL RELNITAAKEIEVGGGRKAIIFVPVP QLKSFKIQVRLVRELEKKFQWES MSVFIAQ\RRILPKPTRKSRTKNKQ KRPRSRTLTAVHDAILEDLVFPSEIV GKRIRVKLDGSRLIKVHLDKAQQN NVEHKVETFSGVYKKHRDLMA
3618	9115	A	3889	1	93	GFTMLP/RLVLNSWVQMICLPWPPK MLSLQA
3619	9116	A	3890	1	252	PTLEQYAMRAFADALEVIPMALSE NSGMNPIQTMTEVRAR/QDMKQQH VIETLIGKKQQISLATQMVRMILKID DIRKPGSEEE
3620	9117	B	3891	18	1121	MASMGTLAFDEYGRPFLIKDQDRK SRLMGLEALKSHIMAAKAVANTMR TSLGPNGLDKMMVDKDGDTVTVTN DGATILSMMDVDHQIAKLMVELSK SQDDEIGDGTGTVVVLGALLEEA EQLLDRGIHPRIADGYEQAAARVAIE HLDKISDSVLVDIKDTEPLIQTAKTT LGSKVVNSCHRQMAEIAVNAVLT ADMERRDVFELIKVEGKVGGRLE DTKLIKGVVDKDFSHPMPPKVED AKIAILTCPFPPKPKTKHKLDVTSV EDYKALQKYEEKFEEMIQIKETG ANLAICQWGFDDDEANHLLQNNLP AVRWVGPEIELIAIATGGRIVPRFS ELTAEKLGFAGLDKRISFGDT*
3621	9118	A	3892	1	282	LPSSHTIPGYP\NPLHPRPFSSRLPP GIIGGEYDQRPTLPYVGDPISSLIPGP GETPSQFPPLRPRFDPV/GPNDRFPF RPSRGRPTDGRLSFM
3622	9119	A	3893	3	166	PRPFPSRLPPGIIGGEYD\QRPNPILP \GRGGPNDRFPFARPSRGRPTDGRLS FM
3623	9120	A	3894	101	1926	SPVRGRRRLGRELLGPAAPVPAAS GSRPLGPPAAVMRLRVLLKRTWP LEVPEPTEPLGHLRSHLRQSLLCTW GYSSNTRFTITLNYKDPLTGDEETL ASYGIVSGDLICLILQDDIPAPNIPSS TDSEHSSLQNNEQPSLATSSNQTSM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QDEQPSDSFQGQAAQSGVWNDDSLMLGPSQNFESAESIQDNAHMAEGTGFYPSEPMLCSESVEGQVPHSLETLYQSADCS DANDALIVLIHLLMLESGLIPQGTEAKALSMPEKWKLSGVYKLYQYMHPLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICK EKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTTRQALNLPDVFGLVVLPLELKLRIFRLLDVRSVLSLSAVCRDLFTASNDPLLWRFLYLRDFRDNTVRGQDQTDWKELYRKRHIQRKESPKGRVFMLLPSSTHTIPFYPNLHPRIPFPSSRLAPPGINGGEYDPKNTNTPMLGDPISSLIPWVLGETPQPSFPPTETHALNPSWPPISRDPNPQSCPGAEGGPPN/TRFPPLRPQPGGRANLMAGLVISCGLDLLIFISWSLPFVFCFLNYRCQRPWGADLRVLFS
3624	9121	A	3895	2	442	LSQLCGDPQRFDDFLRAYVEKYKFTSVVAQDLLDSFLSFFPELKEQSVD CRAGPPLAEPDLSQGSSLTRPVEALFQL/WTAEPLDQAAASASAI DISKWRTFQTALFLDRLLDGSPLPQEVVMSLSKCYSSLLDSMNAEIRIRWLQIV
3625	9122	A	3896	1	1035	GEFLVIDVIHEVAHSWFGNAVNTATWEEMWLSEGLATYAQRRTTETTYGAAFTCLETAFRLDALHRQMKLLGEDSPVSKLQVKLEPGVNPShLRNLFTYEKGYCFVYLSQLCGDPQRFDDFLRAYVGEYKFTSVVAQDLLDSFLSFFPELKEQSVD CRAGLEFERWLNATGPPLAEPDLSQGSSLTRPVEALFQLWTAEPLDQAAASASAI DISKWRTFQTALFLDRLLDGSPLPQEVVMSLSKCYSSLLDSMNAEIRIRWLQIVVRNDYYSLT/FHRVRRFPGRARCHACYTIPLYEDLCTGALKSFALVFYQTQGRHPNLRRAIQQLSQGLGFQHRARP
3626	9123	A	3897	2	912	CSRSSRTGGWWPAPCSAASRRPTGPAAAAAATTD/VVTAGCGFGKDFRKGLLKKGACYGDDACFVARHRSA DVLGVADGVGGWRDYGVDPSQFSGTLMRTCERLVKEGRFVPSNPIGILTTSYCELLQNKVPLLSSTACIVVLDRTSHRLHTANLGD SGFLVVRGGEV VHRSD EQHYFNTPFQLSIAPPEAE GVVLSDSPDAADSTSFVDVQLGDIILTATDGLFDNMPDYMILQELKCLKNS NYESIQQTARSIAEQAHELAYDPNYSMPFAQFACDNGLNVRGGKPDITVLLSIVA EYTD
3627	9124	A	3898	2	220	YMSKKFSALLQSQRNCLIIINWCSSLCLRVRLYLRQVTVIPRICKVSD/SPCAPEADAMFAFNADGVGDAKG
3628	9125	A	3899	1	346	SANATTKTSETNHTSRPRLKNVDRSTAQQLAVTVGNVTVIITDFKIEKTRSSITSSSTVTS\SAGSIEQQNQSSSGV

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						QRAPDKGLPPRSLPTPKGDMS\AVN DEIFPEIATWNCEKL
3629	9126	A	3900	76	368	
3630	9127	A	3901	1	1182	MFAKGRGSAVPSDGOAWEKLASV VYEYLLHVRVQKSAETFLSEIRWEK NITLGEPPGFLHSWWCVFGDLYCA APQRRDTCEHSSEAKAFHDYSAAA APSPVLGNIPPNDGMPGGPIPPGFFQ GPPGSQPSPHAQPPPHNPSSMMGPH SQPFMSPRYAGGPRPPVIRMGNOPPG GVPG\TQPLL\NSMDPTRQQGHP\N MGGSMQRMNPSRPLGPMGPRPHR ITGSGMRPPNSLGPA\MP\GINMGP GAGRPWPNPNSANSIPYSSSSPGTY VGPPGGGGPPGTPIMPSPADSTNSS DNI\YTM\N\NPVPPGGSRSNFQMGP STGPMDSMGGMEPHHMIG\SLGSG DIDGLPKIFPNNISGISNPPGTPRDDG ELGGNFLHSFQNDNYSPTSMTMSV
3631	9128	A	3902	2	470	IPTFGLPGSIQSDNGP\SFISQITQQVS QSLGIQWRLHIPCWPTSGKVERAN GILKAQLTKLTLEVQKPWDLALLPH RHWESIRRP/GPKGTLLSFSSIWSLIY GTPFPLTNRPPSNSQLGGIPSQQSSL MEVIFLWPTRPTRAFFPKPHGGGLPIP K
3632	9129	A	3903	69	523	PLGCASSQISASRNTLCTTASSCCP QVLAHS\KAAEYMTRWKVQQMPH SQDRALQSVFCAPFHS*LVALPTG HR*MTPAQFSECFQATSGGSD*DPF LAPSFL\VPGLPVAPGLLLPLGPVHS RATMEEGQATHEELTVFIGLRPGVR GS
3633	9130	A	3904	101	1469	RTHPTFPHPGTGPTSAPPSGALEGTA GTITSNEWSSPTSPEGSTASGGSQAL DKPIDNDGEGVWSPDIEQSFQEALA IYPPCGRRKIILSDEGKMYGRNELIA RYIKLRTGKTRTRKQVSSHQVRLAR RKAREIQAKLKDQAAKDQALQSM AAMSSAQIISATAFHSSMRLARGPG RPAVSGFWQGALPGQAETSHDVKP FSQQTYAVQPPLPLPGFESPAGPAPS PSAPPAPPWQGR\SVASSKLWMLEF SAFLEQQQDPDTYNKHLFVHIGQSS PSYLRPYLEAVDIRQIYDKFPEKKG GLKDLFERGSPNAFFLVKFWADLN TNIEDEGSSFYGVSSQYESPENMIT CSTKVCSFGKQVVEKVETEYARYE NGHYSYRIHRSPLCEYMINFIHKLK HLPEKYMMSVLENFTILQVVTNR DTQETLLCIAVFEVSASEHGAQHH IYRLVKE
3634	9131	A	3905	1	1290	
3635	9132	A	3906	2	270	ISLADLKEGPHTHLKPPDYSVAVQR SKMMHNSLSRLPPASLSSNLVACVP SKIIVTQQRHNLQPFHPKLGVDVTA DSEED\ENEQVSAV
3636	9133	A	3907	2	288	RWGLALSLR/AGAQWFHHGSLQPQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PPMLKSSSRLSLPSSRNHRHTQPCPA NFFIFVEMGFHHVAQAGLELLSSLT VWASQSAGITGVSHRTHPLLS
3637	9134	A	3908	3	222	FFFETESRSVTRLECSGTISAHCKLH LPGSCHSPASASRVAGTTGAHCHTQ RIFVEMGFHRVSQDGLDLKLN
3638	9135	A	3909	3	175	GTSPKDCEVRDFCPSEGLYST*WGG SILPSLDT/FKKMWVSKKKYEEDGA RSIHRKTF
3639	9136	A	3910	2	533	RAAEFFETFNVPALFISMRAVLSLY ATGRTTGVLDSGDGVTHAVPIYE GFAMPHSIMCIDIADRDVSRFLRL YLRK\EGYDFHSS\SEFEIVKAIKERA CYLSINPQKDETELEKAQYYLPD GSTIEISAPQERLYSTWIGGSILASLD TFKKMWVSKKEYEEDGARSIRKTF
3640	9137	A	3911	1	1213	EFGALRRTRLGSSFPRRRDSSAMES YDVIANQPVIDNGSGVIKAGFAGD QIPKYCFPNYVGRPKHVRVMAGAL EGDIFIGPKAEHRGLLSIRYPMEHG IVKDWNDMERIWQYVYSKD\QLQT FSEEHVLLTEAPLNPRKNRERAAE VFFETFNVPALFISMQAVALSLYATG R\TTGVVLDSGDGVTHAVPIYEGFA MPHSIMRIDIAGRDVSRLRLYLRK EGYDFHSSSE\FEIVKAIKERACYLF HKTPKRD\ETLETEKASVTTWLDGS TIEIGPFR\FRAP\ELLFGPRI*LEKESE GIHEVPGVRPFRKSDMGPAGARLF SNIVL/SQGGSTPVQKFSSLPISGFGD RLLC*VKKL\APKDVKIRISAPQERH VYPRGLGGSILASLDTFKKMWVLQ KGDMR*DGSTIEIGPFRIPGPLSCSSG PEFDWKRKVKASHEVPGVRPFRKS DMGPAGARLFSNIVLFREALPLFKS SPLCPFQVLVTGSFVIVKKLSSKRCE DQDICTSGETCISTWIGGLHPCPLPGH HLRRCGCSKKEI
3641	9138	A	3912	2	262	LEKRSHSVTKLGYSGVIIAHC SLNF LSSSQPPTSASQTAGTTGICHSTQLIF KIFLVEMG/LHYVAQAGLDLLGSSN VEPPKVLLGL
3642	9139	A	3913	1379	2175	TTAGIQMPIKAPGVLPQTPASGGST AT*KNAQEQKRVL*HL/QPVVLLPD VETPSEEDCMFGNGKGYRGKRATT VTGTPCQDWAAQEPHRHSIFTPETN PRAGLEKNYCRNPDGDVGGPWCY TTNPRKLYDYCDVPQCAAPSFDG KPQVEPKKCPGRVVGCVAPHSW PWQVSLRTRSPRPSYKVILGAHQE VNLEPHVQEIEVSRLFLEPTRKDIAL LKLSSPAVITDKVIPACLPSPNYVVA DRTECFITGWGETQEHFYFN
3643	9140	A	3914	1	387	TPEKEPPLWHAFTKEELVQKLSST TKSADQLNGLLRETEATVHAVLME QIKLLKSEIRRLERNQEESAANVEH LKNVLLQFIFLKPGRSERESLLPVINT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=/possible nucleotide insertion)
						MLQLSPEEKGKLAAVAQGLQETSIP KKK
3644	9141	A	3915	360	885	NVFLVLEANQRTSTVTLATVSASGQ MPSTFGGLDSSIQKLIAIAHFILNH RELGFLEKASSKSTLGFSPASDETFG PVSDHIIWGWQTSWDYFVSDDGRT A*L*QGNIFSCGLQEQRHFYFLNM RF/DDSLLGVHPG*PCRMKALGTSP SSGQQSTPTLGISRCLHRSFQTLF
3645	9142	A	3916	1669	4914	
3646	9143	A	3917	1379	2175	TTAGIQMPIKAPGVLPQTPASGGST AT*KNAQEQKRVL*HL/QPVLLPD VETPSEEDCMFNGNGGYRGKRATT VTGTPCQDWAQEPHRHSIFTPETN PRAGLEKNYCRNPDGDVGGPWYCY TTNPRKLYDYCDVPQCAAPSFDCG KPQVEPKKCPGRVVGCVAHPHSW PWQVSLRTRSPRPSSYKVILGAHQE VNLEPHVQEIEVSRFLFLEPTRKDIAL LKLSSPAVITDKVIPACLPSPNYVVA DRTECFITGWGETQEHFYFN
3647	9144	A	3918	1	387	TPEKEPPLWHAFTKEELVQKLSST TKSADQLNG\LLRETEATHAVLME QIKLLKSEIRRLERNQEESAANVEH LKNVLLQFIFLKPGSERESLLPVINT MLQLSPEEKGKLAAVAQGLQETSIP KKK
3648	9145	A	3919	360	885	NVFLVLEANQRTSTVTLATVSASGQ MPSTFGGLDSSIQKLIAIAHFILNH RELGFLEKASSKSTLGFSPASDETFG PVSDHIIWGWQTSWDYFVSDDGRT A*L*QGNIFSCGLQEQRHFYFLNM RF/DDSLLGVHPG*PCRMKALGTSP SSGQQSTPTLGISRCLHRSFQTLF
3649	9146	A	3920	1669	4914	
3650	9147	A	3921	1	246	FLETEFHSAQAGVQWCHLGLSLQP PPPGFKQLS\CLSLPSSWDYRGTPPY LANFCIFSRDGVSLCWPGWSQTPDL KQSSGNL
3651	9148	A	3922	10	476	DRVLLSVAQAGLQWRDLGSLQPPP P/GFKRFSCLSLPNSWDYRCVPPCLA NFFVFLVETGFHHVQAGLELLTSG DPPLPQPPKVLGAGITGMSHHTWLI SLIFYQTKWRQTAIASVGIPGSPLCH PLPLIRKGVAGKAVLCPRKDGHTH KTQLRP
3652	9149	A	3923	2	465	ARARADSARAARAEFEDIMKRNRA ISSPISKAVSGASAGDYSDAETLLT AIAVIKQSRVAK\DERCRVLISLKD CLHG\IEGQVPTVWGAQLGALSRRK HPFPGERSPARSRETSRRHRDLLHN EDR\HDDYFQERNREHERHRDRER DRHH
3653	9150	A	3924	3	218	LPPPLSNIHSTLSTPFLPPAPL/SP/YP SRASPPSTYSPLPTPPPLPTSQPSTPT LPLPTPCSTPSGQALFF
3654	9151	A	3925	1379	2175	TTAGIQMPIKAPGVLPQTPASGGST

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AT*KNAQEQKRVL*HL/QPVVLLPD VETPSEEDCMFGNGKGYRGKRATT VTGTPCQDWAAQEPHRHSIFTPETN PRAGLEKNYCRNPDGDVGGPWCY TTNPRKLYDYCDVPQCAAPSFDCG KPQVEPKKCPGRVVGCVAHPSW PWQVSLRTRSPRPSSYKVILGAHQE VNLEPHVQEIEVSRLFLEPTRKDIAL LKLSSPAVITDKVIPACLPSPNYVVA DRTECFITGWGETQEHFYFN
3655	9152	A	3926	1	387	TPEKEPPLWHAFTKEELVQKLSST TKSADQLNG\LLRETEATHAVLME QIKLLKSEIRRLERNQEESAANVEH LKNVLLQFIFLKPGSERESLLPVINT MLQLSPEEKGLAAVAQGLQETSIP KKK
3656	9153	A	3927	360	885	NVFFVLEANQRTSTVTLATVSASGQ MPSTEFGGLDSSIQKLIAIAHFILNH RELGFLEKASSKSTLGFSPASDETFG PVSDHIIWGWQTSWDYFVSDDGRT A*L*QGNIFSCGLQEQRHFYFLNM RF/DDSSLGVHPG*PCRMKALGTSP SSGQQSTPTLGISRCLHRSFQTLF
3657	9154	A	3928	1669	4914	
3658	9155	A	3929	1	1542	
3659	9156	A	3930	3	1771	
3660	9157	A	3931	2	1869	RLVVVEAKMAAQAAAAAQAAAA QAAQAEAADSWYLALLGFAEHFRT SSPPKIRLCVHCLQAVFPFKPPQRIE ARTHLQLGSVLYHHTKNSEQARSH LEKAWLISQQIPQFEDVKFEASLLS ELYCQENSVDAAKPLLRKAIQISQQ TPYWHCRLLFQLAQLHTLEKDLVS ACDLLGVGAEYARVVGSEYTRALF LLSKGMLLLMERKLQEVHPLLTLCL GQIVENWQGNPIQKESLRVFFLVLQ VTHYLDAGQVKSVPCLKQLQQCI QTISTLHDDEILPSNPADLFHWLPKE HMCVLVYLVTVMHSMQAGYLEKA QKYTDKALMQLEKLMLDCSPILS SFQVILHEIIMCRLVTGHKATALQE ISQVCQLCQQSPRLFSNHAAQLHTL LGLYCVSVNCMDNAEAQFTTALRL TNHQELWAFIVTNLASVYIREGNRH QEVVLYSLLERINPDHSFPVSSHCL RAAAFYVRGLFSFFQGRYNEAKRF LRETLKMSNAEDLNRLTACSLVLL GHIFYVLGNHRESNNMGGVAMQL ASKIPDMSVQLWSSALLRDLNKAC GNAMDAHEAAQMHQNFSSQQLLQD HIEACSLPEHNLITWTDGPPPVQFQ AQNGPNTSLASLL
3661	9158	A	3932	2	614	
3662	9159	A	3933	1	4992	VSSNNVLLNSQADDRVVINKPESAG FRDVGSEEIQDAENSAKTLKEIRTL MEAEENMALKRCNFPAPLARFRDIS DISFIQSKKVVCFKEPSSTGVSNGDL LHRQPFTEESPSSRCIQKDGTQTNL

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KCRRGIEWFEISSTTVRSPLQEAES KVSMAL EETLRQYQAASVMRSEP EGCSGTIGNKIIIPMMTVIKSDSSSD ASDGN GSCSWDSNLPESLESVSDVL LNFFPYVSPKTSITDSREEEGVSESE DGGGSSVDSLAAHVKNLLQCESSL NHAKEILRNAEEEEESRVRAHAWNM KFNLAHDCGYSISELNEDDRRKVEE IKAELFGHGRTTDL SKGLQSPRGMG CKPEAVCSHIIIESHEKGCFTLTSE HPQLDRHPCAFRSAGPSEMTRGRQ NPSSCRAKHVNLSASLDQNNSHFK VWNSLQLKSHSPFQNFIPDEFKISKG LRMPFDEKMDPWLSELVEPAFVPP KEVDFHSSSQMPSPEPMKKFTTSITF SSHRHSKCISNSSVVKVGVTESQSC TGASVGVFNSHFTTEQNPPRDLKQK TSSPSSFKMHSNSQDKEVTILAEGR RQSQKLPVDFERSFQEEKPLERSDF TGSHPSTRANC SNFKEIQISDNHT LISMGRPSSTLG VNRSSRLGVKEK NVTITPDLPCIFLEQRELFEQSKAP RADDHVRKHHSPPQH QDYVAPDL PCIFLEQRELFEQCKAPYVDHQMR ENHSPLPQQQDSIASDLPSPISLEQC QSKAPGVDDQMKNHHPFPQGGQD CVVEKNNQH KPKSHISNINVEAKFN TVVSQSAPNHCTLAASASTPPSNRK ALSCVHITLCPKTSSKLD SGTLDERF HSLDAASKARMNSEFNFDLHTVSS RSLEPTSK\LLTSKPVAQDQESLGFL GPKSSLDFQVVQPSLPDSNTITQDL KTIPSQNSQIVTSRQIQVNISDFEGHS NPEGTPVFADRLPEKMKTPLSAFSE KLSSDAVTQITTESPEKTLFSSEIFIN AEDRGHEIIEPGNQKL RKAPVKFAS SSSVQQVTFSRGTDGQPLLLPYKPS GSTKMYYPQLRQIPSPDSKSDTT VESSHSGSND AIAPDFPAQVLGTRD DDLSATVNIKHKEGIYSKRVVTKAS LPVGEKPLQENADASVQVLITGDE NLSDKKQQEIHSTRAVTEAAAKE KESLQKDTADSSAAAAAEHSAQVG DPEMKNL PDKAITQKEEIHRRKKT PEEAWPNNKESLQINIEESECHSEFE NTTRS VFRSAKFYIHPVHLPSPDQDI CHESLGKSVFMRHSWKDFFQHPD KHREHMCLPLPYQNMDKTKTDYT RIKSLSINVNLGNKEVMDTTKSQVR DYPKHNGQISDPQRDQKVTP EQTT QHTVSLNELWNKYRERQRQQRQPE LGDRKELSLVDRLDRLAKILQNPIT HSLQVSESTHDDSRGERSVKEWSG RQQQRNKLQKKKRFKSLEKSHKNT GELKKS KVLSHHRAGRSNQIKIEQI KFDKYILSKQPGFNYSNTSSDCRPS EESELLTDTTNNILSGTTSTVESDILT QTDREVALHERSSSVSTIDTARLIQA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						FGHERVCLSPRIKLYSSITNQQRIR YLEKRSKHASKESAGLTGHPLVTSE HTRRRHIQPPTSATACRQPLMTFCF YGFAYSGPFI
3663	9160	A	3938	2	354	NRILVITSKAGEVIKHGDLRCVRDE GMPYKAPLEKGIILIIQFLVIFPEKPL ALSGKSFLQLEALLPPRQKVRITDD MDQVELKEFCPNEQNWRQHREAY EEDGDPQAGVQFQTA
3664	9161	A	3939	204	374	DHGFLIPLTQGDQKGPPRVHPL*AC YHWNQREKVISSCIGCICMSQIKDP LVKKKKK
3665	9162	A	3940	39	385	AGVQWRDLSSPQPPPGFKRVSCLS LPSSWDYRPPRLANFC/DFLVEMG FCHVDQAGLELLTSGDPPASASQS AGITGVSHRTQPCLLFLKTKTWGK WEKDGMFWEMNGAQDQEQ
3666	9163	A	3941	1	200	FETGSYSVTRLVFSVQISAHCNLC PGSPDPTSASEVVGTSVCHR\TQLI VIYPLQLPKLFRLQV
3667	9164	A	3942	2	458	LFYGVYFLFPLNSCILFVSFTVNHLO IFFFGGGMKSWSVRRLECSGVILAH CNLRPLGSSDSPASASRVAGTTGTC HR\ARLIFVFLVEMGFHHVG/RRDG LGSPDLVIHPPR\TPKGVGGGLQGVSH CGPGSPQGFYLIKELGSSQGGGEQ FP
3668	9165	A	3943	1	2499	
3669	9166	A	3944	855	2479	PGGSGPGFPTLEGSSKAGRELIGY EPGSSGVGAPLTPHKMKKRKELN ALIGLAGDSRRKKPKKGPSHRLLR TEPPDSSESSSEEEFVVGNRSR FAKGDYLRCKICYPLCGFVILAAC VVACVGLVWMQVALKEDLDALKE KFRTMESNQKSSFQEIPLNEELLSK QKQLEKIESGEMGLNKVWINITEM NKQISLLTSAVNHLKANVKSADLI SLPTTVEGLQKSVASIGNTLNSVHL AVEALQKTVDEHKKTMEQLQSDM NQHFLKETPGSNQIIPSPSATSELDN KTHSENKQDILYLHNSLEEVNSAL VGYQRQNDLKLEGMNETVSNLTQR VNLIESDVVAMSKVEKKANLSFSM MGDRSATLKRQSLDQVTNRTDTVK IQSIQKEDSSNSQVSKLRE*LQLISAL TNK\PESNRPPETADEEQVESCTSKP SALPKFSQFLGDPVEKGCPKLRTYS P*QGVSKH*KIFQDLFR\KTGQDV GKLTQEIWTSLSGAMPEPESLRAF D\SDGDGRYSFLELRVALGI
3670	9167	A	3945	336	519	AALPCEPAFSPLEQVQRGLQDRGQ NQTQRPFFLNVVQA\VSQEGACV YAVSELRKEWGRPQ
3671	9168	A	3946	252	2104	LCASSCPFICPIRPSVCPAAPLLLG CRAMARGYGATVSLVLLGLGLALA VIVLAVVLSRHQAPCGPQAFAHAA VAADSKVCSDIGRAILQQQSPVDA

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me- thod	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						TIAALVCTSVVNPQSMGLGGGVIFT IYNVTTGKVEVINARETVPAHAPS LLDQCAQALPLGTGAQWIGVPGEL RGYAEAHRRHGRPLWAQLFQPTIA LLRGGHVVPVLSRFLHNSILRPSL QASTLRQLFFNGTEPLRPQDPLPWP ALATTLETVATEGVEVFYTGRLGQ MLVEDIAKEGSQTLQDLAKFQPEV VDALEVPLGDYTLSPPPPAGGAIL SFILNVLRGFNFSTESMARPEGRVN VYHHLVETLKFARGQRWRLGDPRS HPKLQNASRDLLGETLAQLIRQQID GRGDHQLSHYSLAEAWGHGTGTSH VSVLGEDGSAVAATSTINTPFGAMV YSPRTGIILNNELLDLCERCPWVGSGT TPSPVSGDRVGGAPGRCWPPVGE RSPSSMVPSILINKAQGSKLVIGGAG GELIISAVAQAIMSKLWLGFDLRAA IAAPILHVNSKGCVEYEPNFSQEVQ RGLQDRGQNQTQRPFFLNVVQ\AVS QEGACVYA\VSDLARKSGEAARS
3672	9169	A	3947	2	97	GLGRWLT/PVIPTLWEAKKGRSPEV RSSRPVKS
3673	9170	A	3948	3	308	PEDSDEKSLSSSVVHVRRPSRRVP RMPRGSRSTSRMAPPASRAPQMR AAPRPAPVAQPP\QPCLYEIKQFLEC AQNQGDIKLCEGFNEVLKQCRLAN GLA
3674	9171	C	3949	38	154	MXSNSFWSVPRTVTSSSVRVSMR CCYDFILCELIRIKS*
3675	9172	A	3950	1	192	GSNAEP/ARPDLY/QEP/QGTQPAQ QQQPCLYEIKQFLECAQNQGDIKLC VGFNEVLKQCRLANGLA
3676	9173	A	3951	1	254	LMARMQTLKLAVLWASAIGHTWV HAFTGAFSGGSNAEPARP/DITYRSL YEIKQFLECAQNQGDIKLCGFNEV LKQCRLANGLA
3677	9174	A	3952	1	142	
3678	9175	A	3953	1	325	FFFEMESCSVAHAGVRWA/DLSSLQ SPFPGFKRFSCLLSSWDYRRLPP HPANFYFLVDTFHHVGGAGLELL T/S/GDPPASASQSAGITGTSHRARPT VNTFNRPPAS
3679	9176	A	3954	3	304	HEGREKRRVLGAEAGGGRSCEIGV PLEWWRPLMRVRVRMCC\MLML RWGASFAWYCCFLSFCNWLASSED TGLMITFMLRISALLMRS\QNPEAM TLPW
3680	9177	A	3955	3	961	LLLLNSRPRRRDRLVTLESWANDPD YLKRQVGFCQWSLDNFLKEGRQ LTYEKNLSSIRAMLNSNDVSEYK ISPHGLEARCDASSFESVCCSFCVD AGVWDYEVTVVTSGVMQIGWATR DSTFLNHEGYGIGDDEYSCAYDGC RQLIWYNARSKPHIHPCWKEGDTV GFLLDLNEKQMIFFLNG/TPA/RPPEE QVFSSTVSGFFAAASFSYQQCEFN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						FGA\SPFKYPPSMKFSTFNDYAFLTA EEKIIL\PRHRLALLKQVSIRETAGS LCCDEVADTQLKPCGHSCLCMDCA LQLETCPLCRKEIVSRIRQISHIS
3681	9178	A	3956	4	101	RQSLAMLSRLA\LNSWPQVILLPWP PKVLGLQA
3682	9179	A	3957	21	338	HPVLAITLSIFVAFAYAEELDEIQ P/CIMMKTLNKLIGEMCLNSIKAIY /DKSNANFILNKEKLKAFFLRSGTRQ IRPNFQ/PLLFNIVLEVLAKEIRQEEI KV
3683	9180	A	3958	90	360	ALICLVDIENSTTRPRFASHDQV CIALLRTA\GILCLETFDSPSHGSRH FLFVLSPPPLTLFPLLHIYLLAVVPI VSPLLSLSDPP
3684	9181	A	3959	1	424	CGRRFSTRSDLTKHRRDTG\EKPN RCELCKGRFTCVSNLNVHRRNHAG HKPHKCPECSKAFSVASKLALHRKT HLGERPAECARVGQVLQPAPLS QHQRGPHAPPAPLPPLPSPAVGHC PQSFEGGRLEQEKAKGSL
3685	9182	A	3960	153	328	SIASYFTLVCHLLRKCHPRLGTVAH TYPNSTLGGGRGRWIMR\QEFETSLT NMVKPCRY
3686	9183	A	3961	1	936	
3687	9184	A	3962	1	1023	
3688	9185	A	3963	15	337	RINNTISWLIYVCKFCLSSFSIYLIIII IIFETESHVAQAGVQWRNLGSLQ PPPPRFKRFSCLSFPSSWDYRCPPR PANFCIFSRDGVSPCWPGWFRTPDL R
3689	9186	A	3964	3	1105	HASALTPVVCMLSAIAFSNVFEHYL GDDMKRENPPVEDSSDEDDKRNQG NLYDKAGKVRKHATEQEKEEGLG PNIKSIVTMLMLMLLMFAVHCTW VTSNAYSSPSVVLASYNHDGTRNIL DDFREAYFWLRQNTDEHARVMSW WDYGYHIAGMANRTTLVDNNTW NNSHIALVGKAMSSNETAAYKIMR TLDVDYVLVIFGGVIGYSGDDINKF LWMVRIAEGEHPKDIRESDYFTPQG EFRVDKAGFPTLLNCLMYKMSYYR FGEMQLDFRTPPGFDRTRNAEIGNK DIKFKHLEEAFTSEHWLVRIYKVKA PDNRETLDHKPRVTNIFPKQKYLK KTTKRKRGYIKNLVFKKGKKISK KTV
3690	9187	A	3965	1	181	ANVFTQLLIWYGVDVRSRDARGL TALAYARRAGSQECADILIQHG\CS AEGCGLSSTCY
3691	9188	A	3966	640	961	DGVSASCCPGLGVQWVRLGSL\QP SASWGFKQFSCSLPSSWDYRRALP PPRPANF/SVFLVKMGFLHVG\QAG LELLTSGHPAASASQSAGITGVSHR TRPAASIL
3692	9189	A	3967	2	334	VGLYGRIEASSPMGEGNRW*SGTPA NQG*QEQGIARPKPRGEPGLRNEGG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PGAILPGRWAGV*GPTGQEGR*RGSGESCPCPAQSSCSHRVAGLDVGGSHGHSAAFPATP
3693	9190	A	3968	1	361	ARARLRHLRDLRAPAGPVGGLCAA GTACGWPGPGPLLGERVRAFLRR* RAQHLLHHHRVRAPLPGWREAAG GAPPFLGTYPESQVRLDAVVPEA GGQDSGSSGSASLRPRSSFSCSCS
3694	9191	C	3969	151	373	MPTAVXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXVLPFLV LEV MQCLCPVLLLYDPNSKTRYV FFKTR*
3695	9192	A	3970	50	441	IPSPDGGFFSNLGRKPFPCNFSCQ NILLTRKILLKSFLYPFFFLRWSLA LPPAVLSAHCNLCPPGSSDSLASAS* VAGITGVHHQAWPVLPFLVLEVMQ CLCPVLLLYDPNSTPRYVFFKTRT FIA
3696	9193	A	3971	3	224	FLRWSLALPPAVLSAHCNLCPPGSS DSLASAS*VAGITGVHHQAWPVLPF LVLEVMQCLCPVLLLYDPNSFV
3697	9194	A	3972	1	214	PIQFKQLRPFGLFVVF*EGVLLCH PGWTAVTEDRSWLTATSTSWAQVI LQSSCLSLPGS*DYRQCLPGV
3698	9195	A	3973	154	341	KNFFRGQFWFVA*AGVQWGHFRSL QPQPSGVKQFFPLGLPKPLDCRCES HRVPFLFLGLETL
3699	9196	A	3974	3	379	FALVAQAGVQWCSFDSLQPPPPGF K*FSCLSLPSSWNYRHLPRLANFV FLVEMGFHYVGQASLELLTSGDPPA SASQSAGIRGLSHCTWPHVSGFIMQ YEYTLCFMVFIMSFWRNCRKVAKY LK
3700	9197	A	3975	2	35	LKQAPCLCLPSS*DYRHLPCLSNF* NFL*R*GLSLLPRLVSNS*PQAICPRR PPKVLRL*AQTSPLPLPTK
3701	9198	A	3976	1958	2316	IHSSPTKATFFLRQSLALSPRLEYSG AISAHCNLCFPGSSDSRALAS*AAG TTGACHHIRLIFFLVFLVETGFHH VGQAGLELLVSSDPILVLSARITG VSHHAQPPPKLLNALL
3702	9199	A	3977	2	80	SLCICMCVCACIRTHA*MYVCVCV HTHACMNATSPSWVF
3703	9200	A	3978	123	452	KTGSNFAPQLEAQGCNLG*LNPWP PG*KQFSGLTLLITWINGAPPPPRAN FGIFNKKGVTPCGGGPKTRDLGIG PSKPPKGLEFRAQPPEPALMGKFYP MVNLSNVPPF
3704	9201	A	3979	3	250	AIAAH*NLHLLGSSNSSASVSRVAGI TGARHHTQLIFVFLVETGFHHVCQA GIEFLTSGDTSTSASQSARITGMSHH TWPQKQ
3705	9202	A	3980	2	257	PRSSPTCPACLCVQVNPPAQDPEDP APQLSPQPDPAKPPQPYPNPYPY PNLGCGL*PQNYCIIVCMVSIVYYH MGIETVKSQ
3706	9203	A	3981	2	147	LVEMGFHHVSQAGLKLLDSGNLSA

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						S*RSAGITGISHRAHPPNSTNIYA
3707	9204	A	3982	3	446	QVVRGFGRVSKQMGIPTANFPEQV VDNLPADISTGIYYGGASVSGDVH KMOVSI*WNPYYKNTKKSMEHIM HTFKEDFYGEILNVAIGD*LRPDKN FDCLESLISPVQGD*AKIRLELPE HLRI*EDTFFQVSLNRTMIVTDDK
3708	9205	A	3983	1	162	FFFRVKASICCPGWSTVAQ**LTAA SDSWAQKSSCSLWSSWDNRRLP HLANK
3709	9206	C	3984	131	442	MNIPLSMSLVVSNMQDVFWXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXX*
3710	9207	A	3985	141	429	TGSHFVAQAGMQWCNLSMQLLP AGLR*FPYLSLPSSWDYRHAPPCST HFLYFFVEMGFCHVAQVGLELLAS SDVPTYASQSAGITGVSNHPRPF
3711	9208	A	3986	1577	1879	
3712	9209	A	3987	1	219	EM*SCRVTQAGVQWCNLSLQLPS PGFKQFSCLSVPSGWGYRCMPHP ANFCIFSRDRASPRWPGWSQTPDLR
3713	9210	A	3988	1	414	FF*TGSCFVSQAGTQQQDHSSLP* TPGLKPSSHLCLLSSWDNRHLIFKFF VEMGSRHVAQAGLQLGSNNPPTL AS*SARIISWSHRAQPTCTLCSWLC DSGAGTAESFLWQPALSRVANRGC CRRPGKLKEKQGT
3714	9211	A	3989	3	666	FFVETGFCHVGQAGLELLGSGNLPA AASQSAGITGMSHRVRQHS*YETHR KVFYS
3715	9212	A	3990	1	436	FFFFFLRQNLTLSPRL*CSGTILAH NLQHPGSSDSPASASQVAGITGVRH HIWLIFVFLVEMRFHHVQGASLELL NSGYLPTSASQSAEITGVSHCAQLQ PGILMHGLRRLTDLDDNVHHPRSRL KVTSSSAHPGAASSSFLHL
3716	9213	A	3991	167	563	SESASEFSIFYLFIIIIIIIIETRSCSVA QTGVQWCDHGLLQPRPPWFRPSCH LSLLSSRDYR*APHPANTFNFFLE IGSHYVWGSLELLGSSDPPASASQ SVEIIGVSHRGPDSQKSFIHLSPRFP
3717	9214	A	3992	3	456	
3718	9215	A	3993	78	129	
3719	9216	A	3994	96	251	MDQYSRNSPLEVNGQQLLGWYQH ALRCKWNF*APLCYCSHTVFNSQPT HTEE
3720	9217	C	3995	94	351	MKRISTTQYYHCODYDLRHSKHM CLVSTAFQKVPLYKYLEILQENLD PQGKDSRWFSVISSPRSQNVKVR HLQSCLTSHCKH*
3721	9218	B	3996	1	431	MAVASTKSRWETGEVQAQSAAKT LSCKDIVAGDMSNKSFEQGGGSK TSSTITAQIAFLQGERKGQENLKKD LVRMIRMLEYALKQKRAKYHKLK YGTELNQGAMKPPSYDSDEAQQQA

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						MRSVHGPLHLSAPPASQQKRPTER*
3722	9219	A	3997	772	1391	IANNKDALRKWTWNPKFTRLRSHFDGI RALAFHPIEPVLITASEDHTLKMWN LQKTAPAKK*EYSTLTLEFYFK*HA
3723	9220	A	3998	3215	3491	SAKVLRLPTFFFFFFFFFAIESHCVT QAGVQWCNLAQLQSPTEFK*FSC GLPSSWDYRCVPPHPANFYIFSRDR VSPCWPGWSKTPDLK
3724	9221	A	3999	1	779	MNNGRNYRCQNLVDKGVGENRGP ADNRMLVAHQCSREEKLKEPDEQV TPAVCQQDSLAMERLGRSPTAEK VPETTRFWAPGVEAPGDDAERRR REASGPATRHSPPLTAGITAPKAGS AKVQLSILKPSKLDKCSHKTSHTKS SYHYFLHYPVSSTVQPVAAAATPSY ALIGSSLWPVNERGRQESRTCHDQ SAWHVGRAEIRKLLPYCSTQGGK YSDVTSGMVKDPPDVL/DRQKCLD ALAALRHAKWSSEIRF
3725	9222	A	4000	1	1286	MEMRRYEEDMYWRRMEEEQHWW DDRRRMPDGGYPHGPPGLGLGV RPGMPQPQGPAPLRRPDSSDDRYV MTKHATYPTTEELQAVQKIVSITER ALKLVSDSLSEHEKNKNKEGDDKK EGGKDRALKGVLRVGVFAKGLLLR GDRNVNLVLLCSEKPSKTLISR NLPKQLAFISPEKYDIKCAVSEAAH LNSCVPKMQVTITLTSPIREENMR EGDVTSGMVKDPPDVLDRQKCLDA LAALRHAKWFQARANGLQSCVHIR ILRDLQCRVPTWS\DFPSWAMELLV EKAISSASPSQSPGDAL\RRVFECIS SGVILK\GSPG\LLDPCEKDPFDTLG QQ*PDPAASRED/LSTSQCCHSLPLETS LAFPPRYHKV\LGMDPITRK*AQR N\HNRRKR\RRD\SDGVDGFEEAGK KDKDYDNF
3726	9223	A	4001	2	379	DLPASATQNAIGTVSHHIWPRIIFL LW*KTFITLTLFSLVQYSSNYIHPVC NRALELFKSYKTETKLNFPSPPPPI VNLHCIFFF*GLTFLGFFSLPKYRG FTNFVSPCTVAMLTRGGGGGEF
3727	9224	A	4002	229	445	RPGPNFGLLETLTWGLKGTWLWNP PKNWELGAHPPTPGNFWIF*KGGF WNVSQGGSKTRGLRELPPFSWKKG
3728	9225	A	4003	192	529	HEVLNFLTSCVLTTLVFLIADIWLS CRTRSLPFVATTLEVLPLSLIGLCHH TILVFISNAFFI*KAYFVTSSFIMFP*S FFLFNISVLSYMYLTFSHLTSFVIAY FSYSHI
3729	9226	A	4004	330	754	SDLSQKSSSSLSKFLVTEKNSSLGS GGCDMANKENELACAGHLPEKLH HDSRTYLVNSSDSGSSQTESPSSKYS GFFSGGFLRDHETMAQVLFSDMR LNVALTFWRKRSISELVAYLLRIED LGVVVDCLPVLTNCLQE

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3730	9227	A	4005	296	861	VSQDHETMAQVLF SRNMRLNVALT FWRKRSISELVA YLLRIEDLG VVVD CLPVL TNCLQEEKQYISLGCCVDLL PLVKSLLKSKFEE*CY*WVLTGLQA VIKRW WSELSSKTEINDGNIQILKQ QLSGL WEQENHL TLVPGYTGNIAK DVDAYLFPVTIEGFHLLKSIWFFKTS LELYNLQKKKVS
3731	9228	A	4006	2	265	NNFFSFSETESHSVTQAEAQWYDNS SLQP*ILGLKQSFCLSLPSNWDHRC APPHPQFSFLIPGLYVSQFILGNKPSS LPCQMFKSAV
3732	9229	A	4007	3	295	HFNLSHRSAAKGNRYKEAEALTN AAVHVDDMPNALNALIDLRAHNLG QDPVNFKRLSHCLLVTLAAHLLAEL TPAVHA*LDKFLASVSTVLTSKYT
3733	9230	A	4008	1	1077	
3734	9231	A	4009	3	285	ETESRLATQAGVQCCDLGSLQPLSP GFK*FSCFSLPSSWDYRYPPSCQAN FCILVEMGFHHVGQASLELLTSGDP PASASQSARITGVSHRAQ
3735	9232	A	4010	1	338	VIATYHGGLCTQKSQPPPPQALWSA STSTINLMVSTEPLALTETHICKLPK D*GTCRDFILPWDYDSNTKSCARF WYGRCSANENDFGSQSECEKVCAP VLCKPGVISEMAT
3736	9233	C	4011	269	526	MLARLVSNLSPQVIHHTQPRVGSPT RIPTLSLNLPLPLALTSRLWRDRHQLR GQGHWGAQELRAITGFKDHQVWQ TLNCSLCVPKP*
3737	9234	A	4012	2	51	
3738	9235	A	4013	83	5229	
3739	9236	A	4014	3	45	EVVHALRCRWWSWGLKDLLTPEP EPICGPALLSRSSLRGSHPTAFLLPP QVSQ*RGELGPSTFRAFAEFPTSRG SKDNKEKNQEQDMAKPATGTGQ G*GADGGAGA
3740	9237	A	4015	3	323	LLWKVESSWRDQKDIMSWEWDKR RRRHHLTDRSQLCSKVKFQVDCDLI EWGTWIINLKQYNAYHCEGECHNP VG*KFHQSNHAYIQVGCQVLGEE AVIWHWGTGL
3741	9238	A	4016	2	279	FFFFEAKSHSVTRMLECNGAISAPC NLHLPGSSDSPASASQVVGITGVYH HTQLIFISVETGFCHVGQDGLNLPD LMIHPPWPPKVLG*QA
3742	9239	A	4017	166	939	
3743	9240	A	4018	2	225	KELTGRRC AEPHPRPSPQLL TEEP TKGRFSGEWGRNAASMTGPFAE HSNQLWNISAVPSWSKVNQGLIRM YKAEP*EGADRKALCRASPPPIPPV TDRGAIYKRPI LWVERQERSVYED WPICRALQPAVEHQRRPFLVQSEPG SHPHV
3744	9241	A	4019	142	1336	KARGDCKHPGRCWPEQMAEGEQ PPPSSEEAPPATQNFIPKKEIHTVP DMGKWKRSQAYADYIGFILTLNEG

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						VKGKKLTFEYRVSEAIEKLLALLNT LDRWIDETPPVDQPSRFGNKAYRT WYAKLDDEAENLVATVVPHTLAA AVPEVAVYLKESVGNSTRIDYGTG HEAAFAAFLCCLCKIGVLRVDDQIA IVFKVFNRYLEVMRKLQKTYRMEP AGSQGVWGLDDFQFLPFIWGSSQLI DHPYLEPRHFVDEKAVNENHKDY MFLECILFITEMKTGPFAEHSNQLW NISAVPSWSKVNQGLIRMYKAEC \EKFPVIQH/FSKFGSLLPIHPVHVGL GGAKPKPEPRGTVSCCLPFPPTPAVA PPSPSPSVSSRLMRGCLLGLGGEMG LRGLRA
3745	9242	A	4020	80	283	
3746	9243	A	4021	61	626	DLICVIGVPEEEKETGAKNIFKEIMG ENSPHLVKDVIVHIEIHSQIDEN*** Q*KSYK**QKGIIKLRVDLLETMEA KCSRTPSLKCLGKESFGESWESRILH PAEISHRNECHMKIILDFKSEKGPDA VAHTCNPSILGGHTAGGSLEARSFE TNLPETLSLLKKNLKEKEFVASYP PLVEMLK
3747	9244	A	4022	18	161	TSFKNPPPPPGGLKKIPSPPPKKK KFKDVS*PTYFLYLNASSVT
3748	9245	A	4023	30	262	NRRQAGPFAKLGRPSKGGFPNFF KSSSSKSSF*KNPKGQGWGFPPLIPG FQGPQVGGSLGAPGLKPPWGTPQN PF
3749	9246	C	4024	193	366	MYNYSIPKNKYTYTYTKSYPNKIF SRLILYIPLGTVSQISTLNCVPRFVLL TWKAL*
3750	9247	A	4025	3	258	TIDSLKGLPCKQNEPWHTIQCGYL GNSSKWN*YQSGKDFIRIAFCVCIC I/CYF*E*IYSCT*IPVRNTLNELNPLA KCPCPFH
3751	9248	C	4026	164	313	MEGTRIFGKVVKLIQIPNRNSCTTI DLFLKINIHIHTQKAILMKSFDP*
3752	9249	A	4027	9	373	DRVSLCRPTLEVQWRDLGSLQPPSP QVQSNPALSLPSSWDYRRVPPCPS *FFVFLSRRWRFRVGGTALFLIKM MGKKILKIKSNYTLGLYVGPSYSER MIKPQEFESSLGQHCKTPSQK
3753	9250	A	4028	1	336	DRILLHRPCWSTLARS*LTIPSNHLG SVFPPSALLES*DCRHTPTTPD*FLKI FL*RRGLTVFPRVLNVAWTQAIQPL PLKALGLQDTFFKNINCDRLKVSEY YSDTEIEI
3754	9251	A	4029	514	742	LPKC*DHRHEPPHQAFFNFFVEMG SCHVPQSGQLLLGSSDLPASAFYSA GIAGMSHHTWPPYLFKSRHKSFRCP S
3755	9252	A	4030	1	264	QAQGHKPGSFGPPFAGLKGFPGGLGF PRTGNSGGFPQGGKYKGFLIKNGVP PSFQGGF*IPGPGSHQRLGFRG*VGR AL*TPGFRATLF
3756	9253	A	4031	7	417	RQDLALSPRLECSDTIIAHCSIKLLG

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						SNGAPSAAS*VAGTTGTRHHAQLIF LKIFVETRSLYVAQASCVFPASSNPP TSASQSTGITGMSCCARPTSYVPGS DLSVLCILTHLILKIPLYRRYYYFVS LTYSKAEVQ
3757	9254	A	4032	123	376	KTGSNFVPQAEAQGGNSG*LNPLPP G*KQFSGLTLLITWINRAPPPPRANF GIFKKKGVSPCC*GGLKTPNSGFSPF KPPKGLE
3758	9255	A	4033	3	292	QWHKHGLLQPQPPGLK*SSHLSLPR SWDHRHVSPCLTNFF*FSVSMGSCY VAQAGLKHKLASSDPPASASVGTIG MSTT*SKTTLYTEKLANIILTK
3759	9256	A	4034	1	230	FFF*TDSCSVAQAGLQWRDYRPEPP CPANFITIKQVQNKSVTFARNLNK MRGASIMLYPIGLSLNDLMQLLSEG F
3760	9257	A	4035	3	189	SWDYRRLPHARLIFVFLVGTGFHHV VQAGLELLTS*FTRLGLPRCWDYRR EHIAPGHIWY
3761	9258	A	4036	2	148	PGSSNPPTSASQLAGTAGTHHA*LI FVCLVETGFCHVA*AGV*VKFF
3762	9259	A	4037	348	696	AEEQDKKGRQ*ERGKEWERETETK IYSRIKGNREGQAKKKWGHGELIH KTKDEKRKKSEEDKKLRWRKR*TN SQKD*IRKRLHKETANSER*EEKHK ERKQWRRGPKARRAISRG
3763	9260	A	4038	1	295	QNQFFIFIYFKTESGSVTRLEYSGLVIS AHCNLCHPGSSQSPASAS*AAGTTG AHHHIQLLFVFLVETGFHHVQAG LELLTSSDLPASASQSAWGLQV
3764	9261	A	4039	6	151	SQGLALLPRLISNPWVQAILLPWPP KVLGL*AEIAQNKMOK
3765	9262	A	4040	101	318	SNHTLGTS*HFFFETVSCIMLHRVE CSGAVIAHCNLELLGSSDSPASTS*V AGTTAVYHHTGLSWLLNLH
3766	9263	A	4041	210	306	SWPGTVAHICNPALGGQGGWIA* GQAFRQA
3767	9264	A	4042	2	147	DFSVKTL*ARREWRDIFTVMKEKNF YPRKVYALKIPFKNEAETKKVEV
3768	9265	A	4043	160	525	NTQTRSFGNRLMAPAQSSHKALTK KVMTCNPSETVHDSQECFFVLFFET VLVCLPGWSAVMLVRCCLLSSW DYRRVPPHLG*FLYF**R*CLTMLA RMVSNS*PQVIHLPRPPKLLGLQA
3769	9266	A	4044	3	72	KTQVHFQGWQHSVHIHPCWEKL ALSITPLR*DNRKLQAWNSPRLGPT CLFPRLALMCVLMML**NIHEYNSFQ RVLWVLLVNC*ISKVGSTLCISSHIP AGRS
3770	9267	A	4045	313	358	
3771	9268	A	4046	7	308	AGGRRARAPHLGGRGAARGRL*RV RGHRERGLRAAPVPRPQQLRRGA AAGAVQPGQGVGRAGPPEGSEGSV AGVGLDLDSscyHHSSDFYICHMP ISS
3772	9269	A	4047	92	390	ETGSHSVNLAGLQWCDHNSLQP*T

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						PGLKQSSYLSLLSS*DYRWVPPCPA NF*IFFVEIRSCHISQAGLDLPRPSDP PVWGSQSAGTIGMSHHAQPREIC
3773	9270	A	4048	65	375	SQLTATSTSRVQ*HDLSSQPPPPGF KRFSCLSLPSGCDYRHPPPHLANFL YFLVETGFCHVGQAGLELLTSSDLP ALASQSAGITGVRYCAWPTFLIMKT CIPSFPLPSTSPIPLP
3774	9271	A	4049	12	292	DIVSPVA*TRMQWHNLGSLQPPPPR FKQSLCFSLPSSWDYRCVPPCPAIF VFLAEMGFCHIGQAGLELLASSNPT TLASQSAEPPLAATDF
3775	9272	A	4050	40	343	SSSSLILSSSVIYLLNLSDIFLVLLY FLVFRFSVCSFCFQFFVKNFNLIYF FKHIKNICFKVCV*RLGFLDPLCAYF GCLLFL*VFSHVLSLHIPDDL
3776	9273	A	4051	97	282	
3777	9274	A	4052	3	336	FFETGSRFVTHAGVKWHNHDSLHP QPPRLK*FSYFSLSSWDHRHVPP RPANLVYLL*RGGPPSMLPRASLEF PGLQVNSSLPSALPKVLGITG*GHRP RPKVTFHQRG
3778	9275	A	4053	3	294	CCFGDGVSLCRPGWSIECSGNHSSL QAVEPRLR*SSRLSLLGSWDPSHV PLHLANF*TFCTHGVLA MLPLAGLK TPWAQTIPPHLSLPKVLGLQG
3779	9276	A	4054	16	308	MPQPN*SNPPVNCRLPRGPPSQVP PRIHLSPKYSPSPEASAPDLQKKGNL QAPRRPGEVLETPRKPESSCMKFP* REIKPLPPRLTPSVHSMVL
3780	9277	A	4055	445	448	IS*HCDASASIFRKKQRKQINKHPTL ASRVLGLAMEMQDETWCSCQSET VN*SQTAQNHPQPGS*PAGVCLWV ASSQHFTPQPLKKPNPDSAKLNSA SDSLTEVILCKIFSAWQTDK
3781	9278	A	4056	3	284	CLSLSSWDYKCLPPRLGYFLYF** RRGFTVLARMVVISRMVVISRMVIS *RRDPPASASQNA GITGVSHCARPK EQKLFYPEVSCLYLGLY
3782	9279	A	4057	428	636	DYHIVSLLHLF*FLETGSHSVTQAGI QWCDHSSL*PRTPLKQSSCLSLPE* LGLQE*VTVPGSYSLFF
3783	9280	A	4058	2	113	FFGRDGVSLCCPDWS*TPGLKGSSC LGLPKCWDYRRE
3784	9281	A	4060	36	359	RSQVQNGFHQAEVLSVRLCFSTEAL GQNPMPPFAPPATSSPGPRPSCHL HSQKL/TLLHAQTLVTPPL*GLGLS AWRTLGGAPGLHPFTTHALSTPET IPGAYRRT
3785	9282	A	4061	17	168	APGMVSGVLSACVVNGWSPGAPPA SVLQA/PQT*PF*SRPHVTSQPLLKA PH
3786	9283	A	4062	2	375	FFFFFENHTNLLSYSSRGSGVQNGF HQPEVLSVRLCFSTEALGQNPMPPF APPATSSPGPRPSCHLHSQKLPLLH AQTLVTPPL*WPPWITQGGPPQST GHLPTTEILKLKHHRRRVPFCHAR

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3787	9284	A	4063	309	620	
3788	9285	A	4064	3	218	LRQSYSVTQAGVQWRNLGSLQLPL PGFKRFSCLSLRKS*DYRRPRLPNFC ILVKTGVHPCWSGWSQTLDLR
3789	9286	A	4065	1	170	NPKATPPQIVNGDQYCGDYELFVE AVEQNTLQEFLKLA*VKPVQSSPAG LHHHTPL
3790	9287	A	4066	29	483	RRLPAVQLPLTAALCPPARLSTPSM SGPARSTARRATGFREIKVPSKSEVT RIL\EGKRIQYQLVDISQDNALRDEM RALAEQPQGHPTPDLSTGDQYCGD Y/DASFVEAVEQNTVAG\FPGSLGL KFKPCSRVSPCWDSSHQHSPPAFQP GQ
3791	9288	C	4067	33	236	MRHHAWLIFVLLVETGFHHVQGAG LEHLISGGPPTSASQSAGITGVSHHA WPIYLFILLSGPSRLCF*
3792	9289	A	4068	1	205	AIGTDKGTRWPSEDDPGNLPEIFLFI LGPTADYV*RERQRSIELESFYRRV WGSPGGEGTGDLEDFD
3793	9290	A	4070	2	44	LSSWDYRHVPRLANFCIFSRDGGF TMLARLVLSN*PQVIHPPQP*VL*L QACATTPG
3794	9291	A	4071	173	369	CSTLI*IRKVWLGAHAHAYNPNTLR GRGGRIA*GQVFKTSLGNVKTCLF LPSPHNQQSLSGFLL
3795	9292	A	4072	1	336	
3796	9293	A	4073	1	200	
3797	9294	A	4074	11	392	
3798	9295	A	4075	1	191	
3799	9296	A	4076	84	264	
3800	9297	A	4077	2	446	DSARNSRVDGCE/IDRQKGTNDSLM MLMRELEDRFASAGYQDNIALR EEEIRHLKDEMARHLREYQDLLNV KMALDVEIATYRKLEGEESRINLPI QTYALNFRETSPEQRGSEVHTKK TVMIKTIETRDGEVVSEATQQQHEV L
3801	9298	A	4080	3	196	SRAKGPKNYNFGQGPPTKVKGPLA SPFFPLLPFPRPPWFPPPF*NPIFPW W*KGPKKPFLN
3802	9299	A	4081	1	187	SIRLFFCFFF*AETGFRHIGQAGFGL LTSSVPPALASQSAGIIGVSHRARC SSLIVLHL
3803	9300	A	4082	156	326	KLEICRRARVSLKIGFIRPGTVAHAY NPSTLEGRGRQIT*DQEFETSLANM VKPCLY
3804	9301	A	4083	3	448	
3805	9302	A	4084	1	4249	AAATIRYLKTTMAWKTLPIYLLLLL SVFVIQVSSQDLSSCAGRCGEGYS RDATCNCDYNCQHMECCPDFKR VCTAELSCKGRCFESFERGREDCD AQCKKYDKCCPDYESFCAEVHNPT SPPSSKKAPPSGASQTIKSTTKRSP KPPNKKKTKKVIIESEEITEHSVSEN QESSSSSSSSSSSTIWKIKSSKNSAA NRELQKKLVKDNKKNRKTKKPTP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KPPVVDEAGSGLDNGDFKVTTPDSTTQHNVSTSPKITTAKPINRPSLPPNSDTSKETS LTVNKETT VETKETTTNKQSTSDGKEKTTS AKETQSIEKTS AKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTT KSAPTT PKEPAPTTTKEPAPTTTPKEPAPTTTKEPAPTTT KSAPTTPKEPAPTTPKKPAPTTPKEPAPTTTPKEPTPTTPKEPAPTKEPAPTTTPKEPAPTAPKKPAPTTTPKEPAPTTTPKEPAPTTTKEPSPTTPKEPAPTTT KSAPTTPKEPAPTTT KSAPTTPKEPSPTTTPKEPAPTTTPKEPAPTTTPKAPAPTTTPKEPAPTTTPKEPAPTTT KKPAPTAPKEPAPTTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPNTPKEPAPTTTPKEPAPTTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTS DKPAPTTPKGTAPTTTPKEPAPTTTPKEPAPTTPKGTA PTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTS DKPAPTTTPKETAPTTTPKEPAPTTPKKPAPTTTPETPPPTTSEVSTPTTKEPTTIHKSPDESTPELSAETPKALENSPKPEGVPTTKTPAATKPEMTTAKDKTTERDLRTPETTTAAPKMTKETATTTTEKTTESKITATTTQVTSTTTQDTPFKITTLKTTTLAPKVTTTKKTITTEIMNKPEETA KPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPTTTPRKMSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIINPMLSDETNICNGKPDVGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRRFERAIGPSQTHIRIQYSPARLAYQDKGVLHNEVKVSILWK\GLPNV\VTSAISLPNIRKPDGYDYAFA\KDQYYNIDVPSRTARAITTRSGQTL SKVWYNCP
3806	9303	C	4085	258	362	MFYRNLMKVRAELNCSAILIEIKAKVLT L FHSN*
3807	9304	A	4086	2	236	QSYNSDSLFFLRRSFALVTQAGVQWRDLGSLQLPSPGFK*FSCLSLPSSWVYRCPPDPANFLVLVETGFHHVGQGS
3808	9305	A	4087	224	464	KIFLFFFFFKRQGLTLSCRLDCSVQ*HNHYPLQSRTPELKQSSCLSHPKYWD*RHEPLCLAPKKEDTLQEQLIRLLIY
3809	9306	A	4088	129	315	ILKILWIFRIFLLSIKCF*TNMHVCV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SCLFIFLTVSFIEQTF*ISFFYASWIML LMSFFF
3810	9307	A	4089	1	190	FFF*IGPHSVAQAGVRWCDLGSCSL NLPGSSDPPASASQVAGTTGVHYYT QLIFKFFIEMRAP
3811	9308	A	4090	1	5229	
3812	9309	A	4091	1	7044	
3813	9310	A	4092	170	422	
3814	9311	A	4093	1	3230	
3815	9312	A	4094	3	151	DTATCCAKWNTEDKVSHVSTGGG AS*ELLEGKALPGVDATSTIYYFPF
3816	9313	A	4095	2	1446	SLRSARRQSAPSLTESPTSLPSCISK MSLSNKLTLDKLDVKGRVVMRV DFNVPMKNNQITNNQRIKAAVPSIK FCLDNGAKSVVLMSHLGRPDPVPM PDKYSLEPVAVELKSLLGKDVFLFK DCVGPEVEKACANPAAGSVILLENL RFHVEEEGKGKDASGNKVKAEPK IEAFRASLSKLGDVYVNDAPGTAHR AHSSMVGVNLPQKAGGFLMKKEL NYFAKALESPPFLAILGGAKVAD KIQLINNMLDKVNEMIIGGGMAFTF LKVLNNMEIGTSLFDEEGAKIVKDL MSKAEKNGVKITLPVDFVTADKFD ENAKTGQSTWASGITPG\WMGLDC CPRESS\RYAE\AVTRAKQM\WNGP V\GYFE\WEAFA\RGTKALMDEVVK A\TSRGLPSPS*GGWRPLPTCCAQM ETREDKSQPM*ATGGWCPVWQLE G*SPFLGVDALSQYLGTFPALLSPC AQPPKVNLGIFLHLPLGH
3817	9314	A	4096	1	747	MDSSRARQQLRRRFLLLPDAAEQL DREGDAGPETSTAVEKKEKPLPRLN IHSGFWILASIVVTTYVDFFKTLKEN FHTSRSPESPAPRRGGVRASVPQKL AEMLSQYGLIVFVAGLLLLLAWA VHAAGVSKSDLLCFLTALMLLQLP VDAVVRGPQLRAPPLPPQGHARG CRLAARQRPPTVSTGRGEHVDSPPP AQRRLSYLPLRLRGAFAEPSPSAPA HRA\TPPPVEVTPTEAGRFRQAKG ALS
3818	9315	A	4097	1103	1295	EQEGTGLERRRGSPMSKDWPPPHL TPPQGPGIPVHSLSPPSFSPGPRNS K*ARRSTAPVDCK
3819	9316	A	4098	1	1302	MVAGSDNYHEVSLHDGVIGARGCP PPSPSARGARSPPPGGCARQPTA GRDAEQPVWADRVRGGAAGL GRARRGLAESDLLCFLTALMLLQM LWYVGRSSAHRRLFRLKDTAGAG WLHRLWIPPAFGCRPEYDNGLEEI VFGFEPWII\VNLAFAFIFYAMHA AASLFEVYSGISETSVLGDWSKPSTF DSKASGLRHLKTSKGSSLVNASIP TPPSFPRPSQPSEPASQPAKPAKPAK PVSQPSQPSQT\PGKPAKPAKPPKPA KPPASQASQASQPGMPAKPAKPAK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						K/PKPGMPAKPARQPSQPAKTAKPA NQPSQSASQASQPASQPSRPACQPT KSARQPRQPSLPAAKRANATYQRS HSASQDRHASEPTSQPSSQHSAAARP AATSQPDSRAANQSAVEQARQPSA KHSGKQQADSEAAAGS
3820	9317	A	4099	684	902	
3821	9318	A	4100	143	551	TNEFPFHSRSPPIQTS*AHFPHLITD PDLLSPLSPSHHRSRPPEPTSPISPIQ TC*AHFPHLITDPDLLSPLSPSHHRS RPPEPTFPISSPVISWAPAFSPNCCC KQTATDSSGFHFCLIVLIAKSPKRISP G
3822	9319	A	4101	14	209	ASFVWLIWE*RPWHGTYPSCKNW GKFASGSVTIWFKLPSGPLALSGIL MRLLLLSLSLHENSVS
3823	9320	A	4102	126	265	
3824	9321	A	4103	74	196	NLGMLAHAYNSRNLGGQVRTII*G QKFETSHENISRPCLV
3825	9322	A	4104	1	217	NIYMFLICFVLIFNFLNELIT*KHIVIF ICWILSLLLTLH*FWCHKFHVSW NLEFCIFYFGFKIKLDTFT
3826	9323	A	4105	3	268	DRVLLCCPGWSAVSQS*LTAPQTPG FK*SSHLSLPSSWDYRHIPPHLAKK QKYFK*RWSLPVLPRLV*NSWAQAI FPCQPPKGLGLQA
3827	9324	A	4106	3	263	DSLALSLRLECSGVISAHCNLCFLGS NNSPAAASRVAGTTGACH*DWLIFE FLVETGFHHIGQAGLELLTEVICLP WPPKVLGLQM
3828	9325	A	4107	22	208	SFSIQGPLLLKPNS*PGVVAHSYNPS TSGGQGRCT*GQEFESSLVHMAKP HLYQKIQKICR
3829	9326	A	4108	122	339	EKGFWFCAQGGKNLPGGNSLEPSA SGLKEIFGLNLLNNWE*RGGPKTPG NFWIWKKGGV*PLWPGWG*NPGL
3830	9327	A	4109	2	210	KEKIFSPGFKHPPPPF*KTPLKGGK RIFFSPPRKNWPPQRIFKAPPSSSSS SSSSSSSAQI*SFNSP
3831	9328	A	4110	3	76	ATSESLDVMASQKR*SRSGSPMARR
3832	9329	B	4111	1	2142	MGGAGSPQVILVSHTPQSASAACEE IAYQVAGVSGNLAPGNQPEKEGRA HQCLECDRAFSSAAVLMHHSKEVH GRERIHGCPVCRKAFKRATHLKEH MQTHQAGPSLSSQKPRVFKCDTCE KAFAPPSQLERHSRIHTGERPFHCT LCEKAFNQKSALQVHMKKHTGERP YKCAVCVMGFTQKSNMKLHMKRA HSYAVAVAMGGTAQCPPGATACL GTAICPSGLRAQRPSNLSVPEAAKP KSGRNRKIEAPTWALSTSKDPQTEG LRNPQTCVQIRSNPFCAFAQGFSLIS ELRTLNCVGLCDSQSGKQQLGFYS GQPATEAWQKYS LAVCILRSEQEIS ATRLGLKNTNVNKLDGGCGAWN LGGMSEHNSPPSGRAILLPVVFTFV FPGPWTPQQGSHICRMNLAPTQAF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LPKTGFIDPQELLQGPIERTIWPGT VYTFRSAIVTARA VVVRPRMDRRA DLSSATQSASAEKFGGRVSAGHCA LPLPARPVTASVYGRRLARLRCLED SYPSALSAQVFLDSPAVGCGLETRL FIEAALGPPCRATVTSRGHLLDISIT KSPGRPCFLSVCLHGSDDQQRKGA AATAKRKSKGGGVNVEGRLCTWPP EDPPKSWSLAFGLQEKTTTELNLHP RCWARCLSHWELPPGPRGRAQAPD WTGSKSFREQLLTFTLWGVQEKISK HQANQGKEAPAYTGLESDPGGGLC AV*
3833	9330	A	4112	1	551	
3834	9331	A	4113	3	288	CIGLGVAHACGPGTLGGRGGRIT* AREFGTSLGNIARSHLYKKRKNSES QMSLHLLTDLTPYISAAFASPVDA DTQLSACTFQLKETPMPSF
3835	9332	A	4114	3	344	VQYYGPAT*VQDGS*GYRTHMYMI NQIWLQAVLKIITNKTGRALTILTQ QETQMRNAIYQNRALDYLLAAEG EVC RKFN LINCCLHIDNQGQVFEDI VRDMTKLAHVPMQV
3836	9333	A	4115	6	185	LAGHDRVRL*SQLFRRLRREDCLSS GGRGCSEP*SHHHTPVWTKLGPV SKEKKYNQIV
3837	9334	A	4116	1	176	QSIFQICIFFKFTVYMFKTFLKFQTV FLCGRCWFL*KGLIIFFTLYFKTFHH IVRGIK
3838	9335	A	4117	1	312	GGEKNQDFTFKMESPSDSAVVLPST PQASCLSLPSN*DYRHPPPCPANFCI FSRDWVSTHVGPGWSRTPDPQVIH RLGLPKTIRGSEEGIPDEYQLKGTLI YKL
3839	9336	A	4118	1	112	GKTFKQKQKQEQKKQK*ELK*KAM GKGPLAAGEIKKS
3840	9337	A	4119	3	355	SQSTKNLPSLARDMDIQIEAQRSP KRSPPRHIIFELTKVKDEKNPKVPV EKHQVIYKGFIRITAETSQARKKW DDISKFLKEKKKYRSKILCTANQSIR N*VEIASHSGSCL*SMILTA*PATVA HAYNP
3841	9338	B	4120	638	3862	MKGTCVIAWLFSSGLWRLAHPEA QGTTQCQRTEHPVISYKEIGPWLRE FRAKNAADFSQLTFDPGQKELVVG ARNYLFRLLQLEDLSLIQAVEWECDE ATKKACYSKGSKEECQNYIRVLL VGGDRLFTCGTNAFTPVCTNRSLSN LAEIHDQISGMARCPYSPQHNSAL LTAGGELYAATAMDFPGRDPAIYR SLGILPPLRTAQYNSKWLNEPNFVS SYDIGNFTYFFFRENAVEHDCGKT FSRAARVCKNDIGGRFLEDWTTF MKARLNCSRPGEVFFYYNELQSTFF LPELDLIYGIFTTNVNSIAASA VCVF NLSAIAQAFSGPFKYQENSRSALP YPNPNPHFQCGTVDQGLYVNLTER

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						NLQDAQKFILVHEVVQPVTTVPSFM EDNSRFSHVAVDVVQGREALVHIY LATDYGTIKKVRVPLNQTSSSCLLE EIELFPERRREPIRSLQILHSQSVLFV GLREHVVKIPLKRCQFYRTRSTCIG AQDPYCGWDVVMKKCTSLEESLS MTQWEQSIACPTRNLVDGHFGV WSPWTPCTHTDGS AVGSCLCRTRS CDSPAPQCGGWQCEGPGMEIANCS RNGGWTPWTSWSPCSTTCGIGFQV RQRSCSNPTPRHGGRVCVGQNREE RYCNEHLLCPPHMFWTGWGPWER CTAQCGGGIQARRRICENGPDCAGC NVEYQSCNTNPCPELKKTPWTPW TPVNISDNGDHYEQRFYRTCKARL ADPNLLEVGRQRIEMRYCSSDGTSG CSTDGLSGDFLRAGRYSAHTVNGA WSAWTSWSQCSRDCSRGIRNRKR CNNPEPKYGGMPCLGPSLEYQECN TLPCPVDGVWSCWSPWTKCSATCG GGHYMRTRSCSNPAPAYGGDICLG LHTEEALCNTQPCPESWSEWSDWS ECEASGVQVRARQCILLFPMGSQCS GNTTESRPCVFDSENFPEVSVARSSS VEEKRCGEFNMFMIAVGLSSSILG CLLTLLVYTYCQRYQQQSHDATVI HPVSPAPLNTSITNHINKLDDKYDSVE AIKAFNKNNLILEERNKYFNPHTLG KTYSNAYFTDLNNYDEY*
3842	9339	A	4121	3	124	NVNRPVSSNEIKIIKSLPVKKSP*LN GFNAEFTKHVKNL
3843	9340	A	4122	1	197	GFKQLS*LSLPNSWDHRHTTTTPRE MGFHHVVGQAGPELPISGDPAPASQ SAGITGVSHRTRPRI
3844	9341	A	4123	1	268	QLYHLSLQSSRDHRCEPPRPANFLII CRDEVYVAQAGLKLPSDDPPASAS KSAGSTGVSHCTQAKFYFF*NLMG EMRGKNNKHLTSFK
3845	9342	A	4124	3	301	TEEIHGVLSWNLVPDNYPPYYHPPP PSYIYGAQHLLRLFLVKLPEILGKMT FSDKNLKALLKHFDLFLKHLAEYH DDFFPE*AYVAACEAHYCTHNPRSI
3846	9343	A	4126	2	214	FFFFKEMGSHYVA*AAVKWLFTGA IITL*SLKLLDSNNTPALSECKLIITQ EASVLKIKKVEIKKTKNRN
3847	9344	A	4127	2	382	TMVLSPADKTNVKAA/WGMFLSFP TTKTYFPFHDLSHGSAQVKGHGKK VADALTNVAHVDDMPNALSALS DLHAHKLRVDPVNFKLLSHCLLV LAAHLPAEFTPAVHASLDKFLASVS TVLTSKYR
3848	9345	A	4128	2	253	
3849	9346	B	4129	317	683	AHKLRVDPVNFKLLSHCLLVTLAA HLP AEFTPAVHASLDKFLASVMHR ADLQIPLSWSLATGCQKLEI VDDER KLRTFY*
3850	9347	A	4130	1	82	VDGWVDGWVDG*MDR*VGRWID

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						GWVDG
3851	9348	A	4131	1	240	ASTFFFFSIDRVLLCCPGWTRTPGFI* SSCFGLPKCWDYRSEPPCLATFFFIK KKYKEEHFILLCQIVNMILILYQPT Q
3852	9349	A	4132	3	180	REPPLPAANFVFFVEMRSHHVRQA GPEPPSSDLPASASQSAGITGVHCH AWP*YTYL
3853	9350	A	4133	2	238	SPCAGILEDDRADYQGTRKTSEYSS VTP*EACHT*EGPIAFISWP*KVPIQL TFNERNRARGFQVPYGTDRGLPG TH
3854	9351	A	4134	7	259	IVTAALFTLAPNQK*SKYPSSGKLIN KFWYIYKME*TSISNKQVSTTYSMQ AWVNLKSITLS*RHKGVIYII*SHLYD ILEKTEL
3855	9352	A	4135	141	309	AFDEAIAKLYSVNE*SYKGSTVIMQ LVRVNLAVSATSTGFIVSFVFTYPIIP CYLQ
3856	9353	A	4136	113	205	HNLLMLFDLCLLYWL*LIFLIHELAE NLLN
3857	9354	A	4137	3	215	FETGSCSVTQAGVHWRDHSSLQP*S LGFKQPSNLSLPSSWDYRCTPPHLA NLCIFCKDRVTSYCPGWHPV
3858	9355	A	4138	3	386	
3859	9356	A	4139	1	255	IRLMKEGRMKGQAFIGLPNEKAAA KALKEANGYVLF GKPMVVQFARSA RPKQDPKEG*RRKRTWLFNKVGK WELAPKPMGLDFSL
3860	9357	A	4140	78	153	
3861	9358	A	4141	1	293	LRLPGSSHSPASVS*VAGIAGACHH AWPNFCVFSRDQGFTHVGRAGLGA PDPLDPALPWSPKVMGFTRCEAHP CPSPRMRFLKYVSVPSMVGRPE
3862	9359	A	4142	3	48	PLPRKSVEPGGGTKYKTEQKKRQE RRDRGSK*RKQKAATSEEQQRK* AKTQEDGGTKRSPDGEEDPEKKIHR NREGTRKKGQDPRNGVNNKNREK EQN*RTHTS*SQKVRRTRRGNEV
3863	9360	A	4143	1	276	GTRDSV*GGLKLIPIFLMDFWKEPL GPALAHQLQYPGRD*SSDIWIRTA SLHTLPIVGPILLGLASFCTLLTPD PCQHVPFRSRADTVEMG
3864	9361	A	4144	1	154	LVWS*EASKIPGGAEAAHPPTTF
3865	9362	A	4145	2	231	FFFESGSRSVTQAGVQ*HSLGSLQPL PPRFK*FSCLSLPSSWDYTHVPTPA NFCIFSGDGVSSCWPGWSRTPNLR
3866	9363	A	4146	1	303	GTRGSVKEGAKYTSHRDMGLSTFD RDADQWKENCANVYG*GCRYNNC QAANLNGIYYPGGSYDPRNNSAYE TDNGVVVVSFTGAHYSRLAARMKI RPLVTQ
3867	9364	A	4147	3	372	HAGLGAHPLHHPVIQEGFLPAPRG FGYRSEVD*IRIPAESTGQNSQCQLR K*KDDSYFHCYFCGCVCTCRGRL QSSTSHQCQAAL*LLLPVCLTMLRC ISSLIYT*NLKTVHSVRLNFIYN

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3868	9365	A	4148	2	98	RRPFFFFFFFASCI*NLISPNVQLSNFT CILRN
3869	9366	A	4149	1	230	SGRPFLFFQGKERVYFIPVVVLFYT VVVQ*LRKNVVRWQKTMEPPRSW LMQLGHTTEGPGYPLLGETETKLF R TA
3870	9367	A	4150	1034	2354	DRV LAPVAQTGVQWHDLSLQPPP PGFKRFFCLSLPSSWDYRRPP*RPAN FC*FLVETGFRHVGQAGLGLLTSGD PPASASQSSRITGVSHRARTMGLSR ALYRIPALKVWLLINVELKKQMMA HVDVTCLINKSPSLTRPMGKRLSAE TGKGQKEKQKQTGAGCAVLPSRGF PPKAHHGRQPLTLAPSPPTFTSPSP PHTHTHTHTCSPICPRQSRSFQGR MPDPDPGDATCGAGPGGSAPARAA GPRSAPRRAKARVQARVQARAQAR WVRALTLLAAHPRLQPVARIARR AAQSSSSPPATPAKSPPEASGAAA PPALGLERFPGASPNHLTRSTCALR HVGAGGAALGGPGAPRLPHRLEV G REEGRGRRGDGLGHGGCVPAWEP GWRLPSTIKLFIKSKVSSEALEMPFL CICEHLLSYTYSRKHRNVI
3871	9368	A	4151	387	478	
3872	9369	A	4152	757	1477	HKENRNSLELRQNOSSPIWALPLHG LERKGLGRDHSSPHLPLLPSERL*K ASASQGP EWCCPSRAAGPESGRCD QLWESPMASATWKPYRPQPSRSPQ RQRVVLPPLVKGKTPPLFKLLQESV PGDLLPGELSL*PWEKPI*NNFAFNF SQQCKGMFKFPQFRSLARGSNPTSL TGVGPLPLPREFPGEEREGAPQIFKQ NTANGLGPSA*MRAGTAQGCWES* GGNTAPGPGAVNTAN
3873	9370	A	4153	32	255	SRRHDSLHRVTFCISDPHYRKWTNP DGTTSKIFGFVAKKPASPWENVCHL FAKLDPY*PAGAIVTFITNVPTAP
3874	9371	A	4154	1	265	CDTVLLCHPGWSAVAQSQLTTTSA SQIKRFSCNLNPSSQNTRRASHPAN FFYF**R*GFTMLVRLVSNSCPQVIH PPLPPKVLGLQA
3875	9372	A	4155	92	333	FLSFFFF*MGCHSVTQCGVKWHDLS SLQPPHLTFKWFSRLSLLSGWDYRC LAQHQAACCIFSRDGISPF*PCWYQT PDLR
3876	9373	A	4156	16	181	ICSLPSTVDVIEFLDYVVKVSLKL*SI IKICDSKHTHIHTYGYVYIFSPGK PV
3877	9374	A	4157	1	355	TVSLSCSVAQAGVQWHNLGSLQPL PPGFK*FSCLSLPSSWDHRCPPCLA NFCIFL*RWGFARFCHVGEAGLELL TSSDLHTSDSQSAGIIGTSHHAWPH LLVLTCAHTLFRHFYL
3878	9375	A	4158	1	194	FFFFFTISYIFIYTLTTCWEFKQLAGN I/HL*GTVAFFYLKLLKLQDRLTNSF SSATTNVLAENS

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3879	9376	A	4159	112	270	ILGNSLFKNYK*YLSAAVTHACNP NTLGGQGGPVT*AQEFETSLGNIVR PCL
3880	9377	A	4160	1	211	RFSCSLSS*DYRRVPPRAIFVFL VETRFHYVGQDGLDFTSCSARLYL PKCRDYRRELLCPAPASLL
3881	9378	A	4161	2	253	ETDSCSVAQTRVQWYDLGSLQOPP PRFKRFSCSLSPNSWDYKCVPTPI* FFLFLVEMEFHCAGQADLELLGSGD PPASAPK
3882	9379	A	4162	198	276	KPFMAQCSF*IYEAFSCTSSEIRY
3883	9380	A	4163	3	193	HFGRRRADCLRSSV*DQPGQHGET PSTKNTKISQAWWWVPVPTT*EA EAGESLEPGGQRLQ
3884	9381	A	4164	2	515	DTEKMSPWDMELIPNNAVFPEELG TRVPLTDGECKTLIYKPLDGEWGTN PRDEECERIVAGINQVMTLDIASTFV APVDLQAYPMYCTGVAYPTDLSSI KQRLNRFYRRVSSLMWEVRYIEH NTRTFNEP*KPNRPAKSGTDLLH FIKDQTCYNIPLYNMCKKVL
3885	9382	A	4165	3	418	HEADKTNVVTGKTEVGAHAGEYG AQALERMFLSFPTTKTYFPHFDLSH GSAQVKGHGKKVADALTNVTRIK EMRNALCTLSDLAHKLLGDSCTL *LLSHCMLVTLAN*PSSEFTPVAHTL VAKILAFVSTELTSKY
3886	9383	A	4166	1	191	CLETECRYVSQAGMQWHYPG*LQP *PPGYKLSSHLSLPSSWDYRHVPEH PTNFVYFFVERKSH
3887	9384	A	4167	3160	3732	
3888	9385	A	4168	2	326	PRSGSEFSCQLSPFFFFGDRVSLC GPG*SAVV*LQLM*PGPPKLKQSSC LCLPSSWDHRWAAPHLA*FFKFFFI ETGSYHLPQLVSNPWAQASLLPWP PKVLGLQV
3889	9386	A	4169	2	163	LIFVFIVGTGFHHVGQAGLECLTSS DPSASASQSAGITGVNHHTRPPSAF GC*T*GTGFHHVGQAGLECLTSSDP SASASQSAGITGVNHHTRPPSAFGC
3890	9387	A	4170	126	348	HISIFETGSYSVTQAGAQLDGHGSL QP*PPGLK*SSCLSLPSSWDYRHMP CPANFYIFCRDGVSPRCSCGNF
3891	9388	A	4171	1659	1970	MLKGGAKIRSRRTGVSHSLHSDL NFFFFWDKSIALSHRLEYNGAISAH CNLRLLGSSDSPASAS*VARITGMR HHTQLILVFFSRNGVLPCWPGWSRT PDLR
3892	9389	A	4172	153	278	MRPDTVAHTCNPSTLGGQGGRIT*T HEFETSLGDMMKPYLYK
3893	9390	A	4173	3	254	LQYLVFISSKAWPS*KLEDGET*SA GENNNYNTIL*LDLFSHREGKWSKI PYV*AFFALQNNRKLCCQCHDLALI AVISSQT
3894	9391	A	4174	3	225	SLTHLTATSILLK*FSCLGLPSSWDH RCPPPRLANFFAFLVETDFTMLARL V*NS*PEVIRSPRPSKVLGLRA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3895	9392	A	4175	1	344	GGALSGGTGPGFSPSPGKTAAPGQS GNPPGGF*RVSPGGSQRGGFPGNT PAPGPLSSSSSSKGGFGDCTPRDKS RKGGKPPFS*GGFFPQGSAPVKHLA APTNRYSFHPQK
3896	9393	A	4176	2	201	QPGQYGKHPVLIKNSKIKPFWDPP VVPNAREG*A*KMVEPGKVRVQSA QIKALEFNLGPKKKVPF
3897	9394	A	4177	39	225	KSIQSYAI*YNVTCGFFKSALNGVG SVAFCSHHAEHFLGFVFINHEKSQ FCQMILLCMTR
3898	9395	A	4178	322	451	INSTDWAPWLTIVISALWEAEAA/G SRGQEITILANTVKPRLY
3899	9396	A	4179	234	383	
3900	9397	A	4180	86	216	KQTLGQAWWLTPHIALWEAEVGR S*DQEITILPNTVKPHRY
3901	9398	A	4181	1	4123	MEEVEEDRFKENLEGALAGQLLGD EATQALQVLAVELDVVVPALHPQ RLHRLGAALVERQPVREVDHLVLP AVDDEHGRRDLGHLLDVREGVEA VGLLGVAEGDAHARGERRVQHHR GTLVARGQVHGHRADALPVQDD AVRADAVPGGAGAGSAAASNARA PFPAGVPGSSGCDPPVSPLSQVSA HWELCGPHILNASYLPARVRKPFV HWPGQRTFLPAALAHPLGHEEFR QLCPQMSPPNFGLESERPVRCQCN PGQHRGWWRRLWHPLPPAPSLGSG QVLGHLSTTSSHPGAPSPGHWCAA PDPADPAPVTRPPRAQSQARGTHLP PCPCRDPTLLPHALGSDPRQTPSC KAGAWAGRSPQLPPGCHHSNERDT SPVEALGTLWPPPHGSGPRFLQDKG AAGQMAEQTELRAHGHRMAKLRS HRASWASPPDLAAASPHLAPSAA SADGLPATRAQTPRPPPTPSRQAELP PGSPSPGAQGLPGGVVDVGIEVPLGR PARAGTVAGGVVGEDVAVEAGAQ ANVEAAHLAQVHGIAVREEDRVPG TRHAANIHAGDTVAAGALGGEDLD GVQLALAVLEVGTLRQGFWWTLR GTDVETYFAPSAPRAASHGVGRHEEL PDPTGPCGGRLLSLTIHGVTIRYHAL LWARGPIMSKSQVLGEWEPVQGGK SSENDKWTMSDPGAEAPTCSRAAS GVDKEQQGRWQGLWNSHIKPLKIR MVKQNNIIPGETQILLRFTGWESKV NAKKQLPVGIKCEPMDQENEQTGG HETDGHRIVSVLHIFPLISILSYATW GLSLLECIPGSPVCTLLVRFSNVGTR WSLEVRGSPCGFGSNKVCVMTPEI KMVCVCEGKAGKAVGSGGVEGTK EVSTGNAEGPVRHEAVDGGVHLAF ALLQGLLWSLLGPPGLAGWGGGE LDAVPDSTSSATNVSMVVSAGPWS SEKAEMNILEINEKLRPLAENKQQ FRNLKERCFLTQLAGFLANROKKY KYEECKDLIKFMLRNERQFKEECLA

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						EQLKQAEELRQYKVLVHSQERELT QLREKLREGRDASRLNEHLQALLT PDEPKSQGQDLQEQLAEG\LDWH STLSKSSAQKMTKMRMKMFK/CEE DEKVLESSAPREVQKAESKVPEDS LEECAITCSNSHGPCDSIQPHKNKIT FEEDKVNSSLVVDRESSHDGCQ/EC SKHSPSPWPHLFCHKRQHGG/DQPA LCPARRQR*TF*KSMRNCA/HQLAE KKQQFRSLKEKCFVTQVACFLAKQ QNKYKYEECKDLIKSMLRNERQFK EEKLAEQLKQAEELRQYKVLVHSQ ERELTQLREKLREGRDASRLNEHL QALLTPDEPKSQGQDLQEQLAEG CRLAQHLVQKLSPENDEDEDVQ VEEDEKVLESSAPREVQKAESKVP EDSLEECAITCSNSHGPCDSIQPHKN IKITFEEDKVNSSLVVDRESSHDGC QDALNILPVPGPTSSATNVSMVSA GPLSSEKAEMNILEINEKLCPLAEK KQQFRSLKEKCFVTQVACFLAKQQ NKYKYEECKDLIKSMLRNERQFKE EKLAEQLKQAEELRQYKVLVHSQ RELTLREKLREGRDASRLNEHLQ ALLTPDEPKSQGQDLQEQLAEGC RLAQHLVQKLS
3902	9399	B	4182	1	799	MLQIPKQQQNEKYQVPQFDQSTIKN IESAKGLDVWDSWPLQNADGTVAE YNGYHVVFALAGSPKDADDTSIYM FYQKVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWGSATFTSD GKIRLFYTDYSGKHGKQSLTTAQI HFPLISILSYATWGLSLECIPIGSPVC TLLVRFSNGGPPMDPGSERKGFCRF RNHHQTGFSPAGANQRGPLAATLS GPGGEGQSAVARLTGEKKNHGPAQ YANRLSPRVGRFINAAGTTX*
3903	9400	A	4183	260	387	REVGRVRWLTVPVIRWEAEVGRS *GQEIKTILANTVKPRLY
3904	9401	A	4184	1212	1442	
3905	9402	A	4185	3844	4180	KYKKCVGCGGRSL*S*LLRRLRQEN RLSPGGGDCSEPRSSHCTPAWVTER /GDSVSKKKKNLLTWLVNKLCP CRAWWLTVPVIRWEAEAGRSRGQ EITILANTVKPRLY
3906	9403	A	4186	8	385	
3907	9404	A	4187	2	284	
3908	9405	A	4188	1477	1697	
3909	9406	A	4189	17	385	
3910	9407	A	4190	1	837	GKVVLELERFLPQPFTGEIRGMCDF MNLSLADCLLVNLAYESSVFTSIV AQDSRGHIYHGRNLDYAFGNVLRK LTVDVQFLKNGQIAFTGTTFIGYVG LWTGQSPHKFTVSGDERDKGWW ENAIAALFRRHIPVSWLIRATLSESE NFEAAVGKLAKSPLIADVNIAGG TCPREGVVVTRNRDGPDIGPLNPL

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						NGAWLRVETDYYHWKPAPKEDDR RTSA\IKALNATGQANLKLEALFQIL TVVPVYNNLTITYTTAMSAGSPYKY MTRIRNPS
3911	9408	A	4191	653	727	
3912	9409	A	4192	26	161	
3913	9410	A	4193	3	186	
3914	9411	A	4194	28	186	
3915	9412	A	4195	356	428	
3916	9413	C	4196	35	430	MKSCRXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXSETNSWEATRKPNFSSNSESAFIS RSQGHKDAKKEFVPLXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXLQSHPLVR*
3917	9414	A	4197	213	394	
3918	9415	A	4198	28	123	
3919	9416	A	4199	1578	1835	SNKSLPHNCIPPQMRNYSRGNLLQY IDYVQLHRNLYAGEIYFHC*RKSL CNSSWREGAVGCLPMDFPRLHLSL SPSSLHCRNKP
3920	9417	A	4200	213	305	
3921	9418	A	4201	1715	1850	
3922	9419	A	4202	4016	4315	
3923	9420	A	4203	28	239	
3924	9421	A	4204	7	216	
3925	9422	A	4205	1	576	
3926	9423	A	4206	1	500	
3927	9424	A	4207	1	1266	
3928	9425	A	4208	1	162	
3929	9426	A	4209	1	229	
3930	9427	A	4210	197	416	
3931	9428	A	4211	1	131	
3932	9429	A	4212	76	274	
3933	9430	A	4213	295	2530	RPATMAARPLPVSPARALLALAG ALLAPCEARGVSLWNEGRADEVVS ASVRSGDLWIPVKSFDKSNHPEVLN IRLQRESKELIINLERNEGLIASSFTE THYLQDGTVDVSLARNYTVILGHY YHGHVIRGYSDSAVSLSTCSGLRGLI VFENESYVLEPMKSATNRYKLFP KKLKSVRGSCGSHHNTPNLAANKV FPPPSQTWARRHKRETLKATKYVE LVIVADNREFQRQGDLEKVKQRLI ELANHVDFKFRPLNIRIVLVGVEVW NDMDKCSVSQDPFTSLHEFLDWRK MKLLPRKSHDNAQLVSGVYFQGT IGMAPIMSMCTADQSGGIVMDHSD NPLGAAVTLAHELGHNFNMNHDTL DRGCSCQMAVEKGCCIMNASTGYP FPMVFSSCSRKDLETSLEKGMGVCL FNLPEVRESFGGQKCGNRFVEEGEE CDCGEPEECMNRCCNATTCTLKPD AVCAHGLCCEDCQLKPAGTACRDS SNSCDLPEFCTGASPHCPANVYLHD GHSCQDVGDCYNGICQTHEQQCV TLWGPAGKAPAGICFERVNSAGDPY

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						GNCCKVSKSSFAKCEMRDAKCGKI QCQGGASRPVIGTNAVSIETNPLQQ GGRILCRGTHVYLGDDMPDPGLVL AGTKCADGKICLNRCQNISVFGV HECAMQCHGRGVCNNRKNCHCEA HWAPPFCDFGFGGSTDGSPIRQAG KEARQEAESNRERGGQ\EPLGSQ EHASTASLTLI
3934	9431	A	4217	2	119	
3935	9432	A	4218	2	147	
3936	9433	A	4219	10	216	
3937	9434	A	4220	245	455	
3938	9435	A	4221	1	2867	MIFPAESSCALPQEGSAGPGSPGSAP PSRKRSWSSEESNQATGTSRWDG VSKKAPRHLSVPCTRPREARQAE DSTRLSAESGETDQDAGDVGPDI PDSYYGLLGTLPQEQALSHICSLPSE VLRHVFAFLPVEDLYWNLSLVCHL WREIISDPLFIPWKKLYHRYLMNEE QAVSKVDGILSNCGIEKESDLCVLN LIRYTATTKCSPSVDPERVLWSLRD HPLLPEAEACVRQHLPDLYAAAGG VNIWALVAAVVLLSSSVNDIQRLLF CLRRPSSTVTMPDVTETLYCIAVLL YAMREKGINISNSKKTITLTHEQQLI LNHKMEPLQVVKIMAFAGTGKTST LVKYAEKWSQSRFLYVTFNKSIAK QAERVFPNSVICKTFHSMAYGHIGR KYQSKKKLNLFKLTPFMVNSVLA GKGGFIRAKLVCKTLENFFASADEE LTIDHVPWCKNSQGGQRMVEQSE KLNGVLEASRLWDNMRKLGECTEE AHQMTHDGYLKLWQLSKPSLASFD AIFVDEAQDCTPAIMNIVLSQPCGKI FVGDPHQIYTFRGAVNALFTVPHT HVFYLTQSFRFGVEIAYVGATILDV CKRVRKKTIVGGNHQSGIRGDAKG QVALLSRTNANVFDEAVRVTEGEF PSRIHLIGPEEERRKREYPPGLGALE GRTQVTGTRKKQAQSESGTRFPPEK GELVLLSSHDEGENLVKDKFIRRW VHKEGFSGFKRYVTAEDKELEAKI AVVEKYNIRIPELVQRIEKCHIEDLD FAEYILGTVHKAKGLEFDTVHVLD DFVKVPCARHNLPLPHFRVESFSE DEWNLLYVAVTRAKKRLIMTKSLE NITLAGEYFLQAE LTSNVLKTGV VRCCVG\QCNNALSPVDTVLTMTK KLAPITY*ATGK\ENKGGYLCHSCAE QQHRDPWRFLTASPEQVRAMEPHF GGTSYCPRHEALLFLVF
3939	9436	A	4222	57	302	
3940	9437	A	4223	1	550	DAHIIGRIESYSCKMAGDDKHMFK QFCQEGQPHVLEALSPQTSGLSPS RLSKSQGGEEGPLSDKCSRKTLFY LIATL NESFRPDYDFSTARSHFSRE PSLKLVLGNVNC SLFSAVREDFKD LKPQLWNAVGRGDLPLKCDIYSY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NPDLDSDPSREDGSLWSFNFFYNK RLKRNRL
3941	9438	A	4224	11	511	GRTRSIAGEETTQRPGPNCGGNCLC LHTLAINMRICYSQTPFHLRLKG QRWPFVSSLELFPVGFPAHLLVQS TLPKPRPERAFTAPSLFPVTLGFCLG RILCQRLLLCPSCALATALSINGYSRT QECQSWKGRDTGLHKGKLEALG GTEGFGDRARAKIEDS
3942	9439	A	4225	1	279	
3943	9440	A	4226	1011	1322	
3944	9441	A	4227	3	468	TPLHVYNEVMSVGQKYGIRNAGYY ALRSLRIEKFFAFWGQDINNLVTPL ECGRESRVKLEKGMDFIGRDALLO QKQNGVYKRLTMFILDDHDSLDL WPWWGEPIYRNGQYVGKTTSSAY SYSLEHVCGLGFVHNFSEDTEEQ VVTADFINRG
3945	9442	A	4228	1	1236	
3946	9443	B	4229	1	1742	MKRDNSGGCLPAPASAWPARPRQQ AEWRALTRGPANHCIISTLGEPE TPLIGLRTFQCRLVTDGRVLAGTV SSEPTDGFRSPAGPGRRTSAMVLL KLGKTPGEFFPFLGSSSQPPSHELNI GKRLDDTKILPGNMKDNFWEMGD TGPCGPCSEIHYDRIGGRDAAHLVN QDDPNVLEIWNLVFIQYNRFNCVE LQASAAFNWNNQRCKTRNRYICQF ADLRRNLNIINDITGRVHKDRKLL TGDSFPAANALGKLAAQEMMAAY AVSLPKLTALLRVFSTVVRISIGERFS PIRVLRLLRHTTPNYIYQRLIPYVCV LPTTELSINLNMILTENDIPLFRALFL NNITDADARVLLQKRPREGWLTDD AFLYWAQQDFSGVKPLVAQHWEW MTFSADSVSSVHTLTDDPLESLAD QPGAGNVHLLIPPEGLLYRSLTLPN AKYKLTATLQWLAEETLPDNTQD WHWTVVDDKQNESVEDCLIFLGKP QGKGCKLEKSVWAAGRPFYSYAGDK NRQLTRYSDTRWHEDSVNRNWFVSV MVGPSVRVNEWFSAYAMAGMAYS RVSTFSGDYLRVTDNKG*
3947	9444	A	4230	1	638	
3948	9445	A	4231	1377	1746	
3949	9446	B	4232	1	1716	MSQYYQQRPPHEIELDSHAKFFPH HHLQVADSAHLAASPLRRTHRAL TWAQALPQEEGSGAPSPGAPSPPTP KSFGRMTSASAVFILDVKGKMESC YVVQDVLNSWSPAIPLLQPPKVSDD SGGHIEECQCLPVYSFLYKTIEVGI LRILQGAGGGEHPDNFVIVYELLDE LMDFASRRPPTARSCRIHHSAEQQA GDGQVTGAPTVTNAVSWRSEGIKS MQRQRPSENRNRYHQAQVFLSGMP ELRLGLNDRVSSSLAAGQFKKSQ WPTVWRYLCLYPAMRLPQIQDQCG

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						QRQVCAGRNVIWSIKSFPGGKEYL MRAHFGLPRWKRKRWRAGPPSGSS LDPLLHRLWDPGPIMKIEKSGYQA LPWVRTSPRVAIPTSYQLEGRRDGG LNTGFLTAPDADFRGRAGEEPAGR AGVSGWGAGTESSAAGCTAAAPRE GCSASARLLRADSAGLGRAGGFA GRQCRHAAGGGCAGDRLSGAAAR GDVQECAAFCTGSWCIPSTLQRD GAAGFIVPPQSPFEGHDVWQHRHR PELLKQGASPNVQDTSGTVQSMTQ PALDSWTP*
3950	9447	A	4233	1	372	
3951	9448	B	4234	48	1158	MSASAVFILDVKGKPLISRNYKGDV AMSKIEHFMPLLVQREEGALAPLL SHGQVHFLWIKHSNLYLVATTSKN ANASLVYSFLYKTIEVFCEYFKELE EESIRDNVVIVYELLDELMDFGFPQ TTDSKILQEYITQQSNKLETGKSRVP PTVTNAVSWRSEGIKYKNEVFIDV IESVNLLVNANGSVLLSEIVGTIKLK VFLSGMPELRLGLNDRVLFELTGRS KNKSVELEDVKFHQCVRLSRFDND RTISFIPPDGDFELMSYRLSTHVKPLI WIESVIEKFHSRVEIMVKAKGQFK KQSVANGVEISVPVPSDADSPRFKT SVGQRQVCAGEKRRYFGVLSLGG AREYLMRAHFGLPKCEKERX*
3952	9449	B	4235	153	458	KKDLSLEEIQKKLEAAEERRKSHEA EVLKQLAEKREHEKEVLQKAIEEN NNFSKMAEEKLTHKMEANKENRE AQMAAKLERLREKDKHIEEVRKTK NPRPC*
3953	9450	A	4236	3	182	
3954	9451	A	4237	49	607	NSARGLSLSQLIVQNTLPVACLLFT MASSDIQVKELEKRASGQAFELILS PRAKEFVPEFPLSPPKEEGFFPGGKF REN*EAAIEERRQSP*SCSS*RQLAE KLRAPRKKCFQKAIEENNFQ*NGQ KRKLTPHKMEA\NKETPERPQMA\A KLEPF AEKDKAH*KKCGKNKES\K DP\ADETEAGLI
3955	9452	A	4238	1	356	TELQQEQLQTVVGTYHGSPDQSHQ VTGNHQQPPQNTGFPR/SNQPYYN SRGVSRGSRGARGLMNGYRG PAN GFRGGYDGYRPSFSNTPNSGYTQSQ FSAPRDYSGYQRDGYQQNFIP
3956	9453	A	4239	1	2206	RLPPAFSSLSLRSEDALGHQPQRERS KSSGPPPPSGSSGSEAAAGAGAAAP ASQHPATGTGAVQTEAMKQILGVI DKKLRNLEKKKGKLLDDYQERMNK GERLNQDQLDAVSKYQEVNTNLEF AKELQRSFMALSQDIQKTIKKTARR EQLMREEAEQKRLKTVLELQYVLD KLGDDDEVRTDLKQGLNGVPILSEEE LSLLDEFYKLVDPERDMSLRLENEY EHASIHLDLLEGKEKPVCGTTYK VLKEIVERVFQSNYFDSTHNNHQNGL

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						CEEEADSAPAVEDQVPEAEPEPAE EYTEQSEVESTTEYVNRQFMAETQFT SGEKEQVDEWTVETVEVVNSLQQQ PQAASPSVPEPHSLTPVAQADPLVR RQRVQDLMAQMGGPDNFIQDSML DFENQTLDPALVSAQPMNPTQNMMD MPQLVCPVHSESRLAQPNQVPVQP EATQVPLVSSTSEGYTASQPLYQPS HATEQRPQKEPIDQIQATISLNTDQT TASSSLPAASQPQVFQAGTSKPLHS SGINVNAAPFQSMQTVFNMNAPVP PVNEPE\TLKQ\QNQSQA\SYNQSFS S\QPSPS*QQTELQ\EQ\QT\TVVG\TY HGS\QDQSHQ\VTGNHQ\PPQ\QNT GIST*AIRPYNSRGVSRGGSRGAR GLMNGYRGPIANGFR\GGYDGLPAP SFLCLKPNSGY\SHSPQFQCLPRDYL WPIQRDG\YIQQNFKRGSQSGPRG APRGRG\GPPRPNRGMPQMNTQQV K
3957	9454	A	4240	1	151	
3958	9455	A	4241	5	120	
3959	9456	A	4242	1	315	EQMVSEDVPC/D/HRVHARIIGSR/G KAIRKIMDEFKVDIRFPQSGAPDPN CVTVTGLPENVEEAIDHILNLEEEYL ADVVDSEALQVYMKPPAHEEAWP CPLRTCSTV
3960	9457	A	4243	107	4057	PFCCGFPGLCVGVSTMSVAVLTLQ ESFAEHRSLVPQQIKVATLNSEES DPPTYKDAFPPLPEKAACLESQAEP AGAWGNKIRPIKASVITQVFHVPLE ERKYKDMNQFGEQAKICLEIMQ RTGAHLELSLAKDQGLSIMVSGKL DAVMKARKDIVARLQTQASATVAI PKEHHRFVIGKNGEKLQDLELKTAT KIQIPRPDDPSNQIKITGTKEGIEKAR HEVLLISAEQDKRAVERLEVEKAFH PFIAGPYNRLVGEIMQETGTRINIPP SVNRTEIVFTGEKEQLAQAVARIKK IYEEKKKKTTTIAVEVKKSQHKYVI GPKGNSLQEILERTGVSVEIPSDSIS ETVILRGEPEKLGQALTEVYAKANS FTVSSVAAPSWLHRFIIIGKKGQNL KITQQMPKVHIEFTEGEDKITLEGPT EDVNVAQEIEGMVKDLINRMDYV EINIDHKFHRHLIGKSGANINRIKDQ YKVSVRIPPDSEKSNLIRIEGDPQGV QQA KRELLELASRMENERTKDLIIE QRFHRTIIGQKGERIREIRDKFPEVII NFPDPAQKSDIVQLRGPKNEVEKCT KYMQKMAVADLVENSYSISVPIFKQF HKNIIGKGGANIKKIREESNTKIDLP AENSNSETIIITGKRANCEAARSRLS IQKDLANIAEVEVSIPAKLHNSLIGT KGRILRSIMEECGGVHIHFPVEGSGS DTVVRGPSSDVEKAKKQLLHLAEE KQTKSFTVDIRAKPEYHKFLIGKGG GKIRKVRDSTGARVIFPAAEDKDQD

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						LITIIGKEDAVREAQKELEALIQNLD NVVEDSMLVDPKHHRHFVIRRGQV LREIAEEYGGVMVSFPRSGTQSDKV TLKGAKDCVEAAKKRIQEIIDLEA QVTLECAIPQKFHRSVMGPKGSRIQ QITRDFSVQIKFPDREENAVHSTEPV VQENGDEAGEGREAKDCDPGSPRR CDIIISGRKEKCEAAKEALEALVPV TIEVEVPFDLHRYVIGQKSGSIRKM MDEFEVNIHVPAPELQSDIIAITGLA ANLDRAKAGLLERVKELQAEQEDR ALRSFKLSV\TVDPKLHSPGLSGRK GASNSQI\RGLKHDVNIQFP\DKD\I ANQHQD\QITFTGYEKNHSSLPDGA LRIVG\ELE\QMVSE\DVPLNHRVSR PASFGARGKSHPPKIMYEF\KV\DIRF PNKSGAPKTPNCVNC*RGFP\ENVE ESHSTQHPSILEEE\YL\ADVVDSEA LQ\VYMEPP\AHTEEAKGNFSRG\FD VRDAPL\TA\SSSEKAS\DMSSSEEF SFWG*RWLPKTL\WGPKTIMIKKE QNPLPAC
3961	9458	A	4244	11	323	
3962	9459	A	4245	3	171	
3963	9460	B	4246	148	405	XKLSVERKDPLAALAREYGGSKRN ALLKWCQKKTQGYAKRNLLAFE AAESVGIKPSLELSEMLYTDPRDWQ SVMQYVAQIYKYFET*
3964	9461	A	4247	2	438	AVGGNGGCPRPSRVTSQSTCRFGPR TASHSASRAGLCTASR*VPGWV*CL HFQPLQMPTRDSSFPDYSAPGRGC GQAGRCGAEHRRPGHRSSCC*NW* CQCSHNLVSSSGTISVEHCAWNHRI PGPRLPEGLFFPH*VCFVMSM
3965	9462	A	4248	3	256	
3966	9463	A	4249	3	444	
3967	9464	A	4250	3	828	VKGVPGVKAERFE*RM TAKHCALS LVGEPIMYPEINRFLKLLHQCKISSF LVTNAQFPAEIRNLEPVTQLYVRVD ASTKDSLKKIDRPLFKDFWQRFIDS VKALAVKQQRVTYRLTLVKAWNV IESLQAYAQGLSLGNPDFIEVKGV YCRESSASSLTMAHVPWHEEVVQF VRELVDLIPEYEIACEHEHSNCLLIA HRKFKIGGEWWTWIDYNRFQELIQ EYEDSGGSKTFSKDY MARTPHWA LFGASERGFDPKDTRHQRKNKSKAI SGC
3968	9465	A	4251	1	384	
3969	9466	A	4252	3	1225	
3970	9467	A	4253	1	864	
3971	9468	A	4254	1	1266	GNSPPSELKWKAKSEDLRHRGLKA QAEIKGSTQQIGFTDPRMARSSPYP TDVARVVNAPIFHVNSDDPEAVMY VCKVAAEWRSTFHKDVVVDLV CY RRNGHNEMDEPMFTQPLMYKQIRK QKPV LQKYAELLVSQGVVNQPEYE

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						CVSMHGVNRKPSYNSTKSSMDGLI LHPATGLVFVLSKQCEEIHQPVVWT CEQREAENATAEENRVLLAMVNPT VFFDIAVDGVEPLGRVSFEVGRAAA CGNGAQKVGRGRENFRCESEPLERK GFGL*GVPCFHRLFPRLVCVQGGEL QQRHNGNWWASPILWGRKFERLK NFHP*KPYGSPGILSPWQNAQPQTQ MVPQFFICTAQDCSGWNGQAMWV FGTSEKAMNIVEAHWSRFGISR/N GKTQQRSPFADCGQLLISLTCVFIF NHPDHSL
3972	9469	A	4255	3	275	
3973	9470	A	4256	125	315	
3974	9471	A	4257	3	292	
3975	9472	A	4259	1	3045	MDKFLNTYTLPRLKQEEVESLNRPI TGSDIEAIINSLPTKKKSRTRWIHSRI LPEVQGGAEKEGILPNSFYEASIJLIP KPASDTTKKENFRPISLMNINAKILN KILAKQIRQHIKKLIHHDQVGFIPGM HGLFNICKSVNIIQHINRTNDKNHMI ISIDAEKPFDKIQHFMLKTLNKL QNLKLLIGNFSKVSQYKINVQKSQA FLYTNNRQTESQIMNEFPFTIASKRI KYLGIQLTRDVKDLFKENYKALLN EIKEDTNKWKNIPCS\WEKTTLKFI W/NQKRAHIAKSIISQKNKAGGITLP DFKLYCKATVTKTAWYWYQNRDI DQWNRTESEIMPHIYNHLIFDKPD KKKKWGKDSLKNKWCWENWLAIC RKLKLDPFLTPDTKINSRRIKDLNVR PEMIKTLEENLGNTIQDIGMGKDFM SKTPKAMATKAKIDKWDLIKLSF CTAKETTIRVNRQPTWEKIFAIYSS DKGLISRIYNELKQIYKKKTNNPIEK WAKDMNRHFSKEDIYAAKKHMKK CSSSLVIREIQIKTTMRYHLTPVRMA IHKSGNNRCWRGCGEIGTLLHCW WDCKLVQPLWKSVMRFLRDLELEI PFDPAIPLLAAPSLPSGLRSPSKSSPS PPSRCTLVILLHVFDIVFFDGCEK KRWYILLIVLLTRLLVSACTFTEGY TVGFSTFEALRLGLSRYWLPCCSAC RRPIVGLQLVMINSQNFQVIAMEGT VASECCHGNGKLTWHRPVLVCSF SRCTVQAAGGSAILEDGDPPLTAPL GSTPQAAVCRGPRGRELRAAPADS HLFQRDLWPFNKVIVHGEKGSNQT SQGLLNTGSEMTIVLENPKYHSGPP VRVSPDGGQVIEVLADPSYTGPTA LNNVFFAFQCNFYFDHIPENCGFSD PSDPQNLQKGEPCPSLVRASAPPQ EKATEQPLLCKTTESPFGMTVGPCT DETLDHGAPSKHVPGTAHNELALL DLRVIKSAGSAAVHHKLKVLHWRS SLSNNKGTGRLYEQVA
3976	9473	A	4260	1	2526	
3977	9474	A	4261	1	3111	

MISSING AT THE TIME OF PUBLICATION

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						VDTIAADESFSQVDFGGRLMKDYG ACMSLLSVRVFFKKCPSIVQNFAVF PETMTGAESTSLVIARGTCIPNAEEV DVPIKLYCNGDGEWMVPIGRCTCK PGYEPENSVACKGPVNNTEKAKSG EMWFSPEEYGWEYAAFLALRKCSQ CPEDAVAASGA VALENLMEHGHIR LDKASKDSESSTPHDPTLLFHSGPQP NFRHFQGWNTVTSEGLIHLPKSKT QSQCPGLFGGSLDSRIDIGGAWYFC HTHTASSASTPSEEAGSLADPSNETE SLLFACTALCSPWECQLLDLASLFQ GIMLMPRAVQFFKCWDKVTVRNQ WRMHSHGSPCLGVSFQKGLCQEM VYISTRGSSSGLRPLVLSLHGWAVD TAIHTCIPFPTDIWIQDLIAGLKDEW FDTHPGRRIGRPAQLCSSRSRGVH
3980	9477	A	4264	1	2653	MGD FNTPLSTLDRSMRQKVNKDIQ ELNSALHQADLIDIYRN LHPESTEYT FFSAPHHTYSKIDHILGSKAPLSKYR RSEIKINCLSDHSAIKLELRIKKLTQ NRSTTWKLNLLNDYWVHNEMK AEIKMFFETNENKDTTYQNLWDTL KAVCRGKFIALNAHKRKQERSKIDT LTSQLKELEKQE QTHSKASRRQEIS KIRGELKEIETQKTLQKINESRGWFF EKINKIDRL LARLIKKKREKNQIHAI KNDKGDMSTNHTIEIQTIREYYKHL YANKLENLKEIDKFLETYSLPRLNQ EEVESLNRPI TGSEIEAIINSLPNKRS PGPDGFTAKFYQRYKEELLISNFSK VSGYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRMKYLGIQPTRD MKDLFKENYKPLLNEIKEDTNKWK NIPCSWVGRINIVKMAILPKNWKKT TLKFIWNQKRARIAKSILSQKNKAG GIMLPDFKLYYKATITKTAWYWYQ NRDIDQWNRTEPSEIMPHIYNHLIFD KPDKNKKWGKDSL FNKWCWENW LAICRKLKLDPFLTPYTKINSRWIKD LNVRPKTIKLEENPGNTIQDIGMG EDFMSKTPEAMATKAKIDKWDLIK LKSFCTAKETTIRLNRPPTEWEKIFA IYSSDKGLISRIYNELQQIYEKKTN PIKKWAKDMNRHLSKEDIYAAKRH MKKCASSLAIREIQIKTTMRYHLTP VRMAIHKSGNNRCWRGCGEIGTLL HCWWDCKL VQPLWKS VWRFLRDL ELEIPFDPAIPLLGIYPKDYKSCCYE DTCTHMFIVALFTIAKTWNQPKCPT MIDWIKKMWHIYTMEYYADIKKDE FMSFVRTRMKLETIILSKISQEKKT KHRMFSLIGGN
3981	9478	A	4265	1	2988	
3982	9479	A	4266	1	2515	MGD FNTPLSTLDRSTRQKVNKDTQ ELNSAPHQADLIDIYRTLHPKSTEYT FFSAPHHTYSKTDHILGSKALLSEC KRTEIITNYLSDDSAIKLELRIKNLT

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						QNRSTTWKLNLLDDYVWHNEM KAEIKMFFETNENKDDTTYQNLWDA FKAVCRGKFVALNAHKRKQGRSKI DTLTSQLELEKQEQTHSKASRRQE ITKIRAELEIETQKTVQKINESRSW FFERINKIDRQLARLIKKKREKNLID AIKNDKGDITTDPTIEIQTIREYYKH LYANKLENLEEMDKFLDTYTLPRL NQEEVESLNRPIITGSEIVAINSLTTK KSPGPDGFTAIFYQRAIRQEKEIKGI QLGKEEVKLSLFADDMMIVYLENPV SAQKLISNFSKVSQYKINVQKSQAF LYTNNRQTESQIMSELPFTIASKRIK YLGQQLTRDVKDLFKENYKPLLKEI KEDTNKWKNIPCSWVGRINIVKMAI LPKVIYRFNAIPIKLPMTFFTELKKT TLNFIWNQKRAHIAKS/VLSQKNKA GGITLPDFKLYYKATVTKTAWYWY QNRDIDQWNRTEPSEIMPRIYNYLI FDKPEKNKQWGKDSL FNKWCWKN WLAICRKLKLDPFLTPYTKINSRWI KDLNIRPKTIKTEENLGITIQDIGM GKDFMSKTPKAMATKAKIDKWDLI KLKSFCTAKETTNRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKT NNPIKKWAKDMNRHFSKEDIYAAK KHMKKCSSLAIREMQIKTTMRYH LTLVRMAIHKSGNNRCWRGRGEIG TLLHCWWDCKLVSQSLWKS VWQFL RDLELEIPFDPAIPLL
3983	9480	B	4267	1	2634	MGDFNTPLSTLDRSMRQKVNKDTQ ELNSALHQGLIDIYRTLHPKSTEYI FFSAPHHTYSKIDHILGSKALLSKCK RTEIITNDLSDHSAIKLELRIKNTQ NCATTQKLNLLNDYVWHNEMK AEIKMFFETNENKDDTTYQNLWDAF KAVCRGKFIALHAHKRKQERSKIDT LTSQLELEKQEQTHSKASRRQEIT KIRAELEIETQKTLQKINESRSWFF ERINKIDRLLARLIKKKREKNQIDAI KNDKGDITTDPTIEIRTTVREYYKHL YANKLENLEEMDTFLDTYTLPRLN QEEVESLNRPIITGAEIVAINSLPTKK SPGPDGFTAIFYQFRKGLRQNSTT FMPKTLNKLGDGTYLKIIRAIYDKP TANIILNGQKLEAFPLKTGTRQGW LSPLLFNIVLEVLARAIRQEKEIKGIQ LGKEEVKLSLFADDMMIVYLENPVS AQNLLKLISNFSKVSQYKINVQKSQ AFLYTNNRQTESQIMSELPFTIASKR IKYLGQQLTRDVKDLFKENYKPLLK KIKEDTNKWKNIPCSWVGRINIVKM AILPKVIYRFHAIPIKLPMTFFTELEK TTLKFIWNQKRACIAKSILNQKNKA GGITLPDFKLYYKAI VTKTAWYWY QNRDIDQWIRTEPSEITLHIYKYLIF DKPEKNKQWGKDSL FNK WY WEN WLAICRKLKLDPFLTPYTKINSRWI

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						KDLNIRPKTIKLEENLGFTIQDIGM GKNFMSKTPKAMATEAKIDKWDLI KLKSFCTAKETTIRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKT NNPLKKWAKDMNRHFSKEDIYAAK KKHMKKCSPLAIREMQIKTTMRY HLTPVRMTIHSQETTGAAGEDVEK*
3984	9481	A	4268	1	2429	
3985	9482	A	4269	1	2745	
3986	9483	A	4270	1	3210	MVKGSIQQEELTILNIYAPNTGALRF IKQVLRDLQRDLDSHTIIMGDFHTP LSTLDRSTRQKVNKDIQELNSALHQ EDLIDIYRTLHPKSTEYTFFSAPHHT YSKIDHIVGSKALLSKCKRTEITNC LSDHSAIKLELRIKNTQNRSTTWK LNNLLLNDYWVHNEMKAEIKMFFE TNENKDTTYQNLWDTFKA VCRGKF IALNAHKRKQERSKIDTLTSQKEL EKQEQTTHSKASRRQEITKIRAEKKEI ETQKTLQNINESRSWFFERINKIDRP LARLIKKKREKNQIDAIKNDKGDIT TDPTEIQTTIREYYKHL YANKLENL EEMDKFLNTYTLPTLNQEEVESLNR PITGAIEIVAINSLPTKKSPGPDGFTA EFYQRYKEELVPFLLPFQSIEKEGI LPNSFYEASIIIPKPGRDTTKKNFR PISLMNIDAKILNKILAKRIQQHIKN LIHHDQVGFIQGMQGWFNIRKSINVI QHINRAKDKNHMISIDA EKA FDKI QQPFMLKTLNKLDDMIVYLENPIVS AQNLKLISNFSKVS GYKINIQSQA FLYTNNRQTESQIMSELPFTIASKRI KYLGIQLTRDVKDLFK\ENHKPLL N EIKEDTNKWKNI PCSWVGRINIVKM AILPKVIYR/FNAIPIKLPMTFFTELE KTTLKFIWNQKRARIAKSILSQKNK AGGITLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSETPHIYNYL IFDKREKNKQWGKDSL FNKWCWE NWLAI CRKLKLD PFLTPYTKINSRW IKDLNVRPKTIKLEENLGFTIQDIG MGKDFISKTPKAMATKAKIDKWDL IKLKSFC TAKETTIRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKT NNPIKKWAKDMNRHFSKEDIYAAK KHMKKCSPLAIREMQIKTTMRYH LTPVRMAIHKSGNNRCWRGCGEIG TLLHCWWDC KL VQPLWKA VWRFL RDLELEIPFDPAIPLLGIYPKDYKSC CYKDTCTRRKQLDCAEPVEPRKVG DGEWSLTKWTRPGSRALPWPPEQA KPYPPTLPTLAQDF
3987	9484	A	4271	3	3655	
3988	9485	A	4272	1	3615	
3989	9486	A	4273	1	4038	
3990	9487	A	4274	1	3317	MGDFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDIYRTLQPKSTEYT FFSAPHHTYSKIDHIVGSKALLSKCK

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						RTEIITNYLSDHSAIKLELRKLNLTQS RSTTWKLNLLNDYWVHNEMKA EIKMFFETNENKDTTYQNLWDAFK AVCRGKFIALNAHKRKQERSKIDTL TSQKLELEKQEQTHSKASRRQEITKI RAELKEIETQKTLQKINESRSWFFER INKIDRPLARLIKKKREKNQIDTIKN DKGDITDPTEIQTIREYYKHLYA NKLENLEMDKFLHTYTLPRLNQE EVESLNGPITGAEIVAIIDSLPTKKSP GPDGFTAIFYQRYKEELVPFLKLKLF QSIEKEGILPNSFYEASIIIPKLGRDT TKKENFRPLSLMNIDAKILNKILAK RIQQHIKKLIHHDQVGFIPGMQGWFW NIRKSINVIQHINRGKDKNHMISID AEKAFDKIQPFMLKTLNKLIGDGT YFKIIRAIYDKPTANIILNGQKLEAFP LKTGTRQGCPLSPLFNIVLEVLRAR AIRQEKEIKAQNLLKLISNFRKVSFY KINVQKSQAFLYTNNRQTESQIMRE LPFTIASKRIKYLGIQLTRDVKDLFK ENYKPLLNEIKEDTNKWNIPCSWI GRINIVKMAILPKVIYRFNAIPIKLPT TFFTELEKTILKFIWNQKRAHIAKTI LSQKNKAGGIMLPDFKLYYKATVT KTAWYWYQKRDIDQWNRIELSEIIP HIYNHLIFDKPDKNKKWGKDSVFN KRCWENWLAICRKLKLDFTLTPYT KINSRWIKDLHVRPKAIKTLEENLGI TIQDIGMGKDFTSKTPKAMATKAKI DKWDLIKLKSFCTAKETTIRVNRQP TKWEKIFAIYSSDKGLISRIYKELKQ IYKKKTNNPIKKWAKDMNRHFSKE DIYAANRHMKKCSSLAIREMQIKT TMRYHLTPVRKAIIKKSGNNRCWR GCGEIGTLLHCWWDCKLVQPLWK TVWQFLRDLELEIPFYPAIPLGIYP KDYKSCCYKDTCTRMFIAALFTIAK TWNQPKCPTMIDWIKKMWHIYTM EYYAAIKNDEFMSFVGTWMKLEIII LSKLSQEQTKEHGIFSLIGGN
3991	9488	A	4275	959	2955	
3992	9489	A	4276	1	2870	MKAIEIKMFFDTSENKDTTYWNLW DAFKAVCRGKFIALNAHKRKQERS KIDTLTSQKLELEKQEQTHSKASRR QEITKIRAELEIETQKTLQKINESRS WFFERINKIDRPLARLIKKKREKNQI DAIKNDKGDITDPTEIQTIREYYK HLYANKLENLEMDKFLDTYTLPR LNQEEVESLNRPTGSEIVAIINSLPT KKSPGPDGFTAIFYQSWAETQPKK ENFRPISLMNIDAKILNKILAKRIQQ HIKKLIHHDQVGFIPGMQGWFWNIRK SINVTQHINRAKDKNHMISIDAIEKA FDKIQQPFMLKTLNKLIGDGTIFYKII RAIYDNPTANIILNGQKLEAFPLKTG TRQGCPLSPLFNIVLEVLRARIRQE KEIKGIQLGKEEVKLSLFADNMIVY

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						LENPIVSAQNLLKLISNFSKVSQYKI NVQKSQAFLYTNNRQTESQIMSQLP FTIASKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNI PCSG\EG RINIVKMAILPKNWKKTTLKFIWNQ KRARIAKSILSQKNKAGGITLPDFKL YYKATATKTAWYWYQNRDLQW NRTEPSEITPHIYNLYLFDKPDKNKQ WGKDSL FNKWCWENWLAICRKLK LDPFLTPYTKINSRWIKDLNIRPKTI KTLEENLGITQDIGMGKDFMSKTP KAMATKAKIDKWDLIKQESFCTAK ETTIRVNRQPTKWEKIFATYSSDKG LISRIYSELKQIYKKKTNNPIKKWAK DMNRHFSKEDIYAAKKHMKKCPSS LAIREMQIKTTMRYHLTPVRMAIHK KSGNNRCWRGCGEIGTLLHCWWD CKLVQPLWKS VWRFLRDLELEIPFD PAIPLLGIHPKDYKSCCYNDCTRM FIAALFTIAKTWNQPKCPTIIDWIKK MWHIYTMEYYAAIKNDEFVSFVGT WMKLEIIILSKLSQEQTTHRIFSLIG GN
3993	9490	A	4277	1	2982	
3994	9491	A	4278	1614	4577	TEPKTKTT*LSQ*MQKKPLTKFSNPS C*KLSIN/IVLEVLARAI RQEKEIKGI QLGKEEVKLSLFADD MIVYLENPIV SAQNLLKLISNFSKVSQYKINVQKS QAFLYTNNRQTESQIMSELPFTTAS KRIKYLGIQLTRDVKDLFKENYKQL LKEIKEDTSKWKNI PCSWVGRINIV KMAILPKVIYRFNAIPIKLMPFFTE LEKTTLKFIWNQKRACIAKSILSQK NKAGGITLPDFKLYYKATVTKTAW YWYQNRDIDQWNRTEPSEITPHIYN YLFDKPEKNKQWGKDSL FNKWC WENWLAICRKLKLDPFLTPYTKINS RWIKDLNVRPKTIKTLEENLGIIQDI GMGKDFMSKTPKAMATKAKIDKW DLIKLSFCTAKETTIRVNRQPRKW EKIFATYSSDKGLISRIYNELKQIYK KKTNNPIKKWAKDMNRHFSKEDIY AAKKHMKKCSPLAIREMQIKTTM RYHLTPVRMAIHKKSGNNRCWRGC GEIGTLLHCWWDCKLVQPLWNSV WRFLRDLELEIPFDPAIPLLGIYPND YKSCCYKDTCTRM TITSVEEKSQSE KLSYIFLKEKICLMYVGLLNILVSL GKVPFWLYLGSRLATPPTSSQLFFIG GKERSPDEQGV DILIVLIFRYPSTDS AEQIKKKIEKALYQSLKTKQLSLTIN KPSFRLTRCGIRMTSSNMPLPASSST QRIVQGRETAMEGEWPWQASLQLI GSGHQCGASLISNTWLLTAAHCFW KNKDPTQWIATFGATITPPAVKRN RKIILHENYHRETNENDIALVQLSTG VEFSNIVQRVCLPDSSIKLPKTSVF VTGFGSIVDDGPIQNTLRQARVETIS

MISSING AT THE TIME OF PUBLICATION

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						LPCLMIPSQMLLENFSAAIPGHRWCW THMLDNGSAVSTNMTPKALLTISIP PGPNQGGPHQCRRFRQPQWQLLDPN ATATSWSEADTEPCVDGWVYDRSV FTSTIVAKWDLVCSSQGLKPLSQSIF MSGILVGSFIWGLLSYRFGKPKMLS WCCLQLAVAGTSTIFAPTFVIYCGL RFVAAFAGMAGIFLSSLTLMVEWTTT SRRAVTMTVVGCAFSAGQAALGGL AFALRDWRTLQLAASVPFFAISLIS WWLPESARWLIKKGKPDQALQELR KVARINGHKEAKNLTETPPPPPIPI PSPTAPPLSTPTITFTAITSPAPPPIPS LTPQPPSLQNIPTFTTIVTIGNSTIIN STHTVTSITHHLHLHVARHLMGV DVSGETECVYLKVLMSVKEEVAS AKEPRSVLDLFCVPVLRWRSCAML VVKYAVLGRDLTSSLARSFSLISY YGLVFDLQSLGRDIFLLQALFGAVD FLGRATTALLSFLGRRTIQAGSQA MAGLAILANMLVPQDLQTLRVVFA VLGKGCFCGISLTCLTIYKAELFPTPV RMTADGILHTVGRGLGAMMGLILM SRQALPLLPLLYGVISIASSLVVLF LPETQGLPLPDTIQDLESQKSTAAQ GNRQEAVTVESTSL
4009	9506	A	4293	3672	3967	LQPPPHGRRGLLHHLSPGHGPHHP VTPQTRSPAQP/PGQMGPRAPLGCC LPPPPRPPTCRREK*TTETRFSPCWR TRPWGPGPPRPLSRGGPLPCAPA
4010	9507	A	4294	1773	2213	AHWLHLRLPHHRAQWAAALQPG PAGWGWSWQPQLCSAGRLLCHGAI GRP/LSIFCWTDLGASSCGHPAAR SMMASGVTWTSRGMGEKRVSSSTPF PIFFPAASPPPPSRLPNCPFCHRTLA E RAQHLASVRPGLHLSSTCCMKCSC
4011	9508	A	4295	1	616	
4012	9509	A	4296	93	502	EERKRPHLGAWWENRKCFFSFQPD FKAAECRETVARPSLSIPQDCLSVSL ADTNQLCLEVRLARGVCRRAHLS PPVCIQSPLSQGH*LLCSK*SASI GLANFQGTDSLVAEHPVSWIHN SN FVFHFGYFRL
4013	9510	A	4297	1537	2360	TCCTNVVWGAPPHRDSRVSDRVHS QKSRRACYGQRNKRPGG*G*ILISA KKQLLSPRR*LKVWPMRSASLQSM PLASPSVCPGGLLFLWP*QALLPS DCG/PLSLTRLR*GG*PPRPHWCSR FRWLCAVLL
4014	9511	A	4298	1	493	MEAPAEALLAALPALATALALLLAW LLVRRGAAASPEPARAPPEPAPAE ATGAPAPSRPCAPEPAASPAGPEEP GEPAGLGELGEPAGGEPGPDPA AAPAEAE/PGGGGEAGTHRGPRGP LPTPGAPAAAAPRRARERGRGLQ PRLPPGSAEPAARRKCR
4015	9512	A	4299	2	418	
4016	9513	A	4300	8808	9100	RKVLFFFFFEMKSRSA\RLGCSGTI

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						SAHCNLCPLPGSSDSPASASRVAGMT GAHNHIQLIFVFLVGMGFHHVQQA GLELLT*VIHPPQSPKVLGLQV
4017	9514	A	4301	3	101	
4018	9515	C	4302	5673	5894	MWQLTPAILALGEIEAGGLFEPRRV KLAWPAQEELVSTKNTKISWVWW RAPVVPATQEA EVGGSLELERSRLQ *
4019	9516	A	4303	1	241	
4020	9517	A	4304	58	180	
4021	9518	A	4305	2	325	FFFFFFFFFETESLSVTQAGEPGHD LGSLEPPPPRFKQFSCSLPSSWIYR HVPPCPANFFFFLVETGFHHVGGAG LKLLTSNDPPASASQSSGIRGVSHLT RLVS
4022	9519	A	4306	206	386	
4023	9520	A	4307	2	260	
4024	9521	A	4308	5	227	
4025	9522	A	4309	676	1076	FLLCFPPCLSPKFFLFLGKIYSQSN WCVIVNWRIELGWMFNKICDSKIIF SLGSFLCKIKAHWGLWKSPTTSFQE RSPFFSSLFRAMRAKPSRSM/RLFF ELLVKSLPVASPVPEPLSVIAEQSSQI CPCHGI
4026	9523	A	4310	3	205	
4027	9524	A	4311	3	345	
4028	9525	A	4312	118	7473	
4029	9526	A	4313	1	297	
4030	9527	A	4314	366	504	
4031	9528	A	4315	1	2899	MDAPKAGYAFEYLIETLNDSSHKKF FDVSKLGTKYDVLPSYRVLEAAV RNCDFGLMKKEDVMNILDWKTQ SNVEVPFFPARVLLQDFTGIPAMVD FAAMREAVKTLGGDPEKVHPACPT DLTVDHSLQIDFSKCAIQNAPNPGG GDLQKAGKLSPLKVQPKLPCRQ TTCRGSCDSGELGRNSGTFSSQIENT PILCPFHLQVPEPETVLKNQEVFEG RNRERLQFFKWSSRVLKNVAVIPPG TGMAHQINLEYLSRVVFEEKDLLFP DSVVGTD SHITMVNGLGILGWVG GIETEAVMLGLPVSLTPEVVGCEL TGSSNPFTSIDVVLGITKHLRQVG VAGKFVEFFGSGVSQLSIVDRITIA NMCPEYGAILSFFPDVNLKHL TGFSKAKLESMETYLKAVKLFERN QNSSGEPEYSQVIQINLSIVPSVSG PKRPQDRVAVTDMKSDFQACLNEK VGFKGFQIAAEKQKDIVSIHYEGSE YKLSHGSVVIAAVISCTNNCNPVSM LAAGLLAKKAVEAGLRVKPYIRTSL SPGSGMVTHYLSSGVLPYLSKLG EIVGYGCSTCVGNTAPLSDAVLNA VKQGDLVTCGNFIWK\KNFEGRLC DCVRANYLASPPLVVAIAIAGTVNI DFQTEPLGTDPTGKNIYLHDIWPSR EEVHRVEEHVILSMFKALKDKIEM

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						GNKRWNSLEAPDSVLFPPWDLKSTY IRCPSFFDKLTKEPIALQAIENAHVL LYLGDSVTTDHISPAAGSIARNSAAA KYL TNRGLTPREFNSYGARRGND VMTRGTFANIKLFNKFIGKPAPKTIH FPSGQTLDFEAAELYQKEGIPLIIL AGKKYGGNSRDWAAKGPYLLGV KAVLAESYEKIHKDHIGIGIAPLQF LPGENADSLG\LSGRETFSLTFPEELS PG\ITLNIQTSTGKVFSVIASFEDDV\ EITL\YKHG\GLLNFFVARKFS
4032	9529	A	4316	1	178	
4033	9530	A	4317	165	403	PSSRSRAPSPPTLTCGASCCPTCPAC FPAPSRRAGAAGGAG*RPRGGPTST TCYGPTETWLYQLQTVGSRNTTTRT PKST
4034	9531	A	4318	3	404	
4035	9532	A	4319	3	217	
4036	9533	A	4320	3	423	SFFIHRTKGKGPLMSSSFKKLYFSLT TEALSFATPS/CQQGQCDKTRSRV TLQEWNDPLDHDLEAQLIYRHLG VEAMLWERHRELSGGAEAGTMPTS PGKVPEDSLARLLRVLQDLREAHSS SPAGSPSEPNCLELQ
4037	9534	A	4321	2	3040	DPGVWLPPSRDPAMAKRSSLYIRIV EGKNLPAKDITGSSDPYCIVKVDNE PIRTATVWKTLCPFWGEEYQVHLP PTFHAVAFYVMDEDALSRDDVIGK VCLTRDTIASHPKGFGSWAHLTEVD PDEEVQGEIHLRLEVWPGARACRL RCSVLEARDLAPKDRNGTSDPFVR VRYKGRTRETSIVKKSCYPRWNETF EFELQEGAMEALCVEAWDWDLVS RNDFLGKVVIDVQRLRVVQQEEGW FRLQPDQSKSRRHDEGNLGSQLEV RLRDETVPSSYYQPLVHLLCHEVK LGMQPGQQLIPLIEETTSTECRQDV ATNLLKLFLGQGLAKDFDLDFQLE LSRTSETNTLFRSNSLASKSMESFLK VAGMQYLHGVLGPIINKVFEEKKY VELDPSKVEVKDVGCSGLHRPQTE AEVLEQSAQTLRAHLGALLSALSRS VRACPAVVRATFRQLFRRVRERFPG AQHENVPIAVTSFLCLRFFSPAIMS PKLFHLRERHADARTSRTLLLLAKA VQNVGNMDTPASRAKEAWMEPLQ PTVRQGVAAQLKDFITKLVDIEEKDE LDLQRTLSL*APPVKEGPLFIHRTKG KGPLMSSSFKKLYFSLTTEALSFAT MPSSKKSALIKLANIRAAEKVEEKS FGGSHVMQVIYTTDAGRPOQAYLQ C/KGVPCVRVQSHWEK**YQGHQI YLAGSGIPTSVAKGPAAAEIQPTPAS WAPTIPVPSVGTSGAAATKKTRQC VNELNQWLSALRKVSINNTGLLGS YHPGVFRGDKWSCCHQKEKTDTF RSVPQTGVQWRDLGSLQSPPRVK QFSCNLPSWDDRHSPPSLANFFV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: (in USSN 09/770,160)	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						F*LEMGFHHVSQAALVLLLLLLLLL FDTESRSIIQAGVQWCNLGSLQSPFP RLG*FSCLSLPSTTGASHCTQLSQGC DKTRSRVTLQEWNDPLDHDLEAQL IYRHLLGVEAMLWERHRELSGGTE AGTVPTSPGKVPEDSLARLLRVLQD LREAHSSSPAGSPSEPNCLELQT
4038	9535	A	4322	308	658	
4039	9536	A	4323	1	2662	MAKRSSLYIRIVEGKNLPAKDITGSS DPYCIVKVDNEPIIRYRPHQDRGA LSLSSARALPAKGATATVWKTLCPF WGEEYQVHLPPTFHAVAFYVMDE DALSRDDVIGKVCLTRDTIASHPKG FSGWAHLTEVDPDEEVQGEIHLRL VWPGARACRLRCSVLEARDLAPKD RNGTSDPFVRVRYKGRTRETSIVKK SCYPRWNETFEFELQEGAMEALCV EAWDWDLVSRNDFLGKVVIDVQR LRVVQEEGWFRQLPDQSKSRRHD EGNLGSLQLEVRLRDETVLPSSYYQ PLVHLLCHEVKLGMMQGPGLIPLIE ETTSTECRQDVATNLLKFLGQGLA KDFLDLLFQLELSRTSETNLFRRNS LASKSMESFLKFALHVYLAPSWAD TAGKRCKGGCREKVGWSGTGGD RINVTGGPQVAGMQYLHGVLPPII NKVFEEKKYVELDPSKVEVKDVG SGLHRPQTEAEVLEQSAQTLRAHLG ALLSALSRSVRACPAVVRATFRQLF RRVRERFPGAQHENVPIAVTSFLC LRFFSPAIMSPKLFHLRERHADARTS RTLALLAKAVQNVGNMDTPASRAK EAWMEPLQPTVRQGVQALKDFITK LVDIEEKDELDLQRTLSLQAPPVKE GPLFIHRTKGKGPLMSSSFKKLYFSL TTEALSFAKTPSSKKSALIKLANIRA AEKVEEKSFGGSHVMQVIYTDAG RPQAYLQCKCVNELNQWLSALRK VSINNTGLLSYHPGVFRGDKWSC CHQI*ITGQG\CDKTRVTG*PCREW NDLLDRDLESQLIYRHLLGVEAML WERHRELSGGAEAGTVPTKPLAKV PEDSLARLAPGCLQDLREAHSSSPA GSPSEPNNLASLEAADVRPALRSPC
4040	9537	A	4324	69	194	
4041	9538	A	4325	1350	2203	TWRLDPQIISSPKPQPGGTYTLEV KSSKSKKVLSPHP*WPPLRLWQRIG GSPEGGTQAPDGSLLLLPPPPRPKSERV GSPKLSGGKR/EGSHPGGPPHITHP/ DGEEKAKSSWFLREAKDPTQKPS PHPVKPLSAAPVEGSPDRKQSRSSL SIALSSGLEKLKTVTSGSIQPVTPAP QAGQMVDTKRLKDSAVLDQSAKY YHLTHDELISLLLQRERELSQRDEH VQELESYIDRLLVIMETSPDLLQIPP GPPK
4042	9539	A	4326	2	761	
4043	9540	A	4327	2	410	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
4044	9541	A	4328	295	780	
4045	9542	A	4329	1	2203	
4046	9543	A	4330	1	190	RFIMLVRLVFNS*PQ/CDPPASASQS AGITGMSHRARPELSVLTQGFNRW AFRLLQCHSPDF
4047	9544	A	4331	2	269	
4048	9545	A	4332	3	223	DFEPSLQHCSSKLCRNILRASSCHSS WGRM*FPGSV*PTWKI*REESCEWS RTAINPKYKILLHGFVVRTVWR
4049	9546	A	4333	2	366	PCSEPPTRRSGATPSHPGGCGAKL CRNILRASSCHSSWGRM*FPGSV*P TWKI*REESCEWSCTAINPSTRSCCT VCGTNCLEETPTTCPSTRGLQCGRG LTRATGNCPRNDGLTLLSLN
4050	9547	A	4334	3	131	
4051	9548	A	4335	923	1442	GGPCLCRPSWPAVLQVRSGLPSTIPS PWPLFCLPQSILLGPLEMPG*RPLQ RPFYRMSLRTCQRRVRCWTWSVRC RTAWHTRVFLKLPDFTNDSSTTGF *AKPSALLSTGWS*WATA/CGGGA AALLATMLRAAYPAGQVLRLLPSP PAPGAKLCRNILRASSCHSSWGRM
4052	9549	A	4336	1	137	
4053	9550	A	4337	876	1012	
4054	9551	A	4338	148	278	
4055	9552	B	4339	7	673	MVEVTILMIMGLYRIYGFAVAVVS MILSYNVCSEGEVVSVMFSEVVTSS SCGMHRSTLLSSVYSHLIFDSAYVIN NVADALSRGFSMHCMHCDNLKTC HTSHGSVMAETA VINHKRKNPRI VQNDLTEAAYSLSRDQKRMLYLF VDQIRKSDGTLQEHDGICEIHVAKY AEIFGLTSAEASKDIRQALKSFAGKE VVFYRPEEDAGDEKGYESFPWFIKX *
4056	9553	A	4340	786	1088	
4057	9554	A	4342	1	66	
4058	9555	A	4343	2	80	
4059	9556	A	4344	8	258	
4060	9557	A	4345	5	383	
4061	9558	A	4346	99	634	TTTMSSKRTKTKTKKRPPORATSN VFAMFDQSQIQEFKEAFNMIDQNR DGFIDKEDLHDMLASLGKNPTDAY LDAMMNEAPGPINFTMFLTMFGEK LNGTDPEDVIRNAFACFDEEA\TGTI QEDYLRE\LLTTMGDRFTDEEVDEL YREAPY*QKGGISNYIEFTRILTGRP PKHKDD
4062	9559	A	4347	1	966	
4063	9560	A	4348	3	215	
4064	9561	A	4349	1	1416	NSGGSGGGTSGSGSSSGQGKMGQS QSGGHGPGGGKKDDEDKKKKYEP VPTRVGKKKKKTKGPDAAASKLPLV TPHTQCRLKLLKLERIKDYLLMEEE FIRNQEQMKPLEEKQEEERSKVDDL RGTPMSVGTLEEIIDDNHAIVSTSVG SEHYVSILSFVDKDLLEPGCSVLLN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HKVHAVIGVLMDDTDPLVTVMKV EKAPQETYADIGGLDNQIQEIKESV ELPLTHPEYYEEMGIKPPKGVHPFG PTWPRVKTLAKAVANQTSVASFLR VVGVELIQKYLGDGPKLVRELFVRV AEEHAPSIVFIDEIDAIGTKRY\DSN SGGE\REFHRTNVGN*LEPVGMGFD SRG\DV\KVFPWATNR\ETL\DPAL\I RPGRI\DR\KNEFPLPDEKTKKRIFI HTSRMTLADDVTL\DDLIHGLKIDLS GA\DIKAIC\TEAGL\MGL*GERRMK VTNEDFKKSKENVLYKKQEGTPEG LYL
4065	9562	A	4350	2	70	
4066	9563	A	4351	1	1605	
4067	9564	A	4352	3	193	
4068	9565	A	4353	3	127	LFHPCQDSQQHH*CVCCRLTGHGA A*VHGPCQAVQTYRASH
4069	9566	A	4354	2	323	
4070	9567	A	4355	3	85	
4071	9568	A	4356	49	413	
4072	9569	A	4357	3	338	
4073	9570	A	4358	1	3735	
4074	9571	A	4359	2	317	
4075	9572	B	4360	2576	2685	MDGKNSSGSKRYNRKRELSYPKNE SFNNQSRSSSSQSKTFNMPPQRG GGSSKLFSSSFNGGRRDEVAEAQRA EFSPAQFSGPKKINLNHLLNFTFEP GQTGHFEGSGHGSWGKRKNWGHK PFNKELFLQANCQFVVEDQDYTA HFADPDTLVNWDVFVEQVRICSHEV PSCPICLYPPTAAKITRCGHIFCWAC ILHYLSLSEKTSKCPICYSSVHKK DLKSVVATESHQYVVGDTITMQLM KREKGVLVALPKSKWMNVDPHPIHL GDEQHSQYSKLLLASKEQVLHRVV LEEKVALEQQLAEKHTPESCFIEA AIQELKTREEALSGLAGSRREVTGV VAALEQLVLMAPLAKESVFQPRKG VLEYLSAFDEETTEVCSLDTPSRPLA LPLVEEEEAVSEPEPEGLPEACDDLE LADDNLKEGTICTESSQEPITKSGF TRLSSSPCYFYFYQAEDGQHMFLHP VNVRCVLREYGLERSPEKISATVV EIAGYSMSDVRQRHRYLSHLPLTC EFSICELALQPPVSKETLEMFSDDI EKRRQRQRQKKAREERRRERRIEIE NKKQGKCPEVHIPLNLQFPAPKF LYLLLFKPRKETGKNVAMKAENR CRRRPPPALNAMSLGPRRARSAPTA VAAEAPVDAAELPQRRRHRLRHGQ EQRLQQLRLFGQQQRATAAPLRL GGASRRV*
4076	9573	A	4361	3	93	
4077	9574	A	4362	1	289	VGNPQQEVQNIFKAKHPMDTEVTK AKIIGFGSALLEVDPNPANFVGAGI IHTKTTQIGCLVRLEPNLQAQMYRL

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						T/LRTSKEAVSQRLCELLSAQF
4078	9575	A	4363	1	275	
4079	9576	A	4364	2	2803	RGLAVFISDIRNCKSKEAEIKRINKE LANIRSKFKGDKALDGYSKKKYVC KLLFIFLLGHDIDFGHMEAVNLLSS NRYTEKQIGYLFISVLVNSNSELIRLI NNAIKNDLASRNPTFMGLALHCIA VGSREMAEAFAGEIPKVLVAGDTM DSVKQSAALCLLRLYRTSPDLVPM GDWTSRVVHLLNDQHLGVVTAAT SLITTLAQKNPEEFKTSVSLAVSRLS RIVTSASTDLQDYTYFVPAPWLSV KLLRLLQCYPPDPAPVRGRLTECLE TILNKAQEPPKSKKVQHSNAKNAV LFEAISLIHHHDEPNLLVRACNQLG QFLQHRETNLRYLALESMTLASSE FSHEAVKTHIETVINALKTERDVS RQRAVDLLYAMCDRSNAPQIVAEM LSYLETADYSIREEIVLKVAILAEKY AVDYTWYVDLILNLIRIAGDYVSEE VWYRVIQIVINRDDVQGYAAKTVF EALQAPACHENLVKVGGYILGEFG NLIAGDPRSSPLIQFHLHLSKFHLCS VPTRALLSTYIKFVNLFPVKPTIQ DVLRSDSQLRNADVELQQRAVEYL RLSTVASTDILATVLEEMPPPERES SILAKLKKKKGPSTVTDLEDTKRDR SVDVNGGPEPAPASTSAVSTPSPSA DLLGLGAAPPAPAGPPPSSGGSGLL VDVFSDSASVVAPLAPGSEDNFARF VCKNNGVLFENQLLQIGLKSEFRQN LGRMFIFYGNKTSTQFLNFTPTLICS DDLQPNLNLQTKPVDPTVEGGAQV QQVVNIECVSDFTEAPVLNIQVHGS GGTAFQNVSLQLPITLNKFFQPTAEK FCQDFFQRWKQTSNPQQEVHNIFK AKHPMDTEFTK\AKIIGFGSELLAE VDPNPANFVGAG\I\HTKTTQ\GCP LRL*PNLQAQMYRLTLRTSKEAVS\QRLCELLSAQF
4080	9577	A	4365	2	231	
4081	9578	A	4366	1	224	
4082	9579	A	4373	131	381	
4083	9580	A	4374	93	449	
4084	9581	A	4375	11	594	
4085	9582	A	4376	1	1410	
4086	9583	A	4377	1	66	
4087	9584	A	4378	1	553	RRGPLSQNGSFGPSPVSGGECSPPLT VEPPVRPLSATLNRRDMPRSEFGSV DGPLPHPRWSAEASGKPSPSDPGSG TATMMNS\SS*GSSPTRVLDEGMQT VLQEPEVPSVPSITSLAERPVAVNM APKGPPFPFPGVPLMSTPMGGPVPPI RYGPPQQLCGPFGPRALPPPFPGPM RPPLCLRE
4088	9585	A	4379	1	3589	AFLSKVEEDDYPSEELLEDENAINA KRSKEKNPGNQGRQFDVNLQVPDR

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						AVLGTIHPDPEIEESKQETSMILDSE KTSETAAKGVNTGGREPNTMVEKE RPLADKKAQRPFERSDFSISIKIQT ELGEVFQNKDSYDLKNDNPPEHLK TSGLAGEPEGELSKEDHGNTEKYM GTESQGSAAAEPEDDSFHWTPHTSV EPGHSDKREDLLIISFFKEQQLQR FQKYFNVHELEALLQEMSSKLKSA QQESLPYNMEKVLDKVFRASESQIL SIAEKMLDTRVAENRDLGMNENNI FEEAAVLDDIQDLIFVRYKHSTAE ETATLVMAPPLEEGLGGAMEEMQP LHEDNFSREKTAELNVQVPEEPHTL DQRVIGDTHASEVSQKPNTKDLDP GPVTTEDTPMDAIDANKQETAEE PASVTPLENAILLIYSFMFYLTSLV ATLPDDVQPGPDFYGLPWKPVFITA FLGASFAIFLWRTVLVVKDRVYQV TEQQISEKLKTIMKENTELVQKLSN YEQKIKESKKHVQETRKQNMILSDE AIKYKDKIKTLEKNQEILDDTAKNL RVMLESEREQNVKNQDLISENKKSI EKLKDVISMNASEFSEVQIALNEAK LSEEKVKSECHRVQEENARLKKKK EQLQOEIEDWSKLHAELSEQIKSFE KSQKDLEVALTHKDDNINALTNCIT QLNLECESESEGQNKGGNDSDEL ANGEVGGDRNEKMKNQIKQMMDV SRTQTASVVEEDLKLQLKLRAV STKCNLEDQVKKLEDDRNSLQAAK AGLEDECKTLRQKVEILNELYQQKE MALQKKLSQEEYERQEREHRLSAA DEKAVSAAEEVKTYKRRIEMEDE LOKTERSFKNQIATHEKKAHENWL KARAAERAIAEEKREANLRHKL ELTQKMAMLQEEPVIVKPMGKPN TQNPPRRGPLSQNGSFGSPVSGGE CSPPLTVEPPVRPLSATLNRRDMPR SEFGSVDGPLPHPRWSAEASGKPS SDPGSGTATMMNSSSRGSSPTRVL DEGK\VNMGPK\GAPSFPEFPLMS TPMGGPV\PPPIRYGPPQLCGPFGP RHLPPFPGGMRPPLGLREFAPGVP PGRRLPLHPRGFLPGHAPFRPLGS LGPREYFIPGTRLPPPTHGPPQYPPP PAVRDLLPSGSRDEPPASQSTSQD CSQALKQSP
4089	9586	A	4380	3	148	
4090	9587	A	4381	1885	2826	CLQEAIMDGTETIAVSPRSLHSELMC PICLDMLKNTIGSA*ASVPLTDHSG L PFSYPRNKECPTCRKKLVSKRSLRP DPNFDALISKIYPSREEYEAHQDRV LIRLSRLDRGGTLGGGTGPPSPPGA PSPPEPGDPYLQSSSEALWL*ACPP SHSRYVKTTGNATVDHLSKYALRI ALERRQQQEAGEPGGGGGASDTG GPDGCGGEGGGAGGGDGPEEPALP SLFHLLQLSSLFSPLSLLPPPQTLNGS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LTLELVNSPRRPLPRQGLTLRALSLP GSPQHPGKLLTGGCALGFSTPATLH TGKQPYVCAT
4091	9588	A	4382	2	456	DRGGTLGGGTLGPPSPPGAPSPPEP GGDPYLQSSSEALWL*ACPPSHSRY VKTTGNATVDHLSKYALALRIALERR QQQEAGEPGGPGGGASDTGGPDGC GGEGGGAGGGDGPEEPALPSLFHLL QLSSLFSPLSLLPPPQTLNGSLTLEL V
4092	9589	A	4383	58	1262	CLQEAIMDGTEIAVSPRSLHSELMC PICLDMLKNTMTTKECLHRFCSDCI VTALRSGNKECPTCRKKLVSKRSLR PDPNFDALISKIYPSREEYEAHQDRV LIRLSRLHNQALSSSIEGLRMQA MHRAQRVRRPIPGSDQTTMSGGE GEPGEGEDGEDVSSDSAPDSAPGP APKRPRGGGAGGSSVGTGGGGTGG VGGGAGSEDSGDRGGTLGGGTLP PSPPGAPSPPEPGGEIELVFRPHLLV EKGEYCQTRYVKTTGNATVDHLSK YLALRIALERRQQQEAGEPGGPGG GASINTEELNVCGGEGGGAGGGDG\ PKEPALPSLEGVSEKQYTIYIAPGG GAFTTLNGSLTLELVNEKFWKVS RPLELCYAPHPRIQSDPHPGDKPEE RGPLG
4093	9590	A	4384	3	221	
4094	9591	A	4386	2	271	
4095	9592	A	4387	54	990	HSIMMKIPWGSIPVLMLLLLGLIDI SQAQLSCTGPPAIPGIPGTPGPDG QPGTPGIKGEKGLPGLAGDHGEFGE KGDWPWPGNPGKVGPKGPMGPKGG PGAPGAPGPKG\DSGDYKATQKIAF SATRTINVP/LLRRSQTRFRPRCITN MNTNYE\PRSGKFTLQGCPGLY*FN LSTPSSRG\NLCVNLMRGRERAQE/ VWVTFC\DYCLTNTPGSPQGNGP QLKKAPKGGGGGEKKTVPAGPPN KNFTYWGMGGCPTAIFSGFLAFFQI WEGLTCLASHPTPAPPAQQRSLYP QQQPYDQAKCTQ
4096	9593	A	4388	3	493	
4097	9594	B	4389	272	2158	MGPLMVLFCLLFLYPGLADSAPSCP QNVNISGGTFTLSHGWAQSGLLTYS CPQGLYPSPASRLCKSSGQWQTPGA TRSLSKAVCKPVRCPAPVSFENGIY TPRLGSYPVGGNVSFECEDGFILRG SPVRQCRPNGMWDGETAVCDNGA GHCPNPGISLGAVRTGFRFGHGDKV RYRCSSNLVLTGSSERECQNGVW SGTEPICRQPYSDFPEDVAPALGTS FSHMLGATNPTQKTESLGRKIQIQ RSGHLNLYLLDCSQSVSENDLFI KESASLMVDRIFSFEINVSVAITFAS EPKVLMSVLNDNSRDMTEVISSLEN ANYKDHENGTTNTYAALNSVYL MMNNQMRLGOMETMAWQEIRHAI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						ILLTDGKSNMGGSPKTAVDHIREIL NINQKRNDYLDIYAIGVGKLDVDW RELNELGSKKDGERHAFILQDTKAL HQVFEHMLDVSKLTDITICGVGNMS ANASDQERTPWHVTIKPKSQETCR GALISDQWVLTAAHCFRDGNDHSL WRVNVGDPKSQWGKEFLIEKAAIS PGFDVFAKKNQGILEFYGDDIALLK LAQKVKMSTHARPICLPCTMEANL ALRRPQGSTCRDHENELLNKQSVL CTFWSPLNGSKPKI*
4098	9595	A	4390	2	201	
4099	9596	A	4391	1	130	
4100	9597	A	4392	2	215	
4101	9598	A	4393	3	300	
4102	9599	A	4394	3	310	
4103	9600	A	4395	2	228	
4104	9601	A	4396	2	448	PRVRKDAVRDGLRAVKNAIDGCV V/PGAGAVEVAMAEALNKYKLSVK GKAQLGVQAFADALLVIPKVL AQN SGFDLQETLVKI*AEHSESGQLVGV DLNTGEPVVAEAGIWDNDCVKK QLLHSTVIATNILLVDEIMRAGMS SLKG
4105	9602	A	4397	2	100	
4106	9603	A	4398	3	174	
4107	9604	A	4399	1	147	
4108	9605	A	4400	1	104	
4109	9606	A	4401	153	480	TTLKQQFSFMSYKAVKLVFLIMSC YPRNPSHFP*CGA/WVMCPLRVGSE RRLCPFMATS\QSLSNKFHNRKIFMS REIKFRNLLKKNETQLMYLQIFRW YTKQRLFLF
4110	9607	A	4402	1	186	
4111	9608	A	4403	3	478	
4112	9609	B	4404	56	390	XAAYVQPFLDKSGLEKYL PASAA APFPLYPGIPAAAAAFPCLSVLS PPEKAGAAAATLLPHEVAPLGAPHP QHPHGRTHLPFAGPREPGNPESQA EDPSQPGKEAP*
4113	9610	A	4405	2	485	
4114	9611	A	4406	105	183	
4115	9612	A	4407	1	1560	MLRKKEKANYRLLAERTRKRPRKA SAELQRKHYPMLRGHLRLFLPGRL RPLPSNPRLAFPAERGGGHC GPMR HFPVSTQERGTADPVHPASPLPPNQ APNAGHSPPTPRSPNTSSPRRRRRR PESGWGRPGGGFTSILRPDSPLPTRV QYGTERKRRGQSSRDAFSARRQSV GGGANWEGGGA KRARRGTGPAG WRAEGGGAACRGSARASPAFRGRG PLPPFASGRVPGRQCGLRQWLQEK LLGPSDHLSCFQMPGTSVCDCAACL RACTEKP CDSNMWDSQAPWTGLK TRLTYRIFTINDLRQDWWRDYFEK YGKIETIEVMEDRQSGKKRGFAFVT FDDHDTV D KIVGRGGGSGNFMGRG

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						GNFGGGGGNFGRGGNFGGRGGYG GGGGGSRGSYGGGDGGYNGFGGD GGNYGGGPGYSSRGGYGGGGPGY GNQGGGYGG/G/GGGYDGYNEGGN FGGGNYGGGGNYNDFGNYSG\QQ QS\NYGPMKGGSLGGVRSSGSPYGG GYGSG\G\GSGGYGSRRF
4116	9613	A	4408	2	370	
4117	9614	A	4409	1	159	
4118	9615	A	4410	3	261	
4119	9616	A	4411	1	8748	
4120	9617	A	4412	1	2176	
4121	9618	A	4413	37	441	
4122	9619	A	4414	1	1940	PVLRHAVWLKSEGKSSFGLCAPLR KGSFLQKSWIFFRPVMADKLTRIAI VNHDCKCKPKCRQECKKSCPVVR MGKLCIEVTPQSKIAWISETLCIGCG ICIKKCPFGALSIVNLPNLEKETTH RYCANAFKLHRLPIPRPGEVLGLVG TNGIGKSAALKILAGKQKPNLGKY DDPPDWQEILTYFRGSELQNYFTKI LEDDLKAIKPQYVDQIPKA\AKGTV GSILDRKDETKTQAIVCQQLDLTHL KERNVEDLSGGELQRFACAVVICQ KADIFMFDEPSSYLDVKQRLKAAITI RSLINPDRIIVVEHDLVLDYLSDFI CCLYGVPSAYGVVTMPFSVREGINI FLDGYVPTENLRFRDASLVFKVAET ANEEEVKKMCMYKYPGMKKKMG EFELAIVAGEFTDSEIMVMMLGENG MGKTTFIRMLAGRLEPDEEGEVPVL NVSYKLQKISPKSTGSRVQLLREKIR DAYTHPQFVTNVMKPLQIENIDQE VQTLSSGELQRVTLAL*LGQNLDP VYL\DEPPA\YLDSEQRLMAARVV KRFIPHAKKTA\FVVGTTWTFIMATY L\ADRVIVFD\GVPSTKNTVANSPT LLAGMKNKFLSQLEITFRDPNNYRP RINKLNSIKDVEQKSGN\YFFLDD
4123	9620	A	4415	1	122	
4124	9621	A	4416	2	1382	
4125	9622	A	4417	135	282	
4126	9623	A	4418	2	1652	
4127	9624	A	4419	3	279	
4128	9625	A	4420	8	353	
4129	9626	A	4421	1	1542	
4130	9627	A	4422	1	496	
4131	9628	A	4423	70	365	
4132	9629	A	4424	1	3771	
4133	9630	A	4425	2	285	
4134	9631	A	4426	1	724	
4135	9632	A	4427	58	197	
4136	9633	A	4428	640	813	
4137	9634	A	4429	3	268	
4138	9635	A	4430	1	1512	
4139	9636	A	4431	3	1625	
4140	9637	A	4432	1	330	GKTITLEVEPSDTIENVKAKIQDKEG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						IPPDQQRLLFAGKQLEDGRTLSDYNI QKESTLHLVLRRLGGIKYNCCKMI CRKCYARLHPRAVNCRRKKCGHT NNLRPKKKVK
4141	9638	A	4433	2	544	DPRLQFFFFLSSLLQRGDRAGWW RRFFGTQTCRVFVKTLTGKNLHPL RYETQ*HPLKNVQKPKISRTKEGIP PDQAAS**FAGK\QLE\DGRTLSDY\N NIQKESTRAPWLLRL\GGIIEPFSPP GLPKKYN\CDKMI\CRKCYAR/LFHP RCLSTCRK\KKCGSHQTTLRPQRRR SNKGGFFP
4142	9639	A	4434	385	499	
4143	9640	A	4435	2	127	
4144	9641	A	4436	3	424	
4145	9642	A	4437	1	110	
4146	9643	A	4438	1	110	
4147	9644	A	4439	1	110	
4148	9645	A	4440	1	110	
4149	9646	A	4441	1	108	
4150	9647	A	4442	3429	7466	
4151	9648	A	4443	4048	4181	
4152	9649	A	4444	682	829	
4153	9650	A	4445	163	320	EFEGFNPLKLGEAGWARWLTVPVIA L*ETEAGGSRGQEITILANTVKPHL Y
4154	9651	A	4446	1122	1446	
4155	9652	B	4447	124	27844	XRSTVPPRISAYERPVPWPGEWNDP RGPGRRASAVVSPREGNWGVL RDP RLQARKPRMVRSRQMCNTNMSVP TDGAVTTSQIPASEQETLVRPKPLLL KLLKSVGAQKDTYTMKEVLFYLGQ YIMTKRLYDEKQQHIVYCSNDLLG DLFGVPSFSVKEHRKIYTMIRNLV VVNQESSDSGTSVSENCHLEGGS DQKDLVQELQEEKPSSSHLVSRPST SSRRRAISETENSDELSEGERQKRH KSDSISLSFDESLALCVIREICCERS SSESTGTPSNPDLAGVSEHSGDWL DQDSVSDQFSVEFEVESLDSYSL SEEGQELSDDEDDEVYQVTYQAGE SDTDSFEEDPEISLADYWKCTSCNE MNPPLPSHCNRCWALRENWLPEDK GKDKGEISEKAKLENSTQAEFGDV PDCKKTIVNDSRESCVEENDDKITQ ASQSQESDYSPSTSSSIYSSQEDV KEFEREETQDKEESVSSLPLNAIEP CVICQGRPKNGCIVHGKTGHLMAC FTCAKKLKKRNKPCVLTGHIRTEQ PIIILPKKHKKKKERKSLPEEDVAVS SNVDFDTLTKKKVYLNKLERKSV FKGFQGMGQHWTFINLDKPSNPS SHEVVAWIRRLRVEKTGHSGTLDP KVTGCLIVCIERATRLVKSQQSAGK EYVGIVRLHNAIEGGTQLSRALET TGALFQRPLIAAVKRQLRVRTIYES KMIEYDPERRLGIFWVSCEADTYSR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						TLCVHLGLLGVGGQMQLRRVRS GVMSEKDHMTMHDVLDQWLY DNHKDESYLRRVVYPLEKLLTSHK RLVMKDSAVNAICYGAKIMLPGVI RYEDGIEVNQEIVVITTKGEAICMV EHDKEFFHPRYHHREFRDLSKIPE GEAVTAAEFRIYKDYIRERFDNETF RISVYQGIGSLPARQPYLWASEEGW LVFDITATSNHWVVPNRHNLGLQL SVETLDGQTINPKLAGLGRHGPQN KQPFMVAFFKATEVHFIRSIRSTGSK QRSQNRSKTPKNQEALGWPTMCTD ELSFGLIVTLQSLFEKRTAAGTRG RPCCKHELIVSFRDLGWQDWIIAPE GYARYYCEGECAPFLNSYMNATNH AIVQTLVHFNPETVPKPCCAPTQLN AISVLYFDDSSNVILKKYRNMVVRA CGCH*
4156	9653	A	4448	2	129	
4157	9654	B	4449	1	462	MSQQYYVRLCQIQPSPSRVSGRENL VLVGDFPDPTLKRKVGRCACG LTDLPEPTAQVLVEQGQDEALWFH NVISEEFGVGVNIFWKHLPSECYDK TDTYGNKDPTAASRAAQILDRALK TLAELPEEYRDFYARRMVLHIQDK AYSKNSE*
4158	9655	A	4450	3	366	
4159	9656	A	4451	1	167	
4160	9657	A	4452	2	382	TMVLSPADKTNVKAA/WGMFLSFP TTKTYFPHFDLSHGSAQVKGHGKK VADALTNVAHVDDMPNALSALS DLHAHKLVRDPVNFKLLSHCLLV LAAHLPAEFTPAVHASLDKFLASVS TVLTSKYR
4161	9658	A	4453	2	252	
4162	9659	B	4454	31	449	MVLSPADKTNVKAAGWKTYFPHF DLSPGSAQVKGHGKKVADALTN VAHVDDNAQRAVRPKRCTRSTFG WTRSNFKLLSHCLLVTLAAHLPAEF NPCGARLPGQVPGFCYAPC*
4163	9660	A	4455	2	81	
4164	9661	A	4456	2	81	
4165	9662	A	4457	3	452	
4166	9663	A	4458	1	493	RPRIRHEHRLRENPPWFLFPAAKTN VKAGLG*G*GSHPPSNVAKTLERIM FLSFPTTKTYFPQLRTLHGFSQV* GPRSRRLPDALTKRPWRHVDDHAQ TRCPALSDLHAHKLVRDPVNFKLL SHCLLVTLAAHLPAEFTPAVHAYL DKFLASVSTVLTSKYR
4167	9664	B	4459	208	420	MGNPKVKAHGKKVLTSLGDAIKHL DDLKGTFAQLSELHCDKLHVDPEN FKLLGNVLVTSIAIHFGIEFTPE*
4168	9665	A	4460	40	534	SRRHGSVSHREAKATIASLWGKVN VEDAGGETMIRLLVVPWPQRSF ASFSSLFSAIMGNPKVKA/HGKK VLTSLGDAIKHLDDLKGTFAQLSEL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HCDKLHVDPENFKLLGNVLVTVLA IHFGKEFTPEVQAISWQKMVTGV ANALSSSTYHLNSLPMMQNF
4169	9666	A	4461	2	171	
4170	9667	B	4462	10	351	MAPRTLVLGSGALALTQTWAGSH SMRYFYTSVSRPGRGEPRFIAVGYV DDTQFVRFDSDAASQRMEPRAPWI EQEGPEYWDRNTRNVKAHSQTDR VDLGTLRGYRCVSHSL*
4171	9668	A	4463	1	986	
4172	9669	A	4464	3	1282	
4173	9670	A	4465	1	1004	MAVMAPRTLVLGSGALALTQTWAGSH SMRYFYTSVSRPGRGEPRFIAV GYVDDTQFVRFDSDAASQRMEPRAP PWIEQEGPEYWDRNTRNVKAHSQI DRVDLGTLRGYYNQSEAGSHTIQM MYGCDVGSDGRFLRGYQQDAYDYG KDIALNEDLRSWTAADMAAQITQ RKWEAARVAEQLRAYLEGTCVEW LRRHLENGKETLQRTDPPRTHMTH HAVSDHEATLRCWALSFYPAEITLT WQRDGEDQTHCHVQHEGLPKPL TLRWEPSQPTIPVGHAGLVLFQAV ITGAVVAAMWRRKSSDRKGGSYS QAASSDSAQGSVDVSLTACKV
4174	9671	A	4466	1090	2175	
4175	9672	A	4467	1	780	
4176	9673	A	4468	59	169	
4177	9674	A	4469	89	134	
4178	9675	A	4470	864	1885	
4179	9676	A	4471	89	176	
4180	9677	A	4472	1	1127	
4181	9678	A	4473	1	405	
4182	9679	A	4474	3	199	
4183	9680	A	4475	3	607	
4184	9681	A	4476	1017	2029	
4185	9682	A	4477	844	1572	
4186	9683	A	4478	1	846	
4187	9684	A	4479	452	1220	
4188	9685	A	4480	1	1254	
4189	9686	A	4481	1	1383	
4190	9687	A	4482	1	1290	
4191	9688	A	4483	666	1606	
4192	9689	A	4484	1	1236	
4193	9690	A	4485	1	1269	
4194	9691	A	4486	719	1175	
4195	9692	A	4487	1	1182	
4196	9693	A	4488	1	1377	
4197	9694	A	4489	1	1335	
4198	9695	A	4490	1	2456	
4199	9696	A	4491	1	1827	
4200	9697	A	4492	1	1011	
4201	9698	A	4493	452	950	
4202	9699	A	4494	1	1433	
4203	9700	A	4495	1	1933	
4204	9701	A	4496	641	2107	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
4205	9702	A	4497	1	2582	
4206	9703	A	4498	1	1095	
4207	9704	A	4499	1544	525	
4208	9705	A	4500	2	161	
4209	9706	A	4501	3	452	
4210	9707	A	4502	25	622	EFHRLRENPPWFLFPAAKTNVRA\A WG*RSGAHAGEYGAEALER\MLVF PPPTPKPYFPELRT*AHGFCPKVKGP TAKKV\AERA*PNAVA\HVDGHAPN GAVPP*ADLQRRTSFRVDPVNFQAP *ATCLLVTLAAHLPAEFTPAV\HA SLGQVPGLSVSTVLTSKIPVKLEPSV GHAFLPLWAFPPAPPPLSCTRTPVG L
4211	9708	A	4505	2	213	
4212	9709	A	4506	2	382	TMVLSPADKTNVKAA/WGMFLSFP TTKTYFPHFDLSHGSAQVKGHGKK VADALTNVAHVDDMPNALSALS DLHAHKLRVDPVNFKLLSHCLLV LAAHLPAEFTPAVHASLDKFLASVS TVLTSKYR
4213	9710	A	4507	2	252	
4214	9711	A	4508	1	466	WSPQTQREPTMVLSPADKTNVKAA WGKVGAHAGEYGAEALGR\IFLSFP PTKTYFPHFDLSPGSAQVKGHG\KK VADALTNAGAHVDDMPNALSSPE ATLHAHKLRVDPI\NFKLLSHCLLV LAAHLPAEF\TPAVHASLDKFLASV STVLTISKYR
4215	9712	A	4509	256	391	NELHAENLKNEDDVTGLLGFWT LIISLTAGFSCCSFSWTVTYFDSFEP GMFPPTPLSPARFKK*R*CRHWTIRI LDSTYNIPNCWILLQLFLDSDLL
4216	9713	A	4510	2	490	
4217	9714	A	4511	1	160	
4218	9715	A	4512	1	150	
4219	9716	A	4513	1	73	
4220	9717	A	4514	2	213	ISPFYHLCQMLKTADVLRMALWR CRDALLS*GGSSIEIPLFLYGSREL LGFCFTGMNHCAQSIYNRF
4221	9718	C	4515	186	365	MFQLLYDSLXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXIYNRF*
4222	9719	A	4516	251	454	GGSSIEIPLFLYGSRARTWILF*EM AAGRVQWLTSPVAPALWEAEAGGR GQEFKTSIAKRVKPHLY
4223	9720	A	4517	3	192	
4224	9721	A	4518	1	129	
4225	9722	A	4519	23	115	
4226	9723	A	4520	1	1582	GRGWRAVLGWSRRRSGLEPATVGS SMALLFLLPLVMHGVSRAMGTAD LGPSSVPTPTNVTIESYMNPIVY EYQIMPQVPVFTVEVKNYGVKNSE WIDACINISHHYCNISDHVGDPSNSL WVRVKARVGQKESAYAKSEFAV CRDGKIGPPKLDIRKEEKQIMIDIFH PSVFNVDGEQVDYDPETTCYIRVY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NVYVRMNGSEIQYKILTQKEDDCD EIQCQLAIPVSSLNSQYCVSAEGVL HVWGVTTTEKSKEVCITIFNSSIKGSL WIPVVAALLFLVLSLVFICFYIKKI NPLKEKSIILPKSLISVVRSALETKP ESKYVSLITSYQPFSLKEVVCEEPL SPATVPGMHTEDNPGKVEHTEELSS ITEVVTTEENIPDVVPGSHLTPIERE SSSPLSSNQSEPGSIALNSYHSRNC ESDHSRNGFDTDSSCLESHSLSDSE FPPNNKGEIKTEGQELITVIKSPPPSF CYDKP\HVLVDLLVDDSGKESLAG YRPTEDSQRNFEISLSCTQL
4227	9724	A	4521	1	408	
4228	9725	A	4522	2	377	
4229	9726	A	4523	50	326	
4230	9727	A	4524	3	1948	AAAAAAVPASFGLCSRDPAPPQP ASMSGIKKQKTENQQKSTNVVYQA HHSRNKRQGVVGTGGFRGCTV WLTGLSGAGKTTISFALEEYLVSHA IPCYSLDGDNVRHGLNRNLGFSPGD REENIRRIAEVAKLFADAGLVCTSF ISPFKDRENARKIHESAGLPFFEIV DAPLNICESRDVKGLYKRARAGEIK GFTGIDSDYEKPETPERVLKTNLST VSDCVHQVVELLQEQNIVPYTHIKDI HELFPENKLDHVRAEAETLPSLSIT KLDLQWVQVLSEGWATPLKGFM EKEYLQVMHFDTLDDGMALPDGVI NMSIPIVLPVSAEDKTRLEGCSKFVL A\HGRRVAYLTETAEF/HTHRKE ERCS/RVFWGTTCTKHPHKMVM SGDWLVGGDLQVLEKIRWNDGLD QYRLTPLELKQKCKEMNADAVFAF QLRNPVHNGHALLMQDTRRRLLER GYKHPVLLLHPLGGWTKDDDVPLD WRMKQHAADVLEEGVLDPKSTIVAI FSPMLYAGPTEVQWHCSRMIAG ANFYIVGRDPAGMPHPETKKDLYE PTHGGKVLSMAPGLTSVEHPRVA AYNKAKKAMDfyDLARHNEFDfIS GTRMRKLAREGENPPDGFMAPKA WKVLTDYYRSLEKN
4231	9728	A	4525	1	626	
4232	9729	A	4526	66	409	LGLLQVTTTNPSPPTNYLLKMLFK LRTPPFISHHSFILKNYDIQYFSMRDI DRLGIQKVMERTFDLLIGKRQRPIH LSFDIDAFDPTLAAPATGTPVVGGLT YREGMYIAEEIH
4233	9730	A	4527	1	1257	
4234	9731	A	4528	3	1086	FSVLRIMSLRGSLSRLLQTRVHSILK KSVHSVAVIGAPFSQGQKRKGVEH GPAAIREAGLMKRLSSLGCHLKDFG DLSFTVPVKDDLNNLIVNPRSVGL ANQELAEVVSRAVSDGYSCVTLGG DHSLAIGTISGHARHCPDLCVWVW DAHADINTPLTTSSGNLHGQPVSVFL LRELQDKVPQLPGFSWIKPCISSASI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VYIGLRDVPPEHFILKNYDIQ\YFP MKDIDRLGIQKVMERTFDLLIGKRQ RPIHLSFDIDAFDPTLAPATGTPVVG GLTYREGMYIAEEIHNTGLLSALDL VEVNTQLATSNEEAKTTADLAVDV IASSFGQTREGGHIVYDQLPTPSSPD ESENQARVRI
4235	9732	A	4529	1	128	
4236	9733	A	4530	3	126	
4237	9734	A	4531	1	79	
4238	9735	B	4532	214	268	XELEKLVQVVRQLEAEPGLPPVQPV FITVDPERDDVEAMARYVQDFHPR LLGLTGSTKQDEDQDYIVDHSIAIY LLNSDGLFTDYYGRSRAEQISDSV RRHMAAFRSVLS*
4239	9736	A	4533	23	257	AYLIDDTEAQSRGSQAKATPLEGLR TQPSSRPLGGIKLV*YEVLCCLMTA LKA/TQIQLPATSHSAARLRGVLP AIR
4240	9737	A	4534	3	229	
4241	9738	A	4535	1	297	
4242	9739	A	4536	67	552	GPWRFCFSEAVSEPTTVAFDVRPGG VVHSFSHNVGPGDKYTCMFTYASQ GGTNEQWQMSLGTS\EDHQHFT\CT IWRPPRGKSYL\YFT\QFKAEVAGRL RFEYRHGLTFKARILKGESDVPLEN LRNFEVTKTAVGSQGPAGFKLTC PKLVIVAKAS\RTCL
4243	9740	A	4537	2	232	RDGTVHARAANKNRVISVLLPSDLV H*LWEP*PDED*DA*SETGDIDHRV TEESHE*PAFHNFMQESMAQYWKR NNK
4244	9741	A	4538	2	1094	RHPVCLLVLMAGSGKTTFFVQRLT GHLHAQGTTPPYVINLDPVHEVPFP ANIDIRDTVKEYEVMKQYGLGPNG GIVTSLNLFATRFQVMKFIEKAQN MSKYVLIDTPGQIEVFTWSASGTHI EALASSFTVVIYVMDTSRSTNPVT FMSNMLYACSILYKTKLPFIVVMNK TDIHDHSFAVEWMQDFAFQDALN QETTYVSNLTRMSLVLDEFYSSLR VVGVS AVLTGLDEL FVQVTSAAE EYEREYRPEYERLKKSLANAESIQ EREQLERLRKDMGSVALDAGTAKG VFTVDSLSPVLHPSDLILTRGTLDEE DEEADSDTDDIDHRVTEESHEEP AFQNFMQESMAQYWKRNNK
4245	9742	A	4539	710	1053	
4246	9743	A	4540	3	281	
4247	9744	A	4541	30	320	
4248	9745	A	4542	3	115	
4249	9746	A	4543	1	137	
4250	9747	A	4544	3	32	
4251	9748	A	4545	1	135	
4252	9749	A	4546	1	2694	
4253	9750	A	4547	3	544	
4254	9751	A	4548	2	323	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
4255	9752	A	4549	1	384	
4256	9753	A	4550	1	1299	MASPVAQAQAGKLLRALALRPRFLA AGSQAVQLTSRRWLNLEQYQSKKL MSDNGVRVQRFFVADTANEALEAA KRLNAKEIVLKAQILAGGRGKGVF NSGLKGGVHLTKDPNVVGQLAKQ MIGYNLATKQTPKEGVKVNKVMV AEALDISRETYLAILMDRSCNGPVL VGQPQGGVDIEEVAASNPELIFKEQI DIFEGIKDSQAQRMAENLGFVGPLK SQAADQITKLYNLFLKIDATQVEVN PFGETPEGQVVCFDAKINFDDNAEF RQKDIFAMDDKSENEPIENEAAKYD LKYIGLDGNIACFVNGAGLAMATC DIIFLNGGKPANFLDLGGGVKEAQV YQAFKLLTADPKVEAILVNIFGGIV NCAIIANGITKACRELELKVPLVVR EGANVQEAQKILNNSGLPITSAIDL EDAAKKAVASVAMK
4257	9754	A	4551	1	590	RVRTKDPNVVGQLAKQMIGYNLAT KQTPKEGVKVNKVMVAEALDISRE TYLAILMDRSCNGPVLVGSPQGGV DIEEVAASNPELIFKEQIDIFEGIKDS QAQRMAENLGFVGPLKSQVEAILV NIFGGIVNCAIIANGIPKACRELEL VPLVVRLEGTNVQEAQKILNNSGLP ITSAIDLEDA\AKKAVASVAKK
4258	9755	A	4552	3	168	
4259	9756	A	4553	3	95	
4260	9757	A	4554	3	354	
4261	9758	A	4556	1	95	
4262	9759	A	4557	156	364	GPVE*KPVEEESRGLLD*GLPGMD WGWVFGKGGDPPLAQSLNCPSTV SEIIGRDLSGFPAPPGEPPA
4263	9760	A	4558	1	2523	
4264	9761	A	4559	3	469	
4265	9762	A	4560	3	132	
4266	9763	A	4561	1	2961	MGAASCEDEEELFKLVFGEEKEAPP LGAGGLGEELDSEDAPPCCRLALGE PPPYGAAPIGIPRPPPRPGMHSPPPR PAPSPGTWESQPARSVRLGGPGGG AGGAGGGRVLECPISIRITSISPTPEPP AALEDNPDAWGDGSPRDYPPPEGF GGYREAGAQGGGAFFSPSPGSSSL SWSFFSDASDEAALYAACDEVESEL NEAASRFLGSPLSPRASRPWTPE DPWSLYGSPGGRGPEDSWLLLSAP GPTPASPRPASPCGKRRYSSSGTPSS ASPALSRRGSLGEEGSEPPPPPLPL ARDPGSPGPFYVGPAPAESIPQKT RRTSSEQAVALPRSEEPASCNGKLP LGAEESVAPPGGSRKEVAGMDYLA VPSPLAWSKARIGGHSPIFRTSALPP LDWPLPSQYEQLELRIEVQPRAHHR AHYETEGSRGAVKAAAPGHPVVKL LGYSEKPLTLQMFIGHTADERNLRPH AFYQVHRITGKMVATASYEAVVSG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						TKVLEMTLLPENNMAANIDCAGIL KLRNSDIELRKGETDIGRKNTRVRL VFRVHVPQGGGKVSVQAASVPIE CSQRSAQELPQVEAYSPSACSVRGG EELVLTGSNFLPDSKVVFIERGPDG KLQWEEEA TVNRLQSNEVTLLTV PEYSNKRVS RPVQVYFYVSNRRK RSPTQSFRLPVICKEEPLDSSLRGF PSASATPFGTDMDFSPRPYPSPYPH EDPACETPYLSEFGYGMPLYPQT GPPPSYRPLRMFPETRGTGCAQP PAVSFLPRFPSPDPYGGRGSSFPLG/L PFSPPAPFRPPPLPASPPLEGFPFSQS DVHPLPAEG\YNKVGPGYGPGEAGP EQEKSRRGGYSSGFRDSVP IQGITLEE VSEIIGRDL\SGFPETSLEKKPPALKP RETVITLATPAPASALPPFPFLELV ATEAWGQPLAPLSPSFCLSHCLPLPS PSLGCGPQAWLALEGLGGKECVE EGGG
4267	9764	A	4562	19	387	
4268	9765	A	4563	1	373	
4269	9766	A	4564	2	343	
4270	9767	B	4565	19	507	MEANGLGPQGFPPELKNDTFLRAAW GEETDYPVWCMRQAGRYLPEFRE TRAAQDFFSTCRSPEACCELTLQPL RRFLDAAIIFSDILVVPQALGMEVT MVPSKGPSFPEPLREEQDLEALRDP EVEASKLGYGFQAITYPTTTGWDV CRLIGFCWCPHGP*
4271	9768	A	4566	3	339	
4272	9769	A	4567	3	679	
4273	9770	A	4568	1	139	
4274	9771	A	4569	1	526	HERFETTYFKKFP\GYVVTGDGCQR DQDGYWITGRIDMLNVSGHLLS TAEVESALVEH*RLLQEA\AVVGH HPCEGVNASYCFVTLCDGHTFSPKL TEELKKA\VMRKRLAPFATPDYIQN APGLPKTRSGKIMRRVLRKICS/VT DHDLGDMSTVADPS\VISHLFSHRC LTIQ
4275	9772	A	4570	537	2357	GVCHQRR LAPQAWPGAGTDSL LLA TRWATGAPGHCCWHLPARHTCGSP GLSPVPQPASAGPPGGLWERHSRE YIKTWRPR/YFLLKSDGSFIGYKERP/ EAPDQTLPLNNFSVAGCLGMS\EC QLMKTERPRPNT/FVIRCLQWTTVIE RTFH/VDSPDE/REEWMRAIQMVAN SLKQ/RAPGEDPMDYKCGSPSD/SST TEEMEVA VSKARA/KVGTFGKVILV REKAT/GRYYAMKILRKEVIIA/KVR APGIALASLCGGCVCLQDEVAHTV/ TESRVLQNT RHPFLTALKYAFQTHD RL/CFVMEYANGA VFHLSRERVFTE ERAR/FYGAEIVSALEYLHSRD/VVY RDIKLCAQEKGDTHSP*KVSPSLSSR ITLAPTGTQVSTVRGTSDP/AVECS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HSGTPHSSWNEQLHTTVWTRLIG YVEGKPHRGAVPRYMGVGRVLE DN/DYGRAVDWWGLGVVME/MM CGRLPFYNDHERLF/ELILMEEIRF PRTLSP/EAKSLLAGLLKKDPKQ/RL LP/PFKPQVTSEVDTRYFDD/EFTAQ SITITPPDRCECWGPRAESRCLPHAE PSSAAVPDGFAGPLSPQDAWRGR RGWRRRERAGAAGRTRVRRGHLPE VMPAFLAS
4276	9773	A	4571	64	1537	VTAYHAATMNEVSVIKEGWLHKR GEYIKTWRPRYFLKSDGSFIGYKE RPEAPDQTLPLNNFSVAECQLMKT ERPRNTFVIRCLQWTTVIERTFHV DSPDEREWMRAIQMVANSLKQRA PGEDPMDYKCGSPSDSSTEEMEV AVSKARAKVTMNDFDYLKLLGKG TFGKVILVREKATGRYYAMKILRKE VIIAKDEVAHTVTSRVLQNRHPF LTALKYAFQTHDRLCFVMEYANGG ELFFHLSRERVFTTEERARFYGAEIVS ALEYLHSRDVVYRDIKLENMLDK DGHKIDFGLCKEGISDGATMKT CGTPEYLAPEVLEDNDYGRAVDW WGLGVVMEYEMMCGRLPFYNDHE RLFELILMEEIRFRTLSPKASLLA GLLKKDPKQRLG/GGPSDAKEVME HRFFLSINWQDVVQKKLLPPFKPQV TSEVDTRYFDDEFTAQSITITPPDRY DSLGLLELDQRTVHFP/QFSYSASIRE
4277	9774	A	4572	2	423	
4278	9775	A	4573	1	106	
4279	9776	A	4574	3	58	
4280	9777	A	4575	1	191	
4281	9778	A	4576	3	325	
4282	9779	A	4577	3	277	
4283	9780	C	4578	77	292	MVDFCPCSCIFXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXHWSIC IS*
4284	9781	A	4579	645	849	
4285	9782	A	4580	3	140	EANKENREAQMAAKLERLPEKD*A /HLEEVKKNK\ESKDPADETED
4286	9783	A	4581	49	605	NSARGLSLSQLIVQNTLPVACLLFT MASSDIQVKELEKRASGQAFELILSP RSKESVPEFPLSPPKEEGFFPGGKFR EN*EAAEERRQSP*SCSS*RQLAEKR EHGKEVLQKAIEENNNFQ*NGQK RKLTPHKMEA**RDPREATNGLPKL EPFAEEKDKAH*KKCRKNKESQRP CPRDLKPD
4287	9784	A	4582	1	567	VVREPAFSLA/EAQFTARYFSTSSIP NV\NKAPVIRIRRSKHM*QGVTLPI E\HYHEGTDLS*TALV*ARVGNQLA KLKR\NYAKAVELLVQLASLQTSFV TLDEAIKITNRRVNAIEHVIIPIERT LAYIITELDEREREFFYRLKKIQEKK

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						KILKEKSEKDLEQRRAGEVLEPAN LLAEKDEDLLFE
4288	9785	A	4583	1	748	MSGKDRIEIPSRMAQTIMKARLKG AQTGRNLLKKKSDALTLRFQILKK IETKMLMGEVMREAAFLAEAKFT AGDFSTTVIQNVNKAQVKIRAKKD NVAGVTLPVFEHYHEGTDSEYELTG LARGGEQLAKLKRNYAKAVELLV ELASLQTSFVTLDEAIKITNRRVNAI EHVHPRIERTLAYIITELDERVREEF YRLKKIQEKKKILKEKSEKDLEQRR AGEVLEPANLLAEKDEDLLFE
4289	9786	A	4584	166	238	
4290	9787	A	4585	53	203	
4291	9788	A	4586	357	498	
4292	9789	A	4587	262	397	
4293	9790	A	4588	68	422	
4294	9791	A	4589	70	361	
4295	9792	A	4590	259	2603	
4296	9793	A	4591	246	667	
4297	9794	A	4592	25	471	
4298	9795	A	4593	2	3788	
4299	9796	A	4594	1	700	
4300	9797	A	4595	604	1047	SNNRTDNPTSVAYLSKETDVVAKG WPHCLWVVAVAILVLEAIKHQ GK DFTVWTS HDVNGILGAKGNSWLS D KRLRYQALLLEGPVLQIHTCVALN PAIFLPEDGEPIKHDYQQIVAQTYVT *EDLLEVPLANPDLNLYTNGSSFV
4301	9798	A	4596	1	1410	
4302	9799	A	4597	510	755	
4303	9800	A	4598	59	411	SWPSDKQTLVVQRGQKMEQANHP DPTDHMSQLMWT/VLPQGFDRSPH LFGQALAQDLGHFSSPGTLVLQYV DLLLLATSSEASCQATLALLNFLA NQGYK/LSRSKAQLCLQQVKYLCL
4304	9801	A	4599	1	565	
4305	9802	A	4600	126	492	CNNSMTSLQVRLKVCPRPCRTSM/L PIRII*KLPQVCLDLL*IREGEWDMY PCWAKFPCPYSLKGT*PIAWGILWS FGDFFAY/IPLMQQKH*FSSQNTRR NEEGQI*WPLLMHSQKPAPLPVV
4306	9803	A	4601	1	342	
4307	9804	A	4602	55	219	LG NKHLLGSIDPRGSWVTGEYIFLR PPIAA*GRQ*DFLPPELWWTSLNNS WAFS
4308	9805	A	4603	339	1371	ASHPLRGLLCGPSLPNEPCPLLHGT QSHRPLKG*GVRAHSTGLAGSSTCR PLRDPLGEASWAPESAQGL*IHQSA LCI*LKLKPAGQRAKLGDRLDIPDR RKSSSTILGRAGDLQAMPEPPTLSV GSCAAQASPMNPAPCSTAPSPIDHS RAEECGRIARDWQAAPPAGPCGIH WVKPAGLLSLLRDCKYTNRHSVSS SRFANTNQHPASSSGFVNAPIDTLY LANLVGTWRTFVASSGIVNAPISTL SKQTTWLYQSAGCGKESTQASGAQ

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						TGGTSFKSLETTGSISEASSAKHCTE LFSRFTTFNPDSVPDGVVGDAGT VWPGVLKGEPCHLGTCTYRCVLDPH PTPSESDTIQGIHVQVCYMSTLHDA DVCDTNDPVTHTNTKKYIYSTEFTS NNPELRSEDETVFRALEKWKTSSEQT IGEMDFYICNDPHPDALYQNGLSK MQDTVLSLVFSPSVAA
4309	9806	A	4604	749	1002	QLKKGTNSLLVSKPSPVWIPTGTLT QIMGTGVANIC*PVF*KD*GELGKM NYAMMSTITQGKEENPAFLKWLWE ALRKYTPLSP
4310	9807	A	4605	1	1632	
4311	9808	A	4606	307	543	
4312	9809	A	4607	1	1149	
4313	9810	A	4608	119	409	GDICHHLGLTPVGSHSLSCSR*QV A*VGAVTAATIGTGILLQLAFLVC NWLLSGSSENFPRSALICFKSEREK GTCIQVGPNSPPPTACKGHN
4314	9811	A	4609	1	2433	
4315	9812	B	4610	97	1065	MHAVHTSLLVERTILTTTKERGSTL QYPLRPGAHKGLQDIVKRFAQALI RKCSSPCNTPI LGVQKPNGQWRLV QDLRLINEAVIPLYPVVPNPYNLLSQ IPEEAEWFTVLDLKD AFFCIPLHSDS QFLFAFEDPTDHTS QLTWTVLPPGF RDSPLFGQALAQDLGHFSSPGTLV LQYVDDLLATSSEASCQATDLL NFLANQGYKTHSRSDAPVGFTDR HLVATEKIPRGREPLSSLAVYTRGR PTRTGARRTIVSRIRDRFFRYRYLA QREPPYQQSLLIHLQLDSQPALSV VIGKVPNVVELTPNFGTAAQV*
4316	9813	A	4611	1	2403	
4317	9814	A	4612	1	2838	
4318	9815	A	4613	1908	4698	SNDRTEDDCGKHPFMSSPPATEPWV CLIEGQEIDFLDGTTFSVLIPCLG RLSSRSVTIQGILGQPVTRYFSHLLS CNWETLLFSHAFLVMPESTPLLGR DILAKAGAIISMKTGNKLPICCPLE GINPEVWALEGQFGRAKNAHPLQIR LKDPISFPYQRQYPLRPEAHKGLQDI VKHLKAQDSVRKCSSPCNTPI LGVQ KLNSQWRLVQDLRLINEAVIPLYPV VRNPYTLSSQVPEEAEWFTVLDLKD DAFFCIPLHSDSQFLFAFEDPTDHTS QLMWMVLPQFRDSPHLFGQAQA QDLGHFSSPGTLVLQYSEIAKTLYT LIKEMERANTHLVEWEPEAETAFET LKQALVQAPALSLPTGQNFALYVIE RAGIALGVLTQTHRTPQPVAYLSK EIDVVAKGWPHCLRTVVAVAVLVS EAIKIIQKDFTVWTHDVNGILGA KGLWPSDNCLLRYQALLLEPVL QIHMCIAINPATFLPEDGEPIKHDCQ QIIVQTYATQDDLLEVPLANPDFNL YNSGSSFVENGIQRAGYAIVSDVTV

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						LGSKPLSPGTSTQLAELVALTRALE LGKGKRINVYTD SKYAYLILHAHA AIWKEREFLTSGGTPIKYHKEIMELL HTVQKPKEVAVLHCQSHQKGSARR IFCLTRIPGTRVCKNPHVSLSGISEW PLRDHTPLCFRPKALLAVVHEEICS MGCKDPGWNSLVSEEDRKMQUES LETSRDLLNGFDQNVNDNDMSKVQ AEGASDGDEELIGKWRKGLSMLW KILSIENMMNVWKDGTIKDAIIVIEK AVKAIKPETINSCQRNLCPDVVHDF TRFTTEPIKDIKEIGDLAIKLGIFESS NSTQFLNQFVPDDRLSPHNKLLKFY KPEFYSSYPLVSLDHYVDQVGARI SMSFCVTTVTASGSGSWTCGVSQ LKLSYAD
4319	9816	A	4614	1529	2945	
4320	9817	A	4615	3	374	
4321	9818	A	4617	3	112	
4322	9819	A	4618	359	465	
4323	9820	A	4619	3	381	MRILMVGLDAAGKTTILYKLLGEI VTTIPTIGFIFVVD S NDRERI QEVAD ELQKMLLVDEL RDAV LLLFANKQD LPNAMAISEMTDKLGLQSLRNRTW YVQATCATQGTGLYEGLDWLSNEL SKR
4324	9821	A	4620	395	552	
4325	9822	B	4621	1289	1603	MVVTISPNSFLYRMVVLPAASNPTI KMRICFLPNSREKREEIVRPMVVA LVMGRSRRGLGRPRAFSFQAPRQT KREGRERAEEERGRQKRLSGPCAD EDPAQE*
4326	9823	A	4622	2	116	
4327	9824	A	4623	156	403	
4328	9825	A	4624	8	2648	WIQYSSTTLPNDWNKRKKKEKKA MLSARAKTPRKPTV/KKGSQTNLKD PVGVCYCRVRLGFPDQECCIEVINNTT VQLHTPEGYRLNRNGDYKETQYSF KQVFGTHTTQKELFDV VANPLVND LIHGKNGLLFTYGV TSGKTHMT GSPGEGLLPRCLDMIFNSIGSFQAK RYVFKSNDNRNSMDIQCEVDALLER QKREAMPNPKTSSSKRQVDPEFAD MITVQEFCKAEEVDEDSVYG VVVS YIEIYNNYIYDLLEVPFDP/IKPKPP QSKLLREDKNHNMYVAGCTEVEV KSTEEAFEVFWRGQKKRRRIANTHL NRESSRSHSVFNILVQAPLDADGD NVLQEKEQITISQLSLVLAGSERTN RTRAEGNRLREAGNINQSLMTRLTC MDVLRENQMYGTNKMVPYRDSKL THLFKNYFDGEGKVRMIVCVNPKA EDYEENLQVMRFAEVTQEVEVARP VDKAICGLTPGRRYRNQPRGPVGN EPLVTDVVLQSFPLPSCEILDINDE QTLPRLIEALEKRHNLRQMMIDEFN KQSNAFKALLQEFDNAVLSKENHM

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						QGKLEKEKMISGQKLEIERLEKKN KTLEYKIEILEKTTTIYEEDKRNQQ ELETQNLQKLQRQFSEKRRLEARLQ GMVTETTMKWEKECERRVAAKQL EMQNKLWVKDEKLKQLKAIVTEPK TEKPERPSRERDREKVTQRSVSPSP VPLLFPQDQNPPIRLRHRRSRSAG DRWVDHKPASNMQTETVMQPHVP HAITVSVANEKALAKCEKYMLTHQ ELASDGEIETKLIKGDYKTRGGGQS VQFTDIETLKQESPNGSRKRRSSTV APAQPDGAESVWTDVETRCSVGC GR*GAGSQLGPGYQHHAQPKRKK P
4329	9826	A	4625	1	331	
4330	9827	A	4626	142	461	
4331	9828	B	4627	136	906	XPELKPVDKESVVMKFPDGFEEKFS PPILQLDEVDFYYDLKHVIFSRLSVS ADLESRICVVGENGAGKSTMLKLL LGD LAPVRGIRHAHRNLKIGYFSQH HVEQLDLNVSACGTAGHASFLGRP EEEYXGWCDSGVPRMKRFKAGVP GSCGYAKEGGVTRVERKDFDQYRA LLQGTVSAAKAFL*
4332	9829	A	4628	1	233	
4333	9830	A	4629	1	312	
4334	9831	A	4630	2	119	
4335	9832	A	4631	1	145	
4336	9833	B	4632	78	236	MSYIPGQPVTA VVQRVEIHKLRQGE NLILGFSIGGGIDQDPSQNPFS EDT DK*
4337	9834	A	4633	102	583	IRVEMSYIPGQPGTAVVQRGEIHKL RQGENLILGFSIGGGIDQDPSQNPFS EDKTDKGIYVTRVSEGGPAEIALQ IGDKIMQVNGWDMTMVTHDQAR KRLHQA LRRRLVRLVTRQSLQK AVQQSMPVLAATTILRLPAASLYS NATSTLWSPSGFC
4338	9835	A	4634	1	373	
4339	9836	A	4635	3	86	
4340	9837	A	4636	1	204	
4341	9838	A	4637	1	767	
4342	9839	A	4638	20	515	
4343	9840	A	4639	3	391	HEESRSVSQAGVQWRYLGSLQRPP PRFKRFSCLSPSSWDHRCSTTS*LAN F*YLVETGFHHVELLTSSDLPTSAS QSAGITGVSHHAWPWFALNVFKDG CESPWPHNKLEFYTAYYNNFTGTT LRPPL
4344	9841	C	4640	201	368	MGKSKXAFRXKXGIVFIQGTFFPX YNXXPRGIKVSQEXNXXXXXCXKI GGEDVX*
4345	9842	A	4641	1	307	RLFFFFETVSHSVTQARVHLSHLGS LQPLLPTFKQFSCSLPGS*DYRRL LHPANF*FSVETGFHHVGQAGLEL LTSGDPPTSASQSAGITGVSHRAWP ST

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4346	9843	A	4642	1	310	
4347	9844	A	4643	49	360	DRVSVTQAGVQWCNLSLQPLPPR FR*FSCLSLLSSWDYRRPPRPANF* FLVETGFHHVGQAGLKLLTSSDPPT SASQSAEITGVSHRAWPVLSSPQPF FF
4348	9845	A	4644	2	119	
4349	9846	A	4645	1	276	FFFFFFFFLTQSLTHSVTRLECSGVI SAHCNLCLLGSSS*LASAS*VAGTT GANHYAQLIFVFLVEMGFHHVGRA GLKL/HDLK*SKVLGLQA
4350	9847	A	4646	2	273	LRQFSLLLPRVECSGAISAHCNLCLL GSSDSPASASRVSGITGTHQTWLT FFVFLVEMGFHHVGQAGLQLLT*V IRPPRPPKVLGLQA
4351	9848	A	4647	1	106	
4352	9849	A	4648	1	485	SSIDTLGRRVGQPAPGSPGASNHL CESYPWQLLQPCPVQAGARAELVP VPAHHPGDPVKTEP*RGQGASSGSC TCWGCPTAQAQAQPPSPAAPMRK EGPPSL*SERTGRPSRGVTSAGSDG AQPGSA*HSPWPGIVLLSVRYLQETI NHRPGGRPTGFSS
4353	9850	A	4649	1	623	CDLNSQPRSTDGTFDLTVLSNDGVH STVTSNIRVFFAGFSNATVDNSILLR LGVPTVKDFLTNHYLHFLRIASSQL TGLGTAVQLYSAYE/GEQ*NVSFGQ L*SENHNQYVNPGRSHLLERHSK RSF/FRQSGVKVESVDHDCVHGPC QNGGSCRLRLAVSSVLKSRESLPVII VANEPLQPFLCKCLPGYAGSWCEID IDECLPSP
4354	9851	A	4650	1	446	LMLRPRLKLQEPVPHHHLGFQCPSS PLLPPGPPPHKV*PLGFQEGGQHS SSLNFVAHSTPAKP/PPGCVCPSLPA SHAHCLSRVIGGVGLRNCTVVPTRG GGSQLPAWLLPSLIVPLIVHQSPVSS LQPIRHDLPAPGDGTHSSAYC
4355	9852	A	4651	2	388	SHGSYVMYHDQVEFISGMKHW/FN TKIQTIIY*KNEEKNKMIISTNAENG HDKILLPFMIKTHITLGI*GNVLILIT GIHKQFFWQGGWGGACGGGRVL LFPQAGVQWWDHSSLQPQPSLNSF SNSSL
4356	9853	A	4652	115	413	LHIYSQPKFRKGTCKIHW*KDSVFH SSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSPMLIQENTG/IMLQDI GFGKDYLSKTSKAQATKQK*TRKH WEMLQDIGFGKDYLSKTSKAQATK QK
4357	9854	A	4653	3	129	NTLLKKTVSFHQCCWKNWISICRKI KLDSYLSPTYTKIKSLIKNLKVRPET MLIQENTG/IMLQDIGFGKDYLSK TSKAQATKPK*TRLLSLTIYKNQVK VD
4358	9855	A	4654	1	405	LTLKPNSGFRFPQVATR*IKYPGIH PAKEVKDLYRKT*KTLLKGITDGP

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						Q*KTIRGSWIGRINITEMAILPKAIYR FNTTPIKLPMAFVITQLEKTIQKFIWN QKGAQIAKRILSKKTNSQTSHITVL QTIRI
4359	9856	A	4655	3	448	FFFFFAFLLLGLLHQIPDVSPGKYT TLLPLMIILMISGIKEVIYIINDMADK IVKEHKTVMTRLWDTFKWKEVKC GLNTVKALEMGELPSLQDTSPDVFI *QHSNPG*RDCKCKTRQGFDRQLLY QCRDILPPRQQAFLQSLRAQP
4360	9857	A	4656	2	502	KKKKERKRKRTP\IKKWAKDDRHF TGDKIKMVNKNIKICISLVIS*MQI KAITHPTRLAKVKCLPRMGR\KGIL FYCWARKLEQ/SFRKIFIP*NPQVR LLSTNPRKICAPFAKNTRASETWTK LLAALCVVTPN*KQTNCPOSTAGMS NLLASMDHTGRTVSGHA
4361	9858	A	4657	61	364	KTVWFCARVEGQGNLG*WKPRLP GLKHFPGLSSQ/WNRKLPDGPTNPG *FWNFKKKGGFPLWPKRI*IFGPGD PPSRASKRAGITGITHGAGPRFNFKK WR
4362	9859	A	4658	2	436	KLIIFLYTSNEQREFEIKNTIPFTLAPP KIK*LGTNLT\K\WQELYEKIYKSV KNIKELNKWRSSYGKGKSSSSSSSS SSSLDIACSWLRRLKIVKISGLHNLI YRFNIVPIEIPETYLVDVNKLIPQFIW RGKRHRIVNKIVE
4363	9860	A	4659	3	480	GSHDFFDKLILKFIWNSRPRIAKTIL KKKNKVGGTLCDFKTYRATV*I KTVWYWD/QIRHI/DQWSRITSPEIN PYIYQCLIFNRYTKTIQ/YGNNRLFN K*C*DMRRVKSDPFLTY/PYIIN*K MIIDVKAMIMKL/LEGNTGMSLSDF GLRKALDVTTKV
4364	9861	A	4660	362	408	CQVISVLWFYSSVLGWLWVWFCFSL KF*/WSKRSRQANPILKNKTRVLIL PDIKTPK\AGVIKPVW*QCS*KVW GEKVWYWQKMTQIVQWDRTESPQ IDN*SLTKEIQWRKDSLFNKW*GNN WTAPFSS/RSLNLNKDLTAVTKIKSK WVTDLNVKHKTNLL
4365	9862	A	4661	93	367	KVWGEKVWYWQKMTQIVQWDRTE SPQIDN*SLTKEIQWRKDSLFNKR* GNNWTAPFSS/RSLNLNKDLTAVTK IKSKWVTDLNVKHKTIKLL
4366	9863	A	4662	123	397	KVWGEKVWYWQKMTQIVQDRDRA ESPQIGH*SLAKEIQWRKNSLFNKW *GDHWAAAFSSSSSI*TKTLQP/CTKI KSKWVTDLNVKRTIQLL
4367	9864	A	4663	2	433	ETADFGPLVLDSDDDSVDRDIAEAI REYLKAKSGAAQTGAGRGQPGAA QPSRAAGSGSRCKPELSHGSAPTSV CPPKLVPGSGGGPGSQVRSSD*GS AFPVRASSNDSFEQSIKAEIEQLLNE KR*HATPKCDG\SIDKKPDP
4368	9865	A	4664	94	445	HHQLTLESLGKSKNSPRLSPSLGAC

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						LSCIIWQPAKGQGS GDGGNWRG KTAETE/SAAIGGETEWTAKCP*YSC L/GVGPTALTSQPPT/PEAHPQA/GG TYRDLHPDPTWKTGWCHFVFC
4369	9866	A	4665	52	119	
4370	9867	A	4666	987	1324	VSNTPSARNQGRASSPGNSSPE/SSS ESAPAATANGCDEAHLIPGGKFREP LKGQRGPELGPRPRALGGPRGSI/RP GSGGSFRG*LGGQMLLEPAASPGTQ PSGHLPALCGLSN
4371	9868	B	4667	3888	8771	MRLWSWVLHLGLLSAALGCGLAE RPRRARRDPRAGRPPRPAAGPATCA TRGPRPRLAAAAAAGRAWAVR VPRRRQREARGATEEPSPPSRALY FSGRGEQLRVLRADLELPDAFTLQ VWLR AEGGQRSPAVITGLYDKCSYI SRDRGWVVGIHTISDQDNKDPYFF SLKTDRARQVTTINAHRSYLPQW VYLAATYDGQFMKLYVNGAQVAT SGEQVGGIFSPLTQCKVLMGGS LNHNRYGYIEHFSWKVARTQREIL SDMETHGAHTALPQLLLQENWDN VKHAWSPMKDGS SPKVEFSNAHGF LLDTSLEPPLCGQTLCDNTEVIAS NQLSSFRQPKVVRVYRVNLYEDDH KNPTVTREQVDFQHHQLAEAFKQY NISWELDVLEVSNSLRRRLILANC DISKIGDENCDEPCNHTLTGHDGGD CRHLRHAPAFVKKQHNGVCDMDCN YERFNFDDGGECCDPEITNVTQTCFD PDSPHRAYLDVNELKNILKLDGSTH LNIFAKSSEEELAGVATWPWDKE ALMHLGGIVLNPSFYGMPGHTHTM IHEIGHSLGLYHVFRGISEIQSCSDPC METEPSFETGDLCDNTNPAPKHKSC GDPGPGNDTCGFHSFFNTPNYFMS YADDCTDSFTPNQVARMHCYLDL VYQGWQPSRKAPVALAPQVLGHT TDSVTLEWFPIDGHFFERELGSAC HLCLEGRILVQYASNASSPMPCSPS GHWSPREAEGHPDVEQPCSSVRT WSPNSAVNPHTVPPACPEPQGCYLE LEFLYPLVPESLTIWVTFVSTDWDS SGAVNDIKLLAVSGKNISLGPQNVF CDVPLTIRLWDVGEEVYGIQIYTL EHLEIDAAMLSTADTPLCLQCKPL KYKVVRDPPLQMDVASILHLNRKF VDMDLNLGSVYQYWVITISGTEESE PSPAVTYIHGRGYCGDGHQKDQGE QCDDMNKINGDGC SLFCRQEVSN CIDEPSRCYFHDGDGVCEEFEQKTSI KDCGVYTPQGFLDQWASNASVSHQ DQQCPGWVIGQPAASQVCR TKVID LSEGISQHA WYPCTISYPYSQLAQT TFWLRA YFSQPMVAAA VIVHLVTD GTYYGDKQKETISVQLLDTKDQSH DLGLHVLSRNNPLIIPVVDLSQPF YHSQAVRVSFSSPLVAISGVALRSF

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						DNFDPVTLSSCQRGETYSPAEQSCV HFACEKTDCELA VENASLNCSSSD RYHGAQCTVSCRTGYVLQIRRDDE LIKSTGSPSVTVCTEGKWNKQVA CEPVDCSIPDHHQVYAASFSCPEGT TFGSQCSFQCRHPAQLKGNNLLTC MEDGLWSFPEALCELMCLAPPVP NADLQTARCRENKHKVGSFCKYKC KPGYHVPGSSRSKSKRAFKTQCTQ DGSWQEGACVPVTCDDPPPKFHGL YQCTNGFQFNSECRKCEDSDASQG LGSNVIHCRKDG TWNGSFHVCQEM QGQCSVPNELNSNLKQCPDGYAIG SECATSLDHNSHILPMNVTVRDI PHWLNPTTRVERVVCTAGLKWYPHP ALIHCVKGCEPFMGDNYCDAINNR AFCNYDGGDCCTSTVTKTKVTPFP MSCDLQGDCA CRDPQAQEHSRKDL RGYSHG*
4372	9869	A	4668	1	183	GRDGVLPCCPGWP*SPCLKQSA/CL GLPKCWDY/RARATAPGLLFFSYAK ICPLTSCQYSKC
4373	9870	A	4669	3	462	TYQSFSPSHMPLRGYDVW*TTLFQ P*HG*PGLQRFPLANMLCGPSGSHL VLLKL*RSVTLNHREALICLPE*YV EPSGTKICIAGWGETKGTGNDTVLN VSLNDISNQE*NNQHRGHVR*S*M STDGLQASVGAL***YGGPHSWFIH HRG
4374	9871	A	4670	1	360	ARGPQRSERSSRRPAPPSRSSGS*RC SCIPWPTLLLRGPR*RPL*NARYMKI LASPFQLSHPRKGPRRWH/AGVLSP PPAAPPPSSSSVPEAGGPIKKQKAD VTLALNDS DAHSDVVD
4375	9872	A	4671	70	631	RQRPQRSERYWRAAPS*GDKVG PQMASQQPSASLYPYPSTSHITAGS RLGEFHELGWLEVRWFVVDPLAC RENCETGVWAMGLSVFLSVIHS LQSFINTDSVLCHAQRETNVPCAR EGPCL*PSPSARSQRPSPGSRTPQ EKSRRDAAASSAPRAS*RRRRPPII PLRPLWLT SWPRAPPHGDAAAAA TREPEFHL
4376	9873	A	4672	93	338	
4377	9874	A	4673	1	660	FRRFRWRRRLH*AGPASSAGGSPGE ASGTMSGELPPNINIKEPRWDQSTFI GRANHFFTVTDPRNILLTNEQLESA RKIVHDYRQGIVPPGLTENELWRA KYIYDSAFHPDTGEKMILIGKNGQ AQGF PWNMTITGCM DGRFTGTTP AVLFWQWINQSFNAV VNYTNRSGD APLTVNELGTAYVSATTGAVATAL GLNALTKHVSPLIGPFPGFACVA
4378	9875	A	4674	1	387	FFF*RWVSHSVAQA AVRWRNHGSL *PKTLGPK*SSH/CQSP*RAWDS*AH AHYHPA*FLNFFL*RQGPHLSM/FPK MVLNSRPQAVPPT*ASQSDGITGVS HHTLALKV/CLFKMKYFE**TEKGI

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						HFKRTK
4379	9876	A	4675	3	383	GQLQARPPAPAAADCPPWTLRGSA LVPWLVPWRKASPQLSPGSPECP*A PSARPQDPPRPAGQIQDRASEHAAR GGPCGVLRADGALPALPPDRARPQ VCGRGEVAARARW*RSSGRRGTRK RNGE
4380	9877	A	4676	490	1013	WASCSSSREYQCCFQTVPPGFSRVM KFFTFPPGSKHFPAPLAPQACTSF GLAGLPPNALPLILVPAPPA/SSLAN PQLVQPPVPGLVPRPSRSCSAA/RP SA/RLARPPETPAR\PRAPSSAPRTRT PS*GRARSGGSAGNAPSARRTPQGP TRAACSLARILDASGSWRVLRP
4381	9878	A	4677	1	447	KKFVIPDFEFTGHVDRIFEDVKELT GGKVAAYIPQLAKSNPDLWGVSLC TVDGQRHSEGH TKIPFCLQSCVKPL TYAISISTLG/DYVHKFVGKEPSGLR YNKLSLNEEGIPHNPMVNAGAIIVS SLIKMDCNKA*KFDFVLQYLNKMA
4382	9879	A	4678	3	284	QLGQYGETPSLLK/IKIRIQKVAGHG GRHL*SQLRSLRQKNLLNP\GGRS CSEPRLRHCTPAWVTERDSVSKKK KKKKEKERKKKKAGCGGSRL
4383	9880	A	4679	122	196	CWFENVNSKSGFWVLF*FKAKLVN
4384	9881	A	4680	2575	2786	ADTESITL*FYHFFFFLRL/DSVAQA GVQWCDLGLLQV/LPPGFTPFSCLS LPSSWDYR/RPVITPS*FFVFLVEM\G FTALARMVLIS*PCDPPVSASQSAGI TGVSHCAQPTFIPK
4385	9882	A	4681	3	512	YNQKVDLFSLGIIFFEMSYHPMVTA SERIFVLNQLRDPTSPKFPEDFDDGE HAKQKSFISWLLNHDPAKRPTATEL IKSEL\LPPPQMAESEL\HEVL\HHTL\ AN\VDGEGPYRTIDGPRSFQRISP DYTYDQRHS*KGTSSIRA\AKLLHL VRETMIRICTRHGACQT
4386	9883	A	4682	1	382	EESILGEVGEALTSAGEELKIDRFF*I VEGLRHNSSQLNVTSMQLINALDTS PDDLDFRLHIINEFMRCGLKEILPHL *GIKNDGLDMQLKDFDEHNEEDLL EC\HRLDIRAELDESVDVHMLW S
4387	9884	A	4683	1	472	GIMLPDLK\LYDIAMVAKSAWYWH KNGHKVLWNKMAQN/HIYGQLVF VKVPKYTQWGKGS LFNEWNQEN/ WISACRRMKLDPYV\STKINSKWK AYTIR/PETVKLLEENIGKKLIDI/GP G**FLALAPQTQATKA*IDKWDFIK VKTFCTARETVNTEKRH
4388	9885	A	4684	182	345	RFPLCSFPPTLPCEGICFPFA\FCHDC KFPEAFPTRLPEPAEL*VNSTSSLH KL
4389	9886	A	4685	205	395	VNLGIFGKNGAPPG/PEGRGGILGHR NPPPRGLNK*PPLTFQGTGTPGSSSS S*VNLGIFGKNGAPPGGQGGPKTPG PKEWAGLAPQKGGTTGLDPLGPPK

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						KGFNHHPGGIREFPGN
4390	9887	A	4686	35	389	NLFYKVLQSAGFFSMDHEDDVF ARFSQLVTGKRQSLIVSWTT*IQNG DIKNAQEALAAETRMALTLR*LAP DDGTSSKI/LGFCCDYVQILKHLADQ QKAGAAAIMSVATKELMMKT
4391	9888	A	4687	3	547	GGAGRRWAGVGGAPGAGGGPAE AGAAAEAGAEHRGDGAVRAGAGG GRRYRPRRVQDPGGPAE/G*TWPPS PSSRCSSPCVPGRG*/PSEPQDPAAV SLPTSSVPETRGAPAGPIRG\PAPGL RCQP*EARPGCVYWLISGGWCSPLF PWKLPGPRRPKQL*APRAGPCRPSL PCRLATGHDF
4392	9889	A	4688	65	414	WKCADTNVAQGPRVQQVLQLRGT PIPNHCALCLLREKQRQLCPRGSNG PAERSKPRRIQPEDATPAQALPRLP KGGGPGKSPTRGKHLGWGRDLFAS LSPAKATCLPPSIDNKPF
4393	9890	A	4689	75	787	HVAFASGQRCNKSLPTPKVVPVRVG LFPRPRPPWAALVALGLAWHPLAGI PRGCCVPHRHNAPEGKRLPFVSPS GHRARSTWAETRPQGRGSLASLCP AHMDLSIWKTARGATFSFQQGPPG SWRGQT/RGPVSPLRPARPPP*RPDK DGGGGS\PDQRAGRTRKAIEVGGCL ASMRPPPAPLT*TRRGR*RRPAPAP ARTAPSPRCSAPSSAAAPASAGPPP APGAPPTAPRPRPYALRR
4394	9891	A	4690	8	382	QEYWE*LYAYTF*NRDELDEFFDRH ILPNFTQEEYTT*NNPVSVEIEFVI/ NNISTPKKNPK*TSDDPDTSKFC*T FKEELIPVLYKHFQKIVEEEVLPHLF CELSITFLLKLDRCVRLHR
4395	9892	A	4691	2	389	NRKRIELTRKVLFLKHMARDVQNE HLTRFVGACTDPPNICILTEYCPRGS LQDILENESITLDWMFRNSLSSDIC* GMLFIHNAA/IC*HGNNLSFNLSVLR DLRNFN*FSFSSESVPNCIQIIVIIISP
4396	9893	A	4692	2	544	TKAPKYIKQTLIDPKGEVDYNMIV G/DANTPLSKTDRSSIQ*INKETVEL NHILDILGLTAIYRTFHPTATE/YFFS SAHGTLRINYTLGPKPGCEKIVKH RNYIKYPFLNTIELEINNKRNSENT NTWKLNNMFLKD*WNEEIKKEI*K LLETNENGNTM*QNLWDMTKAVL RMKFIT
4397	9894	A	4693	1	373	MPHSVPGMLMSPGIPTGLTAAAAA AAAATNAAIAEAMKVKNIKLQAMS NYHASNNQHGANSHQGMISRVAL DLPLSILPNLYTMPLVLQHSHTYN HLTYS*LHNLQTIP*INLDQRAPSLP
4398	9895	A	4694	185	417	NSELNGKEAALQ/IMILEREIGVEKA LNVQKGRVSESLKLLANRPGMVAH ACNPSTLGGQGGWV\WIRSGVRDQP *PHG
4399	9896	A	4695	88	432	TDLFLFVCLRLSLLSVAQAGVQWF

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						DLSSQPPPPRFKRFSCLSLLSSWNH RCTPPRLV/N/FFVFLVEMGFTMLAR MVSIS*PCDLPTSASQSAGITGINCR TQLTY*F*KFSVDSL
4400	9897	A	4696	3	390	YRIPYVSTDCENLLKRFLELNPVK RLTLKQIMNDRWINARHEEDELKPF AEP*L\DILDQKGIYIIGMGYSQEEI WESLTKMKYDEITATYLLLGRKSS HLDASDSTSSTNLSLAKGRPSTDFN NSTG
4401	9898	A	4697	289	365	SPRLGLPKCWDYRHEPPHPAAFH*G CVLFIFYFIFLKQEL/NSLTQAGVQW RDLSSLQPPPPG\FK*FSRLSLQSS*D YSCVPPRLAFCIFFW*KRGLTMLTR LVSNS*PQ/CDPPALASQSAGITGMS HHTQPHSIVL
4402	9899	A	4698	33	397	NAYNQLKVCASSPWLFFCANFSSY YFYDSHNVIQG*NMTYCT/VM*YLL ITGSLSAHLKNMSLKRMKSYRSGA ESATEEPFTILYESQFSVGGNELDFQ VKTLSLPEVVIVHGSQDNNATA
4403	9900	A	4699	2	371	LNTVIANGVAMASRPYQPTHVNVH IHQUESTLTHLLKAGGTLKKTLEHFG DTVSSSTATIGYEQALWVTQILLGR *E/CVILECVLILGPWTALSASRCF WAESVEIVPRAGAIVHDKQPVKLA
4404	9901	A	4700	3	441	GFEDKVIFYVWFDATIGYLSITANYT DQWERWWKNPEQ/ALGAEDNYTL VSHLIATEYLNIEDGKFSKSRGVGV FGDMAQDTGIPADIWRFYLLYRPE GQDSAFSWTDLLLKNNSSELLNNG NFINRAGMFVSKFFGGYVPEMVLT
4405	9902	A	4701	2	375	CITRDLKWGTPVPLEGFEDKVIFYV WFDATIGYLSITANYTDQWERWW KNPEQVDLYQFMAKDNVPFHSLVF PCSALGAEDNYTLAKLLDLKKQLA VAEGNPLKPLKARRKSKRPWLIESH FNR
4406	9903	A	4702	1	3093	
4407	9904	A	4703	2	2717	GEMRLFVSDGVPGLPVLAAAGRA RGRAEVLSTVGPEDCVVPFLTRPK VPVLQVDSGNLYFSTSAICRYFFLLS GWEQDDL TNQWLEWEATELQPAL SAPLYYL VVQKKGEDVLGSVRRRA LTHIDHLSLRQNCPLAGETESLADI VLWGAQYPLLQDPAYLPEELSALH SWFQTLSTQEPQRAAETVLKQQG VLALRPYLQKQPQSPAEGRAVTNE PEEEELATLSEEEIAMAVTAWEKGL ESLPLRPQQNPVLPVAGERNVLITS ALPYVNVPHLGNIIGCVLSADVFA RYSRLRQWNTLYLCGTDEYGTATE TKALEEGLTPQEICKYHIIHADYR WFNISFDIFGRTTTTPQQTKITQDIFQ QLLKRGFVLQDTVEQLRCEHCARF LADRFEVGVCPFCGYEEARGDQCD KCGKLINAVELKKPQCKVCRSCP VQSSQHLFLDLPKLEKRLLEWLGR

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						LPGSDWTPNAQFITRSWLRDGLKPR CITRDLKWGTPVPLEGFEDK\VFYV WFDATIGCL\ITANYTDQWERWW KNPEQVDLYQFMAKDNPVPHSLVF PCSAL\GAEDNYTLVSHLIATEYLN YEDGK\FSKSRRVGVFGDMAHDTG IPDISRFYLLYIRPEGQDSAFSWTD LLLKNNSSELLNNGNFINRAGMFVS KFFGGYVPEMVLTPDDQRLLGHVT LELQHYHQLLEKVRIRDALRSILTIS RHGNQYIQVNEPWKRIKGSEADRQ RAGTVTGLAVNIAALLSVMQLPYM PTVSATIQAQLQLPPACSILLTNFL CTLPAGHQIGTVSPLFQKLENDQIES LRQRFGGGQAKTSPKPAVVETVTT AKPQQIQALMDEVTKQGNIVRELK AQKADKNEVAEVAKLLDLKKQL AVAEGKPPEAPKGKKKK
4408	9905	A	4704	180	490	VENGNNSLTIMNRRARQKINKEITA DL*NTMNQMDLTDIDGTFYPKAEY TFFSSKCGTF*RTDHMLGHKTS\LD KFKKIKVIQNYLFNHNGVKLEINNS KKMRKF
4409	9906	A	4705	2	405	KNLNNRLFIFP*IKEEIKRQIRK*FEW NEKEKTIYQNLWDAPKAKLKEKCI VLYV\KEETSQITDLSFHLKTPEKEE HVKPKVNRMEIIRIRAEIIAVKYRK PTETNETKSWSFENFSKIDTPLIKMI RKKKVD
4410	9907	C	4706	217	486	MDDPRGHASPVTRTQKPQASRLLV GLRAGGLSWGHWGRGKPPRGRV PAAALGAAVVAAMASDPWPAGP KQPGRWADLAALLCGLRPA*
4411	9908	C	4707	13	216	MLYWDCKRYKVKDKTQAWDFAG NISVKGAELSQTRAASGPRRQAQVT FSVWRGGLQVMAEEGRVDVC*
4412	9909	A	4708	132	1424	VKHGPQGGPRRQAQGGDIQVFGVGV LPGEWPPEGTQKGGPPLKTLGTGD GDKIGEPPTRAP\RFRTGQPGPRDGL VGPGGELAKPWGPPRGLGPASCPP GNTPLPARPEY*HLGWVGCP*RMG QGNLGVPSK/PVFGSSGPNVGSTNC DNFGSFGLSVPMFPNGPIQALFEG DLWDLGRTGHGTTGGQCKPLSPG PKKLQGL*TC*SSLALQG/RLSLGAQ SGGRGKPKQESSEPCPNP*APPVVGC YGITRPVGFRGPSQPG/LMGRPGSSS ALWA*NPELPNCPGLPQPCPQEV QSFPGPGVRGRGLKGGQDCHRG EGSSKCAQGGHPAPA*WNPLVYTP ASPFPRPASGKPRS/RPSCGLRAP* HLRRPCLTPPFRPQGLLGSSPCPKP APDSGLLHSPLTSPRGLSGQCNP LHPQLNQSNRDR
4413	9910	A	4709	1	340	RHEERTTGILTSVGLASDTSLICVIE DFFDTALIISRSSEGGKIQMLDSFLLS L*LLVTEETVNHLLQEDRPCMDTL DCG/LQVAISEALRRLTTSKSRDDL

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						HIWYDDESIV
4414	9911	A	4710	12	398	TYLDLPLPGFCIYDF/VPPFSSECFIF VFMVCFLLAFILSFSSSSSPNSFFDLF FLALPQLPTLRGLFV*ALFQILSWVV FPVKFSLGCVFYLFQFIFKQLAFFH HV*ETFSPVFLICKYWDD*TYFS
4415	9912	A	4711	111	453	YPFIIITFNTLGVAGNCL/KLTYTI** MPTANIILKKLKAFLR*RTR/H/GCP QSI*ARRII*DIQIAKEDVKLYLFTDD MILYVENPEESTQKDLLANKVNVKS GYNINMIIRCISM
4416	9913	A	4712	1	184	SSRDILLCTDIASRGLDSTGVELVNN YDFPPTLQD\ELAARRRRSLPGLASS VKEPLPQAT
4417	9914	A	4713	1	1630	MALTRPVRLFSLVTRLLAPRRGLT VRSPDEPLPVVRIPVALQRQLEQRQ SRRRNLPRLVLRPGPLLVSARRPE LNQPARLTLGRWERAPLASQGWKS RRARRDHFSIERAQEAPAVRKLSS KGSFADLGLPRVLHALQEAPEV VQPTTVQSSTIPSLRGRHVCAAE TGSGKTL SYLLPLLQRLLGQPSLDS LPIAPRGLVLVPSRELAQQVRAVA QPLGRSLGLLVRDLEGGHGMRRIRL QLSRQPSADVLVATPGALWKALKS RLISLEQLSFLVLDEADTLLDESFL LVDYILEKSHIAEGPADLEDPFNPK AQLVLVGATFPE\GVGQLLNKVAS DAVTTITSSKLHCIMPHVKQTFRL KGADKVAELVHILKHRDRAERTGP SGTVLVFCNSSSTVNWLG YILDDHK IQHLRLQGQMPALMRVGIF\QSFQK SSRDILLCTDIASRGLDSTGVELV VNY\DFPPTLQDYIHRAGRVGRVG SEVPGTVISFVTHPVDVSLVQKIEP AARRRRSLPGLASSVKEPLPQAT
4418	9915	A	4714	79	410	IVYWVEVENRDHYAAYLGWEEAP YSDRAYAPQEKDLGPMDIRIGLL*K NWIPLQDDLYPVDMLHTSVG*EME LNNCRNQGV*RMSKDRRETLETYQ QL/L*LLQTSPLYLA
4419	9916	A	4715	185	449	TTILAWGDYLSLENSRSGPN*L*LLS GCTVQSFGLDWNGLLK*DSLTRL ALCSLQLGRK\ETITIIYDCEGLGL KHLWKPAVEAYG
4420	9917	A	4716	154	364	MWRWFSLPPPSLAGVELAPPVSRR SPRGP/TPYGLPRVPLWPLHSTALYC PSPRSTAPFTPHPLPKLRG
4421	9918	A	4717	9	1805	SPATSP*ETAGPVKRSRNGSSPAADP EALSPTARLQRTVPPI*LNQQLSS PLHFAAGGGHAEIVQILLNHPETDR HITDQGRSPLNICEENKQNNWEEA AKLLKEAINKPIEDPLAILILFDEAR YNLLKGFYTAPDAKLITLASLLLQI VYGNYESKKHKQGFLEENLKSIVP VTKLKSAPHWTNRILHEYKNLSTS EGVSKEMHHLQRMFLQNCWEIPT GAAFTGQIFTKASPSNHKVIPVYV

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						GVNIKGLHLLNMETKDFQYFQYYVD
4422	9919	A	4718	200	529	EDVSKPVPWTLNGSCTSPLISHSDN QKCPYPFVIPAMGNPENIEDAYVA VIRPKNTASLNSREYRAKSYEILLHE VPIEGQKKKREKRFYWKRNFKATV K*HKAYWIT
4423	9920	A	4719	177	321	QTCSMDTKWQLYISPHQS**QPEMP SIFSSDPSLQCVCLICKRLLS
4424	9921	A	4720	166	627	MWRWFSLPPFSLAGVELAPPVS/S KDTERSHPYGLPRVPLWPLHSTKW VGQSPGEGGQGPSLSHSSFPFPRHS SPAQLPVAEKPSVAKRKPS*GFPR PTRAPKAQVSGVGDPPAHLFTVLP SPRTSAPFTPHPLPKLRGRSSKALA FHSA
4425	9922	A	4721	3	610	STFNNEP*PEKQEONKHKIRRKQIIK IRA*INKIE/TKNQCKRTMKQKVAFF QKLNKTDKPLARLRKKRQDKIRNE KDITTDAEIQRIIRGYEQLYANKL ENLEEIDNS*THTTY*DLQEEIQNL NRLITSNKVEAIKSLPVKKS LGPDG FTAIFYQTFKEELIPILLKLF*KVEEE RVLPN*FYEASITLMPKPKDKDT
4426	9923	A	4722	1	454	LAHCNICLLGSSNSASVSQVAGITG GCHYTQLIFLFLVEMGFHHVGVQVG LELPTSGDLPALASQSVGITAVSPLC PTRIIFFEAESCLCWPGWSPNGLKQ SPCLGFPKCDWDYQPDLTMP*FY LELEIKFGVHVLWKSFLIKIENYYC
4427	9924	A	4723	1	318	KEECNKEEKESREKK/NEKEKIE*KE EEVRKEEKSLNKDKDKKRRKREK GEGRKKEGILKVKKDGNPSNGHA RMPKER*LYDVRGTPHSSDHGDT AIFQTCIL
4428	9925	A	4724	42	200	LICT*MLIVALLVIARNWKQIRC/SST /DEWLNKLW*IPMEYY*AIEKEPTIG TC
4429	9926	A	4725	50	403	VVYHVMVMVLLKVVICHHFLTFFS FRSLILYLFFILFMISLYLSCFLYNFL FIPSSSIFSHICFLMIIVLI*FFFYALFIII FNPIILYLN\YLLSLFLIESLFDYYLCL ISFVIFY
4430	9927	A	4726	3	282	VQGQEPLTASMLVAA/PPQEQQQM LGERLFPLIQTMHSNLAGKITGMLL EIDNSELLHMLSPESLSKVD EAV AVLQAHAKKEAAQKDSKAK
4431	9928	A	4727	780	1249	LVVFMISPLCSSTHPSILQGLKLVPL EQGQPPPLLFHIVRCSIEQALNHH QVLSFPQC*PTAFPGSQAPQPAVHV QGQEPLTASMLAGAPPQEQQQML GERLFPLIQTMHSNLAGKITGMLLEI DNSELLHMLSPESLSKVSWSGSDP AASVLM
4432	9929	A	4728	510	2771	NLEPSHQDRGEVQSRGEGRIVRRAF CLRCCGRGSRPPPPVSPSPSPPTPA RPRRAGATCEPARARAPAPKAPLCP

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						AAGPIRSPLAGLVVGGGEMNAA SSYPMASLYVGDHLHSDVTEAMLYE KFSPAGPVLIRVCRDMITRRSLGY AYVNFQQPADAERALDTMNFVVIK GKPIRIMWSQRDPRLKSGVGNVFI KNLDKSIDNKALYDTFSAFGNLS KVVCDENGSKGYAFVHFETQEAAD KAIEKMNGMMLLNDRKVFVGRFKSR KEREAEKGAKAKEFTNVYIKNFGEE VDDESLKELFSQFGKTLVKVMRD PNGKSKGFGFVSYEKHEDANKAVE EMNGKEISGKIIFVGRAQKKVERQA ELKRKFEQLKQERISRYQGVNLYIK NLDDTIDDEKLKKEFSFPGSITS AKV MLEDGRSKGFGFVCFSSPEEATKAV TEMNGRIVGSKPLYVALAQRKEER KAHLTNQYMQRVAGMRALPANAI LNQFQPAAGGYFVPAVPQAQGRPP YYTPNQLAQMRPNPRWQQGGRPQ GFQGMPSAIRQSGPRPTLRHLAPT G SECPDRLAMDFGGAGAAQQGLTDS CQSGGVPTAVQNLAPRAAVAAAAP RAVAPYKYASSVAAALILPYSLCRH PS/PAVHVQG\QEPLTASMLAACNPP /QKQKQILGERLFLIPTMHPNLAG KVTGMLLEID\NSELLHMLESPESLR SK\VDEAVAVLQA\HHAQERSCEP GRCCCCYLLDPRKTDKAK
4433	9930	A	4729	7	365	LYTRHPPSPSCIMTACFGSHIRYRS D *VPTPVLRPVIRSVGGGDCSERLG LRPRPI/PELGPHTPTRPPPPWQNV QRADPVAVTPCRSREGSQAELPRG RGAVSSSTTRPGLPAPNRP
4434	9931	A	4730	1	1520	AEGACGPRQPNKGAGAPPQGPAT H LPGRSGLSSTATMTANGTAEAVQI QFGLINCGNKYLTAFAFGKVNAS ASSLKKKQIWTLEQPPDEAGSAAVC LRSHLGRYLAADKDGNTCEREVP GPDCLFLIVAHDDGRWSLQSEHR RYFGGTEDRLSCFAQTVSPAELWS VHIAMHPQVNIYSVTRKRYAHLA RPADEIAVDRDVPWGVDSLITLAFQ DQRYSVQTADHRFLRHDGRLVAP EPATGYTLEFRSGKVAFRDCEGRYL APSGPSGTLKAGKATKVGKDELFA LEQSCAQVVLQAANERNVSTRQGM DLSANQDEARPTRRPSSWRSTATPKS VPSVPTRASTGR*RPPGACSPPPPAR MPAATLTSSGVTGASH*GRPMASL* PPRRMGSWPPRWRQGTQSSSS*SS STAPSSCSAGSMASAAARSAPWT PTAPAMTSSSSWSSTMAPTTSTPQA NTGRWAVTPRSPAAATLLWTSSSS ATITRWPSRWAGAT
4435	9932	A	4731	131	677	PSSLS/CDIFLRSPISTPSPSPLPRT PTS TPVHVKQGTAGSVINNPYVIMDKQ PGQVIGATTPTSGSPTNKISTASQISQ GTGSPVPKIHGSSFVTSTVKVIKQE

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						PGEAPHVPATGAASQSPLPQYVTVK GGHMIASVPQKQVITPGEAIAQSAK VQPSKVL/GQIG*CLPTLARADLLYS VC
4436	9933	A	4732	131	362	PSSLS/CDIFLRSPISTPSPSPLPRTPTS TPVHVKQGTAGSVINNPYVIMDKQ PGQVIGATTSTGVY*IHICTI*RV
4437	9934	A	4733	1	4461	
4438	9935	A	4734	2	614	STTTERENYRPIFLMNTDGRILSIILP SQI***MKKIIYHDQVGFIPGMQRWL NVHK\TMHVIHHINKMKGKNYLIIS ADAEKSLGKTYHCFMMKTLNKLGI EGTL\NIRKGIYD*STANILLTGKN*K AFPLRTGIRQGCPSPLLFNTVWDIQ AKVIRQDKQIKGIENGQEEVKLSHF ADDIILYL*TEKPKDSTKLLKWVN
4439	9936	A	4735	164	613	NLNMEATGTDEVDKLTKFISAWN NMRYSWVLKTKTYFSRNSPVLLLG KCYHFKYEDEDKTLPAESGCTIEDT *LREM*KNFRKDSISRIWLTREEFP QIEGSALTDCGWGCTLRGTGQMLL AQGLILHFLGRAWTPDALNIEKLE L
4440	9937	A	4736	40	359	
4441	9938	A	4737	4274	5256	HTLFGDKLCTVATLRETYGEMADC CAKQEPERNECFLOHKDDNPNLPR LVRPEVDVMCTAFHDNGETFLKK* VIRCL*FKIKKHGVTP*ANTL*KLP* QKYFQH*DLEVLL**FFKEVVFDTT KFYTAKNMIKDILKFIETGYNLSQK FKIDKFFNVFRRYVYMVVIDFVLV SNIILPKFNHLC\TH\TH\TH\TLFST YLKND\RD\TIMCKLSLIG*LAESLEF GGSGENV\DYNYFCNIVCYRK/ADCF SFLKFRYL\YEIARRHPYFYAPELLFF AKRYKAA\TECCQAADKAACLLPK VLCTRIEKKSLLSNLILSILWDLGT LSV
4442	9939	A	4738	133	359	LLNFMLLFHRYYALKVSYFKSSLDL KLELLWNKYWVNTLSSSSLLTVS/ DYTCKECI*ILSKLHSRLISETLFHRK
4443	9940	A	4739	1	353	NWTL*TLKKIFSLKDAIKRIKIQSVR WKKIFAKHTSDKGVES\NIYKELS*I NKASSSSSSSSSS/HSSSSSSSSSSSS SSSSSSSSSSSSSSSSSYHYTSIRVA KMKKTDYVTSW
4444	9941	A	4740	1	375	LVPKRA*YWHKNTSSSSSSSSS/PSS HLHIYSQPKFRKGTKKIHW*KDSVF HSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSPMLIQENTG/MLQD IGFGKDYL\SKT\SKA\QATKQK*TRKH WEM\LDIGFGKDYL\SKT\SKA\QATK QK
4445	9942	A	4741	1	296	FRRSL/DSVAQAGVQRRHLGSLQAP PRGFTPFSCVLSASWDHRSPLPRPA NFFVFLVETGFHVLARMVSI*PCD RPTSGFQSTGNTGVSHRTWPLLL

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4446	9943	A	4742	3	380	FLEEYNPPKVSQEEITSSSSSSSSSSSSSSSSSLSDIES/VIKNTSSNNNNKKNPGPDGFTAKFYQM*KDELISTLLKHSK/IFHSNSFCE*QTTR*FAISITWRAPDKDTPQKEPYRLISLNIHSC
4447	9944	A	4743	3	369	SFTLIKKTKDIIRKANYKTMSLRKIAAVILNKILAN*IEH/RIKRIHHNQIRFISGTQVWLNK*K*INVTHHINRLKKKNYMILIYEEKTFDKIKHPFM/IK/VLSKLGTEFFKLIKHIWRKI
4448	9945	A	4744	70	345	KVWGEKVWYWQKMTPIVQWDRTESPQIGN*SLTKEIQWRKDSLFNKW*GNHWTAPFSS/RSLNLNKDLTAVTKIKSKWVTDLVKHKTIKLL
4449	9946	A	4745	3	345	KFNNLDEMDKFADRQKLPYLAQEE RQNLN/*PYLLKNLNVQNLPISKTSA PDELICKFYETFKNEIILLCSLFQK MELSQHIHDSNLTLTQKI*K*YRTE ENYRDISLINTYAK
4450	9947	A	4746	35	355	PHPPWWSLSSSPPSQHSFLPSPAYM PSPSGNSM/CYLSPSRGM*APSRQGP SSFHQLCPKCLKGCWARHMPSK*G WNGNPFPVSLNYPWARNRPSLLTH FVMWEAPRP
4451	9948	C	4747	27	416	MMKRLGMFNIQHCKKLSSWVLLM KYLGNAPPSSSCLMRGNYSTWKMN SPTISSPSSWENEDRRSASLHLPKLSI TGTYDLKSVLGSTGASLKVFQQWG AGPLPGFTEGGHPXKVFQGPCIKAV LEPFDE*
4452	9949	B	4748	5	763	MPSSVSWGILLAGLCCLVPVSLAE DPQGDAQAQKTDTSHTDQDHPTFNK ITPNLAEFAFSLYRQLAHQSNSTNIF FSPVSIATAFAMLSLGTKADTHDEIL EGLNFNLTEIPEAQIHEGFQELLRTL NQPDSQLQLTTGNGLFLSEGLKLVD KFLEDVKKLYHSEAFVNFVFGDTEE AKKQINANGTRPFEVKDTEEDFPR GPGDHREGAYDEAFRHV*
4453	9950	A	4749	11	368	GLKSLIN*LLAVYPREQTTL EEVMR DPWVNS/GSGVAFDN/TE*QILDHLN PETTQLLVAMGFQADNLSVAVREQ LFSYAMATYLDLEHTLLKKRSTIRS QTLPPGDPTWPLYIEVCTFRLS
4454	9951	A	4750	175	349	PSVAGRPRRKGGGRQPAQTRAVGI AGTEPLYYLGLWGPVGVQDQ*QP ASFPGPPQVPKAPSNTKEA/SPSNA HSSSLGRLPSSPLPPRPASNTGSLSPR QGTMTTL*GATHLPQHSDEESTRE SPPPTLEQLPPSVQLIRMPCLPVT Q
4455	9952	A	4751	2	354	ENCQINNLRFHRLRKPKKEEYTKPTA SRRK*IVNIRIERNGIEQKNNRTSSSS SSSSSSSSSSSSLTFR*MDGRRSSSS SSSSSSSSQ*QRK\KTRLIKI*NERG DITADLTEIK*LLILQKLNNY
4456	9953	A	4752	121	363	WRDFKTKTVIRAK*GYLIITG*NHQ

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						EDTTVINMYA/PKTAPKKYMKQKL TDWKRAV/DSKTTAGDLNILLIMD KTKQKINRV
4457	9954	A	4753	178	439	GPALINALLKWRIPSGEDREP*GRD WEKEKE/R*LEEGRERGGKGEGGK RRNKGRKEGREERGKGGEREEGYIM CIHGIGNRSLAVLGA
4458	9955	A	4754	193	355	GLFSIEEH*HDSTHLGINTLALISRLFI EK*LLKRVYQVTQACELYAWNPNP DQCLPPPLVRPVQHRGAYPGEDWQ IDYTQMPCKGFKY*LVFIDTFTVWI EAFPTKIEKAIKV
4459	9956	A	4755	3	227	NIKIGKEEVKLSLFAGDVYLEKPKD STKKLLELI/NFSKVAAY*INIQKSA FLYANSE*SEKEIRNIIPFTIAT
4460	9957	A	4756	115	487	CSLCFVAEWSPWCGWTQLIYPW*E/ ITHSPVHTQRLGLETHRTAEMRLFS FSLFFFLRQSFALVTQPGVQRCDLG LLQPPSPGFK*FSCFSLPSSWDYRHA PPRLANFVFLVQTGFSLATLVSN
4461	9958	A	4757	2	436	GTEAEQPSYQPGLELPQGDQEEP/G LAGKTGLGPRFPRTTGGSGQTLLEV EGLSHSPFQSPGIPGEFEKARKIL*A GS*HNSC*ATE/GLGERPGGICGVSS SVSTQGPMP*CGQQGN*ALESCRP ATAALSEQSPASPSSRAARA
4462	9959	A	4758	76	194	
4463	9960	A	4759	310	551	SSKQSSAKPPFCLPNPGKVCRSGRS RT*GCNLQKSGSGPEKGRRFGHPPE WTIFPSVQRQQA*FSDSPPTNGIP GEWKG
4464	9961	A	4760	1	1165	LRWQREEGQKAGVHVGMTQHLR PQGA AVLPAALAPPKHQFSLQAS SPSRLGRAGLAGGPSRAGLLC*WRR LSFLPSSFPPSPRSWGARSRRRARGQ VGPREPAGRSAGDRGVGGRFGGPL ALSFFATGLLRASCAPAFQEVTVLG KAVQWRLEPGEPFTEG*ALAGTLG LGKH*QGRQK*GWG*PSLANARQ LGKPLQVLGWLGHVEGRPGRAVK VTGVRSWSCLPSTGVGDRSRATQ LPAGP*VSLRVDQGEAVTGWGGRA GARGSPGRQ\GEPRHSARG*GPESLP LPVTRNSLVGGLSESN*ACPCR*QK ERLSIRGVPERRPFSGPEPGRGPASC SGLPTTGGTEERRKEGKRAAASKA ALPGWARLPDQGPAAATGSK
4465	9962	A	4761	1	389	EETLPLFADDMILYIIKKKQKTKKTT KESTKRY*N**MNVFGKVAGYKV NTQKSIN*QYTI*KVKLASFSSSPQK NKIGINLTKEIQNVYSENYKTLKEIK DLNK*ESIPCSQIRRFNIVKMTVLLK LI
4466	9963	A	4762	1	346	RACL*FQLLGRRLRQGDGLSLGIRGC SGPGWHHHPAWATEKDPVSKTNK QNIKH/LRKSPLSRDEKILREKREEE KILAYHYLEKSAIYSISFFLTKHILN

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						TPVCWFSSEHIIYF
4467	9964	A	4763	2	468	FPSLPSPFSRFLFCITVM\F*VLDPLS LSYLTLILIPHLKIEFNFEK/CVNH/CF LLMLLLLFLL\CTY*MCLGPFFYFLP CLSFSSVFHFLSLCCIIGNLFRYIFKFI NFELC\CYVLYT*DLFYF*KFSLVIF* IY*FFLSIMLSL*VFFHLKHFI
4468	9965	A	4764	3	364	RNLKLISEYCKISG*KVNIENQ\VFL YISNGQVEFEIKNTIPL*AHT*KMKY LDINVTKYVQDPYEENYKILMKKIK EQME/NIPCL*I/GRLNTKTSVLPNLE **ITAIPKIPASYFVDTN
4469	9966	A	4765	1	755	EESILEE\VLEALTSAGEEKKIDRFFC IVEGLRHNSVQLQVACMQLNNGLG TSSGELEFKLHIKNEFMPCGLKEILP NLKCLKNDGLDIQLKGFDEHKKE LVELSHRLEDIRAELEAYVYNM VWSTV*ETRAEGYFISILQHLLIRN DYFIRQQYFKLIDECVSHIVLHRDG MDPDFTYRKRLNLDLTQFVD\CV QAK\KFEFEKALELYKKFEKEFTD PQENSR*NCAKKEAQIYGFNPNSK TF
4470	9967	A	4766	12	321	KSCDWAERLVTLV/WN/PYFKNLSN SYYKQLSPMGGYLNWAHTLTETW IDNILDQLIFPKLQKEVG*ESWETVV ITNHRDLFSLWLHYLSAVKTPGINGI CQHNY
4471	9968	A	4767	2	375	MSSPLSPWSPCLLPQGAPGPTLPVP PAETLSVSPACFLRLPINSPSPQ*APA WRQLTADWGGHSALGLPGCPGPSN TWPSHSASHLLPQRNQGPPMLGYA HLPGLPTNVLPSGHTPALERPK
4472	9969	A	4768	3	338	QSLALSPRLECSGAILAHCHFC/LPG FT*FFCLSLPSSWDYRSPPT/RQLIF VFLVEMGFHHLGQAGLELLTL*SA HLGLPKCWDYRHEPPRPAQRPKLK NLK*LTTVARFTI
4473	9970	A	4769	66	365	LRDEQQHGGPWTSPLSRPPTGKRA RGRSACPQLTH*PGTAARKGASPGR SRALALPTRCPGPACGGREPRLQAR GVP/R*IPPRRGPHGAPSGLPPGPVG C
4474	9971	A	4770	3	345	KRGTPLAGEMAEGHCL\CLPLGTEY LTV\NPVHFLFNSEIG*KIRPVA\KVR HVYSITASIFFTPLRCLCGEKHISGLR ARSGIVLSLELNHGIDSFAHM*SCDL IL\ITLLSYYI
4475	9972	A	4771	2	352	KRGKPLAGEMEEGHCL\CLPLGTEY LSVKPIVHFLFNSEIGKIRPVAGGR HVYSNTASLFFTPLRCLGGEKHKS LRARPGIVLSLELNHGIDSFAHM*FV DLLLIITLLSYYIPFR
4476	9973	A	4772	1	296	QRSVKISISENGNSHMEIVSFSLIFCQ FLLHVFCSTIHYDCYIFLLI*YPINRQ CLFAY*YSDIKFYSDIN/ISYFLCLLC MSFYPLSTCIYMGLVFIF

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4477	9974	A	4773	2	859	GRWPTQPTSLQGGQTLGDVREAFS RRP*NGERQGAPPACPLPRSLGLWR P/WGPLSVTT*NRSWSCYCWLRV/ GWKGSRAVVKALGSPEAAWHLLG PDAALQPCFHSQPQRRRCRGRPPFLP LSGWAGPWECWPTCQAGRT*IPEG GGGSC*GPQVNDLQRHTEENVLRC DLPHPALAAWGTVSPG/SHAPAQ*T EV*RSAQSSFRPQCPLTSPARGTPGS SRRLLCGVPP/CGPLLMCLPLVPEV GLGPFLRELLNTKKNCFVNKQKV PNKPACHLGDGPSLPHQIC
4478	9975	A	4774	158	517	RCRSGYVDQVAGLFCFVLRQSLTF VTQAGVQWHDLSLQPLPRFN*FS CIILLSSWDYRCMPPLANFGIFLR/E RGFTMLGMLVLNC*PQ/CDPPTSAS QSAGITGMGPPHLGLSCSIKK
4479	9976	A	4775	1	165	GSLPLLFNIILEVLAKAIRQEKSIGN EKEKV*LSLLTDHMI/YM*NPTVKK LTT*KLTT
4480	9977	A	4776	2	516	QNPCISERQYCCEKLPLERSSRPQDS AGQPVT/HAHCSLSSTVDLCPLLAT HRISCWH*QDEVQGGRD/SVDKGD LVALSLPAGHGDTDGPISLDVDPGA PDPQRTKAAIDHLHQILKITEQIKI EQEARDNDVAEYLKLANNADKQQ VSRIKQVVQKKNPAAQTIGQLD
4481	9978	A	4777	154	406	CTDIQGYPGSRVAQAGVQWHNL/ CLSLPSSWDYRRPLPRPANFLYF*ER RGFTVLARMVISIS*PCDPPASASQG AGITGVSHRT
4482	9979	A	4778	1	429	ARLETNSRSVAHGGVQCHDLSSQQ PPPGFKGFSGLSLPSSWDYRRPPPC PR*F*YFY*RRGFTVLARMVISIS*PC DPPALASQSAGITGLSHCAR/LERES HSIA/RAGGQWFHLGSLQPPPPRFK* FSCLSLPSSWDHRCPPVD
4483	9980	A	4779	1381	1787	LEYVAHPLHQLLILNMFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVISIS*PRDPPTSA SQSAGITGMSH
4484	9981	A	4780	1147	1553	LEYVAHPLHQLLILNMFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVISIS*PRDPPTSA SQSAGITGMSH
4485	9982	A	4781	1456	1862	LEYVAHPLHQLLILNMFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVISIS*PRDPPTSA SQSAGITGMSH
4486	9983	A	4782	889	1295	LEYVAHPLHQLLILNMFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D

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						SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH
4487	9984	A	4783	743	1149	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH
4488	9985	A	4784	2583	3580	DRVSLLLPRLECNGAILAHCNLCLS GSSDSPASASQVTGITGKCHHTQLIF VFLVEMGFHHIAQAGLELLTS/DSPT LASQSAGITGVNHHAWLFFCS/RD TVSLCYPGWSRVA*SRITATSA/PGL K*FACFSLPSSRDYRHVPPHPGNFCI FGRDEVSPCWPGWF*TPDLR/YPPA SASQSAEIIIGVSHHTWPQEVFLNL FIYLRWSL/DSVAQARVQRRDLGSL QAPPPRFKPFSCSLPSSWDYRRPPP HPANFFVFLVETGFTVLARRVLIS* PRDLPASASQSAGITGVSHHTR/LIF/ NFFETGTHSVTWAAVQWYTI/GSLQ PRTPELK*SSHLILTSNWDYRCTPPC PPNLFYILFIYFHRDEGSLCCPGWS* TPELK
4489	9986	A	4785	1966	2372	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH
4490	9987	A	4786	3	305	FFFLRKSL/GSV/TQAGVQWRGLRSL QPPPPRFKRFSCSLSSWDYRCVPP RPA/NFLYF**RWGFTTLARMVVIS* PCDPPASASQSAGITGISHRAQPIKY
4491	9988	A	4787	1172	1688	VFFGVFVFVFVFVFFPKLTSGTIPWA SPEVMIYPPTHS*VCEAPSPFYVFSH LFS/LQSPSHLVCLFLCSF*DGVS LCR QAGVQWRSLGSLQPLTPWFKRFSC LSLPSGWHH/RRPANFCIF/M*RRGF TMLPRMVSISSPRDPPASASQSAGIT GMSHRARPQSSVFKQSFLSR
4492	9989	A	4788	641	1074	VLNLVEFVTRELAFTNVFFCFFVVF FCFFLRSL/DSVTQAGVHWDLGS LQAPPPRFTPFSCSLPSSWDYRRPP RRPANFLYF**RRGFTRLARMVVIS* PCDPPASASQSAGITGVSHRARPTN VNKAITNGLFTYFFFNEE
4493	9990	A	4789	7273	7925	IVSLFLFILLVFWWWCFFFFFETE SCSVAQAQAGVQWHNLGSL/QAPP PGFTH/LFSCSLPSSWDYRRPPRP VNFFFFHF**RRGFTML/ARMVLIS *PQVICPASASQSAGITGLSHRVQR GPHNLLTNQVNKFFFFFLETESHVS TQAGVQ*HDLGSLQSPPPGLKRFSC LSLLSS*DYRLPPHPH/THF/CVFLVE NGNSPCWPGWS*TPDLR

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4494	9991	A	4790	156	391	IPHSYIRKFYSFKMAILSP/KLIYSINA ISKKIK*AFLKKTDELILTFI*KGKES VLDKPILKKNNIVGLKICDFETY
4495	9992	A	4791	365	506	GRHHACLIVDRALVFPS/CQVGRAA HFLPLPGPCPAWTPPSRSLRPGP
4496	9993	A	4792	2	503	LTHPAGARPVLLTTPESFEGPCFGTP HGQSLSQSAFSRGHSLGDTVGVGTG QVGS/LLSGGGVRAG/GAGGGGGA GFGSRLALKAAGERGEKPREVPPP *QR\GPHTKAPWT*AGQGQPPGRAC SPG/PPAEPASQPLTPGPGRRLPGGK RSRRDRARGAARKMGLLFPLD
4497	9994	A	4793	3	389	FQDLIKR*KATIIKTLWY*HKNRY/D IDQQNRIEN/SKHRLSHLIFDKGTRTI Q/YGREQLSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSP IPDIGFHNDFLNMTPKAQATTCK
4498	9995	A	4794	27	285	VFFFFFFLRRSLALLPRLECSGTIVF LVETGF/TMLARMVISIS*PRDLPALA SQSAGITGVSHRAPASFNFLTINILP PLLLWTF
4499	9996	A	4795	12	336	SPVQL*F*LFLVFC*LWSWSAVVYL GPLGTPSADAHT/AGLSKTPPHWAA RARLDDVFSLRTFSSHSLNMELVQD LTASAPMYSSTSRDPP/CLGLPKCW DYKREPPRAH
4500	9997	A	4796	74	463	HISQHDRSYLQVLLASYKTASFLFFF LRQSL/DSVTQAGVQWRDLGSLQA PPPGFTPFSCPSPK*L/SSWDYRRPP PRPANFFCIFIVEKECFTLLARMVISIS WPRDLPASASQSAGITGMSHRARP AQVS
4501	9998	A	4797	1	337	KKLISGFNVIPIKTPANPCVKIDKLIL KFIWHCKARRIGKAMWNKIKYGGGL IQ*DLKICHKVRJIEIVWY*LQGRQ/I DQ/WEQ/IQSPEIDPNIYSHLTYDKSP TAIQRRIYPF
4502	9999	A	4798	3	331	KNYKTLLREI/KEELN*WKDIPRLW LRLNIVKMSFL/SKFIYRLDSIPIK/ MPSRHLFL*KLILKQILKFIWEGKGP GIAKTILKKNKFGGFTLLNFNTYNK AANSRVLVLG
4503	10000	A	4799	3	340	INRLNIFTMAIFSTLIYRFNTIPIKIPA GFVEMDKLILKLWVKFAHGIGKT TLKKNRVPIPKFSSSSSSSSSYWNE DRNINQWN*IDNLKINPCVCGQLIF NKDAKTNEER
4504	10001	A	4800	46	195	SPATLGRPEVGPDS*GPGDRDHAGL TMVKPPVFYLNKYNWIMRSGDRDHP G
4505	10002	C	4801	353	442	MPLLYVQQLFARTGLCATLFGMM SPLYV*
4506	10003	A	4802	1	273	FFFFFFGTESRSVAQAGLRTAVARS RLTASSASRVHAILLPQPE*LGLQA PATAPG*FFVFLVETGLCKHNEKSP LSVQGRIVLRLNQKG
4507	10004	A	4803	57	231	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
4508	10005	A	4804	2	169	
4509	10006	A	4805	698	1231	
4510	10007	A	4806	58	2674	
4511	10008	A	4807	7	235	
4512	10009	A	4808	1	245	FFFFFFGTESRSVAQAGLRTAVARS RLTASSASRVHAILLPQPPE*LGLQA PATAPG*FFVFLVETGFHLVSQDGL DLLTS
4513	10010	A	4809	175	394	NFLRYSHFKKCNRRPGAVVTPVIPA LWEAEAGGS/CRSGDRDHPG*QGE GKRGSLKFQEVSGAPNKFWSILPL
4514	10011	A	4810	65	2712	SGSGHCLAEAAASMGPGWGWKLRT VALLAAAGTAVGDR CERNEFQCQ DGKCISYKWVCDGSAECQDGSDES QETCLSVTCKSGDFSCGGRVNRCP QFWRCQGQVDCDNGSDEQGCPPKT CSQDEFRCHDGK CISRQFVCDSDRD CLDGSNEASCPVLTCPASFQCNSS TCIPQLWACDNDPCEDGSDWEPQ RCRGLYVFQGDSSPCSAFEFHCLSG ECIHSSWRCDGGPDCKDKSDEENC AVATCRPDEFQCS DGNCIHGSRQCD REYDCKDMSDEVGC VNETLCEGPN KFKCHSGECITLDKVCNMARDCRD WSDEPIKECGTNECLDNNGGCSHV CNDLKIGYECLCPDGFQVLAQRRC DIDECQDPDTC SQLCVNLEGGYKC QCEEGFQLDPHTKACKAVGSIAYLF FTNRHEVARRMTRTRSGYTSFIPNLR NVVALNTEGSPSNRIY WSDLSQRMIC STQLDRAHGVSSYDTVISRDIQAPD GLAVDWIHSNIYWTDSVLGTVSVA DTKGVKRKTLFRENGSKPRAIVDP VHGKHPCT/WPGVLCTCQVTSAT* DVRATIRR*ML/WFPQRTLEKAHLV SGREKQEESIIRCLRVK VWLTYEMQ DLGGG*TRL*ITQAKMNAENWL*L EEDKVFWTDIINEAIFSANRLTGSDV NLLAENLLSPEDMVL FHNLTQPRG VNW CERTTSLNGGCQYLCLPAPQI NPHSPKF TCA CPDGM LLARDMRSC LTEAEAAVATQETSTVRLKVSSTAV RTQHTTTRPVPDTSRLPGATPGLTT VEIVTMSHQALGDVAGRGNEKKPS SVRALSIVLPVLLVFLCLGVFLLWK NWRLKNINSINFDPVYQKTEDEV HICHNQDGYSPSRQMVSLEDDVA
4515	10012	A	4811	49	361	STSYPTGSHAFL*PQNVVDAETNS* HINNVLRLKIIKLEENT EKNCHD LGLSTDYY/SVTPKA*ATTTKIDKL ELIKIKNFCTSKDITYKVKRLLIGNNI CK
4516	10013	A	4812	2	346	EKSSLFNKWCWDKWISTGKRMKL VPPYISSSSSSSSSSSSSSSSSSSS SSSTEKNCHDLGLATDYY/SVTPKA *ATTTKIDKLELIKIKNFCTSKDIT*K VKRQLIGENSCK

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4517	10014	A	4813	2	356	EKSSLFNKWCWDK WISTGKRMKL VPPYISSSSSSSSSSSSSSSSSSSSSSSS SSSTEKNCHDLGLATDYY/SVTPKA *ATTTKIDKLELIKIKNFCTSKDIT*K VKRQLIGENSCKSF
4518	10015	A	4814	1	357	VRPHHTNKKRVRLR/VRVNIKVRD KVSTEVKDKIKNQAAVIVKLG VQIK AGPWVRVKDWVRLEV KIKNRDQV RGEAEVRRIGQQLRTKTRPKLNVHP KRNGSIN*NIHTVECYSTIKKQ
4519	10016	A	4815	1	323	PVRGTEQSNKSWASGLQPGWGRAE QLAWGSFNLSKWPSGGDPQPILLS RVQNMGRRLAR*EAPCQPQPLPSR RSSPVPHQHL\PPCHPCGASLSPALA WPPPPPSRS
4520	10017	A	4816	1908	2324	ILASSLRANPGFIRNFHLFFFFFFYFLR RSL/DSVAQAGVQWHD LGS LQAPPP GFTPFSCSLPNSWDYRRPP/RHHAR LISFFLFLVEMGF\TMLARMVSIF*P WDLATSASQNAGITGVSHHTPRP VIKYLPS SSPNLAG
4521	10018	A	4817	1	273	RPRRRYPHSWWFLQEV AIFTLIEKV VFYYSHRLFLHPAFYKKIRKIHKKW TAPIGVISL*AHPIEHA VSNMLPVDP VNLRSQIRTVLFHQ
4522	10019	A	4818	3	293	DHVSPGVQDQAGQYSKTP\SLQKQ KQKTNRHGSAYLWSELLGSLRQED HLNPGVRGCSELLLGHCSPA WAAK *DPVC*KNKTKNLIAGGHPRSFWIQ
4523	10020	A	4819	2	170	KLGFIIKIDFSSVKDNVKGMR RQAT DW/DFIKIKDFSSVKDNVKGMR RQA TDWEKIFAKETSDKGLLSKIY*KPF KLSKQPN
4524	10021	A	4820	52	228	WASGHVRPYRVLNNFISNQKMD F KEDLSGIAEMFKTPVKELLIVL*TC L IVAFKSDNS
4525	10022	A	4821	22	376	TGTVIKIAWY*HKDRHMDQ*NRINS SETNPNI*SKVQRPFW RASSSSSSS SSSSSSSSSSS/PSSSSSSSSSSSSSS SSSSSSSFIQGNTGINLTDFGLGNV F LDMPKQAQAKE
4526	10023	A	4822	151	379	SIPGIQSWFNIQKSINVFYHIVILNTQ HRSSSSSSSSSSSSSSSY*LMIKF/LNK LGIEGNFLILIKAIHGKPTVNH
4527	10024	A	4823	3	479	RDEVSPHCPGWSQTPGLKQSSCLGL PKC*AYRHEPLGL\ILFFH*ATQETQ ARAGWSYASHFVDERTEAQR/V*G TCPRSHANYVLEDLICVLF*DRVCS VAQAGVQWHD LSSLQPPPPGFK*FS CLSLPSSWDYRRFATTAS*ILAF*VE MGVRHFARLV
4528	10025	A	4824	1	57	GKRYTRSDDELQRLRRAHTGVEKKLV CPECSQRSMRSDRLTGHIRSHQNK K GIH*SDELQRLRRAHTG
4529	10026	A	4825	3	602	VDKNHTLSLLCQPSHGDCSRFSAST CLIRSRHFHFNFTFKIF*KLGDSMLT AVSVARDCGMILPQDKVIIAEALPP

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						KDGKVAKINWHYADSLTQCSHPSA IDPEAIPVRL/CP**LRGSSNDSL SFC NEWIILSDTGIFK/HLVPKGSNLG VCVCSHECIATVF*KNLYYCFQLML HGTVFARMAPDQKTQIEALQNVE
4530	10027	A	4826	3	241	TSFSCLSLSSWDYRCPQAGPANF CIF/M*RRGFTALARMVSVS*PRDLP ASASQSAGITRVSHRTRPLV*CFN*A LFR
4531	10028	A	4827	3	241	TSFSCLSLSSWDYRCPQAGPANF CIF/M*RRGFTALARMVSVS*PRDLP ASASQSAGITRVSHRTRPLV*CFN*A LFR
4532	10029	A	4828	2	321	KAVLRRKFIATNT*KK*TSQIKNLL KKLQEKNKFKPKVSRKTIQRSEQK *IQTRKPGEKINKTKGSSSSSSSSSS SSSSSSQREDLNQIGNEREDITTGTT EIQ
4533	10030	A	4829	132	290	LVTSE**IYQIFFSPEMESHVSQA GVRWSNL\SSLHPLPPGFKRFSCFSL
4534	10031	A	4830	645	1201	GGRDLLRTHSVGPSTPQTIPVLTTPPG *CACKTQDVSPHS/PPMKELWPGA PQGSPGRLSPQPPH*RSPHSPCTLW PAL/PGLASTEGWGAIALYILEKNW GREGLNLPPA*PFCPPQSPHGS L VF PSKCASREAPTSNPCLQPQIPRLPSR PKAQAPATHLGGAATHRISAGVAR VCAGAFGGQA
4535	10032	A	4832	115	454	TMMTSWINCFRKG*DDVEHHALHI NLRGKKFILFLPIQEGLTRGRKQ*AN TVGHFQLGFRLYKISGLEKCLKLSKL STQWLLKPLHPDQL*TRAELLG*ES LDKYDQDPEALIR
4536	10033	A	4833	1	638	ERQSVPGFKASQDRLTLLVRAYTN Q*LKLRLIFHFENPRALKNCAYS TL SVLCQWNNKA WMSAHLFTGW LTKYFKLTIETYCSEKTPFKILLFI DNLAGHPRALMEM*KEMNVFMPA KTTSIMLPLISSFNSYYLRNRIHRTF VVVAQSWLQCPTTAISDIQGPVAM GLLLIPSAFVLCWLSIQQVSKLKH HSHHSYFLRFWRLTA
4537	10034	A	4834	2	6053	KEILQEYLEISSLVQDEVVAIHREM AAAAARIQPEAEYQGFLRQYGSAP DVPPCVTFDESLLEEGEPELGELQL NELTVESVQHTVQLLGKRQVLQEA LQGLQVALCSQAKLQAQQLLQTK LEHLGPGEPPPVLQLQDDRHSSTSSSE QEREGGRTPTEILKSHISGIFRPKFS LPPPLQLIPEVQKPLHEQLWYHGAIP RAEVAELLVHSGDFLVRESQKQE YVLSVLWDGLPRHFIIQSLDGSRPL RMEAADPGSPALQNLRYLEGEFGPS IPLIDHLLSTQQLTKKSGVVLHRA VPKDKWVLNHEDLVLGEQIGRVPQ RGSNSQRAWVRGPNTGAPHPGVGS RMGRKRRREL RDWEGRGRSPRPQ GNFGEVFSGRRLRADNTLVAVKSCR

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						ETLPPDLKAKFLQEARILKQYSHPN VRLIGVCTQKQPIYIVMELVQGGDF LTFLRTEGARLRVKTLQMVGDAA AGMEYLESKCCIHRDLAARNCLVT EKNVLKISDFGMSREEADGVYAAS GGLRQVPVKWTAPEALNYGRYSSE SDVWSFGILLWETFSLGASPYPNLS NQQTREFVEKGGRLPCPELCPDAVF RLMEQCWAYEPGQRPSFSTIYQELQ SIRKRHRPRCSSSAAPAHMLTALHS PGLLPASTLPAGCSAVSSLCPCCCQ GFLFRAETIKPLVPTEHSWHVHSSG RQVSEGTSAAGNIEQARKGKGLEEC AVPTGGSTPLPEGRNDRDLRLPGPE PASEAGGPARGRRTERSGCPGAQL GPRQRPPEQGATGERAPAFACVAA CTRAAVPGRVCVEASMKLKKQVT VCGAAIFCVAVFSLYLMLDRVQHD PTRHQNGGNFPRSQISVLQNRIEQLE QLLEENHEIISHIKDSVLELTANAEG PPAMLPHYTVNGSWVVPPEPRPSFF SISPQDCQFALGGRGQKPELQMLTV SEELPFDNVDGGVWRQGFDISYDP HDWDAEDLQVFVPHSHNDPGWI KTFDKYYTEQTQHILNSMVSKLQE DPRRRFLWAEVSFFAKWLVGNGQL EIATGGWVMPDEANSHYFALIDQLI EGHQWLERNLGATPRSGWAVDPFG YSSTMPYLLRRANLTSMLIQRVHY AIKKHFAATHSLEFMWRQTWSDSDS STDIFCHMMPFYSYDVPHTCGPDPK ICCQDFDKRLPGGRINCPWKVPPRAI TEANVAERAALLLDQYRKKSQLEFR SNVLLVPLGDDFRYDKPQEWDAQF FNYQRLFDFFNSRPNLHVQAQFGTL SDYFDALYKRTGVEPGARPPGFPVL SGDFFSYADREDHYWTGYTSRPF YKSLDRVLEAHLRGAEVLYSLAAA HARRSGLAGRYPLSDFLLTEARRT LGLFQHHDAITGTAKEAVVDYGV RLLRSLVNLKQVIIHAAHYLVLDK ETYHFDPEAPFLQVVGWEEAEPMM VLPFRLTEFQDDTRLSDALPERTVI QLDSSPRFVVLFPLEQERFSMVFL LVNSPRVRVLSEEGQPLAVQISAHW SSATEAVPDVYQVSVVRLPALGLG VLQLQLGLDGHRTLPSVRIYHGR QLSVSRHEAFPLRVIDSGTSDFALSN RYMQVWFSGLTGLLKSIRRVDEEH EQQVDMQVLVYGTRTSKDKSGAY LFLPDGEA\SPTSPRSPCCVSLKALS SQRWFRMTSTFTRRSGFTICQWR GCLWYHPWWTSGTTSTRSWPCTS IQTSTAR/VIFFTDLNGFQVQPRYL KKLPLQANFYPMFVMAIYQDAQKR LTHTAQALGVSSLDKGQLEVILDR RLMQDDNRGLGQGLKDNKRTCNR FRLLLEERTVGSEPDFFSKLAAMFR

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						GLIFHSSRSGNREVQDSHSTSYPSLL SHLTSMYLNAPALALPVARMQLPG PGLRSFHLPLASSLP CDFHLLNRLTLQ AEHCLWAEALLHLRSLKALRPLPW ALSVIQEDTLPSAETALILHRKGFD C GLEAKNLGFNCTTSQGKVALGSLF HGLDVVFLQPTSLTLLYPLASPSNST DVYLEPMEIATFRLRLG
4538	10035	A	4835	1	6606	MGFSSEL CSPQGHGVLQQM QEAE L RLLEGMRKWMAQRVKS DREYAGL LHHMSLQDSGGQSRAISPDSPISQS WAEITIQTEGLSRLLRQHAEDLNSG PLSKLSLLIRERQQLRKYSEQWQQ LQOELTKTHSQDIEKLKSQYRALAR DSAQAKRKYQEASKDKDRDKAKD KYVRSLWKLF AHHNRYVLGVRAA QLHHQH HHQLLLPGLLRSLQDLHE EMACILKEILQEYLEISSLVQDEVVA IHREMAAAAARIQPEAEYQGFLRQ YGSAPDVPPCVTFDES LLEE GEPLEP GELQLNELTVESVQHTLTSVTDELA VATEMVFR RQEMVTQLQQELRNEE ENTHPRERVQLLGKRQVLQEALQG LQVALCSQAKLQAQOELLQTKLEH LGPGEPPP VLLLQDDRHS TSSEQER EGGRTP TLEILKSHISGIFRPKFSLPP PLQLIPEVQKPLHEQLWYHGAIPRA EVAELLVHSGDFLVRESQ GKQEYV LSVLWDGLPRHFIIQSLDGS RPLRM EAADPGSPALQNL YRLEGE GFPSIPL LIDHLLSTQQPLTKKSGVVLHRAVP KDKWVLNHEDLV LGEQIGRV PQRG SNSQRAWVRGPNTGAPHPGVGSRM GRKRRREL RDWEGRGRSPRPFQGN FGEVFSGR LRADNTLVAVKSCRETL PPDLKAKFLQEARILKQYSHPNIVR LIGVCTQKQPIYVMELVQGGDFLT FLRTEGARLRVKTL LQMVGDAAAG MEYLESKCCIHRDLAARNCLVTEK NVLKISDFGMSREEADGVYAASGG LRQVPVKWTAPEALNYGRYSSSED VWSFGILLWETFSLGASYPNLSNQ QTREFVEKGGRLPCPELCPDAVFRL MEQCWAYEPGQRPSFSTIYQELQSI RKRHRKH RAGTERKGTGRGM RCTD RRQHFPARGAQRQRPKATWAGAG FRGWRTRAEP AQRSAAPAARGPAGE LQQRAEQGATGGRAPAFACVA ACT RAAVPGRVCVEASMKLKKQVTV C GAAIFCVAVFSLYLMLDRVQHDPT RHQNGGNFPRSQISVLQNRIEQLEQ LLEENHEIISHIKDSVLELTANAEGP PAML PYYTVNGSWVVPPEPRPSFFS ISPQDCQFALGGRGQKPELQMLTVS EELPFDNVDGGVWRQGFDISYDPH DWDAEDLQVFVPHSHNDPGWIKT FDKYYTEQTQHILNSMVSKLQEDPR RRFLWAEVSFFAKWLVGNQGLEIA

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						TGGWVMPDEANSHYFALIDQLIEG HQWLERNLGATPRSGWAVDPFGYS STMPYLLRRANLTSMLIQRVHYAIK KHFAATHSLEFMWRQTWDSSTD IFCHMMPFYSYDVPHTCGPDPKICC QFDFKRLPGGRINCPWKVPPRAITE ANVAERAALLDQYRKKSRLFRSN VLLVPLGDDFRYDKPQEWDAQFFN YQRLDFDFNSRPNLHVQAQFGTLD YFDALYKRTGVEPGARPPGFPVLSG DFFSYADREDHYWTGYTSTRPFYK SLDRVLEAHLRGAEVLYSLAAHA RRSLAGRYPLSDFTLLTEARRTLG LFQHDAITGTAKEAVVVDYGVRL LRSLVNLKQVIIHAAHYLVLDKET YHFDPEAPFLQVVGWEEAEPMMVL PFRLTEFQDDTRLSDALPERTVIQL DSSPRFVVLFPLEQERFSMVLLV NSPRVRVLSEEGQLAVQISAHWSS ATEAVPDVYQVSVPVRLPALGLGV LQLQLGLDGHRTLPSVRIYLHGRQ LSVSRHEAFPLRVIDSGTSDFALSNR YMQVWFSGLTGLLKSIRRVDEEHE QQVDMQVLVYGTRTSKDKSGAYL FLPDGEA\SPTSPRSPCCVSLKALSS QRWLRTMSTFTRRSFGTICQGWG CLWYHPWWTSGTTSTRSWPCTSI QTSTAR/VIFFTDLNGFQVQPRRYLK KLPLQANFYMPVMAYIQDAQKRL TLHTAQALGVSSLKDGQLEVILDRR LMQDDNRGLGQGLKDNKRTCNR RLLERRTVGSEPFFSKLAAMFRG LIFHSSRSGNREVQDSHSTSYPSLLS HLTSMYLNAPALALPVARMLPGP GLRSFHPASSLPDCFHLLNRLTLQ AEHCLWAEALLHLRSLKALRPLPW ALSVIQEDTLPSAETALILHRKGFDC GLEAKNLGFNCTTSQGKVALGSLF HGLDVVFLQPTSLTLLYPLASPSNST DVYLEPMEIATFRLRLG
4539	10036	B	4836	114	255	VQPRRYLKKLPLQANFYMPVMAY IQDAQKRLTLHTAQALGVSSLKDX*
4540	10037	A	4837	1	452	LDGRQLSV/SRHEG/FP/LRCIDS/GTS ELALS/N/RVMQVWFSGL/TGLLKS RRVDERHEQQVHMQLVYGTRTS KDKSGAYLFMPDGEAKPTSPRSP CCVSLKALSSQRWLRTMSTFTRSG FTICQGWGCLWYHPWWTSGTTS TRSLHFSFN
4541	10038	A	4838	3	3543	QLGRLGPERRGGRALTVCVEASMK LKKQVTVCGAAIFCVAVFSLYML DRVQHDPTRHQNGGNFPRSQISVLQ NRIEQLEQLLEENHEIISHIKDSVLEL TANAEGPPAMLPYYTVNGSWVVP EPRPSFFSISPODCQFALGGRGQKPE LQMLTVSEELPFDNVDGGVWRQGF DISYDPHDWDAEDLQVFVPHSHN DPGWIKTFDKYYTEQTQHILNSMVS

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						KLQEDPRRRFLWAEVSFFAKWWD NINVQKRAAVRRLVGNGQLEIATG GWVMPDEANSHYFALIDQLIEGHQ WLERNLGATPRSGWAVDPFGYSST MPYLLRRANLTSMLIQRVHYAIKK HFAATHSLEFMWRQTWSDSDSTDI FCHMMPFYSYDVPHTCGDPKICC QFDFKRLPGGRINCPWKVPPRAITE ANVAERAALLDQYRKKSQLFERSN VLLVPLGDDFRYDKPQEWDAQFFN YQRLFDFFNSRPNLHVQAQFGTSLD YFDALYKRTGVEPGARPPGFPVLSG DFFSYADREDHYWTGYTTSRPFYK SLDRVLEAHLRGAEVLYSLAAHA RRSLAGRYPLSDFTLLTEARRTL LFQHDAITGTAKAVVVDYGVRL LRSLVNLKQVIIHAAHYLVLDKET YHFDPEAPFLQVDDTRLSDALPER TVIQLDSSPRFVVLNPLEQERFSMV SLLVNSPRVRVLSEEGQPLAVQISA HWSSATEAVPDVYQVSVVRLPAL GLGVLQLQLGLDGHRTLPSVRIYL HGRQLSVSRHEAFPLRVIDSGTSD ALSNNRYMQVWFSGLTGLLKGSGLC FLA\SIRRVDEEHEQQVDMQVLVYG TRTSKDKSGAYLFLPDGEA\SPTSPR SPPSCVSLKALSSQRWLRTMSTFTR RSGFTICQGWGCLWTYHPWWT GTTSTRSWPCTSIQTSTAR/VIFFTDL NGFQVQPRRYLKKLPLQANFYPM VMAYIQDAQKRLTLHTAALGVSS LKDGQLEVILDRRLMQDDNRGLGQ GLKDNKRTCNRFRLLERRTVGSE VQDSHSTSYPSSLSHLTSMYLNAPA LALPVARMLPGPGLRSFHLPLASSL PCDFHLLNLRTLQAEEDTLPSAETA LILHRKGFDCGLEAKNLGFNCTTSQ GKVALGSLFHGLDVVFLQPTSLTLL YPLASPSNSTDVYLEPMEIATFRLRL G
4542	10039	A	4839	2	438	FVPAKVAGAAEPDEDGGRSRLRDC GDYTPSERLGPKGAMLWFQGAIPA AIATAKRSGAVFVVFVSDDEQSTQ MAASWEDDKVTEASSNSFVAIKIDT K/QMHLLKSETSVANGSQSESSVST PSASFEPNNTCENSQSRNAELCEI
4543	10040	A	4840	1	1608	
4544	10041	A	4841	1	3117	MAPEWRPGTTASLPSGPGARSVC RSPEAGSASVFVRLCGPRNLGWFGP HLRLRTSAHARQRHPKTRASAREN TSRHSRNPVSVPQDLSLASRCAG SIPITLESCLPVGLSKDVWPLTIEPKV KVFIENLKLDPSTMKNPASLLFSL FEGEWAI AEVLSDIWCTGVLAINK DQVLTIGFDINEFLSCSSSSKSMSC SLTGSLALQPDQQDHETDSSPAS AYQRIWEAFANQSRAERDAFLQDT FPEGFLWGASTGAFNVEGGWAVG

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						GRGVQPKHVKEAFRLNLSIIRVET PDVNLDQEEIOMEVDEGAGGING HADSPAPVNGINGYNEDINQESAPK ASLRLGFSEYCRISNLIVLHLRKVEE EEDSALKRSELVNWYLKEIESEIDS EELINKKRJEKVHRLTHYVEYFSS LHASQITHYKVFLSWAQLLPAGSTQ NPDEKTVQCYRLLKALKTARLQP MVILHHQTLPLASTLRRTEAFADLFA DYATFAFHSFGDLVGIWFTFSDLEE VIKELPHQESRASQLQTLSDAHRKA YEIYHESYAFQGWLAFTHMSQTLA NKIRVRGMAQESCSHGSSVGYLQH PGSEQVQFPRTTSPCSSQQLQGHQC TAGPPPPPGGGMVMMQLSVNNPQ SCAHSPQWKQNKYYCDHQRGQK CVEFSSVDNIVQTSNCTDPVVCVP SSFFIGDSGIPLEVIAGSVSADELVT RIHKVRQMHLKSETSVANGSQSES SVSTPSASFEPNNTCENSQSRNAEL CEIPTSDTKSDTATGGESAGHATFL FREPSGCSDQRPADLNIRVERLTK KLEERREEKRKEEQREIKKEIERR KTGKEMLDYKRKQEEELTKRMLLE RNREKAEDRAARERIKQQIALDRAE RAARFAKTKEEVEAAKAAALLAKQ AEMEVKRESYARERSTVARIQFRLP DGSSFTNQFSDAPLEEARQFAAQT SVRVTSSEPPNPASSSKSEKREPVRK RVLEKRGDDFKKEGKIYRLRTQDD GEDENNTWNGNSTQQM
4545	10042	A	4842	3	790	GARGTPFLSPASVESSVLLCLLVPHF VLSRGPPASPPSSYHPSLGGP/GGQ *PLPEYGLESSEQN*GLSPGEDPGNP GGPFWGSG/PAGSLMEA*GNKRDA PPPPG/DPSCSAPC/GDPPGMQGIQDS LPCHTASQKGGAFPPGPMAPGRVL HQOQPL*GPSRLSQESPSAGPPMPQ LPSWVLCQVRPRAWGCWEPKGPPG TQFPPRFPDPSGTPCPPGYLEIFLLDP IPPRNWLAPLAAAQ**/PWGRWE MPMALPRGGLPLYT
4546	10043	A	4843	1	1026	
4547	10044	A	4844	1	722	MALEQRLKGGSGAALRSKAPPAEG TAGAKALGQESDWSIGGAVSKPVF VQSVRELVADPCASNPNCHHGNCSSS SSSSSDGYLCICNEGYEGPNCEQAL PSLPATGWTE/CHGTPTASACSCYS GA*Q/QSCLALRQR*HCLPGSRKQG\ KSCRNEMGSSGGDPYCLWECQF* QLCGWPPGIL*SATEHLSQDSARCH CLTDFALEGHGHRIPTVLPHRWTKC DPPSGFRGTGPPGGDARLGE
4548	10045	A	4845	2	2028	CSPAAPRRPVRSCCPWPCCCCCSE RGPEAAPWPTRCPRPCL/LPGPCAA QPCRNGGVCTSRPEPDQHPAPAGE PGYSCTCPAGISGANCLVADPCAS NPCHHGNCSSSSSSSDGYLCICNEG

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						YEGPNCEQALPSLPATGWT/AIHGT PTASACSCYSGA*QNPASLSGNGDT AYLAAENRAESCRNEMGSSGGDPR YCLWECQF*QLCGWPPGIL*SATEH LSQDSARCHCLTDFALEGHGHIPT VLPHRWTKCDPPSGFRGTGPPGGD ARLGE*SLY\CFVNDVSVTKS/NCGFA LNSGGEVSTCVPGESHANDLECSG KGKCTTKPSEATFSCTCEEQYVGT CEEYDACQRKPCQNNASCIDANEK QDGSNFTCVCLPGYNGELCQSKID YCILDPCRNGATCISSLSGFTCQCP GYFGSACEEKVDPACASSP/CQNNGT CYVDGVHFTCNCSPGFTGPTCAQLI DFCALSPCAHGTCRSVGTSYKCLCD PGYHGLYCEEEYNECLSAPCLNAA TCRDLVNGYECVCLA EYKGTHCEL YKDPCA\KSACLNGATCDS DGLNG TCICAPGFTG*ECDIDINEC/ATVTP CHHGG\SLG DQPNGY\TCHCPHGW VGANCEIHLHWEVPGTWAESLTNM PRHFPLTFIHWEFPLRGPFHPYADHP DRGDLPHQPH
4549	10046	A	4846	1	703	TISCPAVRSRRPRRISCLSCPGGGGA ASGLQRAAGGTGLSWVPAGLRVCC SQRSWRPAKEEQPVQTPRRTGKGG EISDMEKPYNKNEGNLENEGKPEDE V*PDDEGKSY*EEKPYA*GNTECEG KLKADGEPGDEGQLEDNGSQEKQG KSECEGKPGGEGKPASQAKPESQPR AAEKRPA*RLCGPGKAKK/NKPDQ GDRTIFPQGLSGGLTGKASEQ*GDD ERMWRCVKGSRGA
4550	10047	A	4847	180	866	GAYVHGGRLCVQSLFQGVSSSDF CPPIPTLVPTLRPRAPCLWCTQDPA PPCQSQRRLGLPFQGA GLKPSPGLL PNILLPESPSKRFNHGQLPVPQTVFG GGGSRGPPLLVPPLPLFVFPFCGCF LSQPRGHRSPSSP*EEG*STPLLSVC HSHTDLWGLSWAVPAGWTGPSALF SPQAVNRLPITRPAPTHPHSFPREAP GRW*TPLPTS YQSLLFY GKDL PVK
4551	10048	A	4848	112	679	KI*NMWCYSDTGQFN VV KLSVLL*I IYIFNKILSSFLVKTGKLSLKS VN/NK QQSRITKTSKEN\KRGGFMR*DIKTF YVFAVIKSVLYMQI*ID*WKIIESSET DLHISHLIFDKDNKMEKSLKK\WDI VYSSHRKIINLDL*HIPYVNINMIWN IDLKIKRFF*IAT/ENIFVTF SNVGN FLKYQLKSKIKKLMRMVVYQMV P
4552	10049	A	4849	33	394	GSVWHHPFEGALRGPIPGAAGKPG LGTPSHPGLSHPAACAACPRLPGL CSCAPGSAPLPRLRP*/PAPCGSSDS VPRTP/GRRGLGSPGPPAPAAPKAE* LLQGGEFFSDPQPLAPEPRQLR
4553	10050	A	4850	2	269	LSGVCTVHIRGVCVWAGGNPSGTE LPGPLPPRPSASPPHPPQ*GVALP\

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						PVLFCFLVLPPHPTPNLIYPPCTVPFS PLPAPFAFFCW
4554	10051	A	4851	1	543	LLSKWIIITPSGAGSGDPPPAASPRR KQRMKIMKTTRSQTTPGRAPAASA SSPTL*TPGRDLESRLRP*PTNLPVR TPPGTAAVCPLLHRP\PQKAPVLGP ARV*ERGE/DANATPKREGLKRA/PP NDTLDLFLWLGTSSSTKIKWTRPPAV EPLLVLHPTPTLPPLPVVPIVTQRVE YQGRFF
4555	10052	A	4852	831	1301	FFVFTFKYKNTILLCVINQGPSSKNL FFFQGRDIHQFILSFVFRAGHLVPSQ ASPTSKRPKPFSLIPNPYLLS*FPLLIE KLVINFLKKKFPTRASP*PNQSTSR SSPFSYPGRRVPPLQT\SSVPELRTPY WTGAPPLNGSSGYVSPPTLPPPLMH
4556	10053	A	4853	1	1222	
4557	10054	A	4854	2	563	AHVIIYRFSMH*VITDVIPMLEVRSV YEINDVGTPEGEQ\TPPLTPVGGSN PQIPAQSHPTSSSSSDGLRDNVPW LKVKNSPLKQSPGYQTELVIQLVW VGGEPPQIASLAVNSSYGLVDFGN CNGIAMVDYLQKAVLLNLGTIELY GSNDPYRREPRSPRKSQPSGAGLC DISEGLVPSKA
4558	10055	A	4855	648	1377	EYLHGGWEHLQKRSLSPATGGGQG QLGAEGGP/GPGGGAAPAHPLLAPN QACGVLIDWRPRWTRGGTAAAG ARTPNLNPAAALTP/GRHSCVSVKK GSESLERSRRR/TLPVVSPPGGGGCE MLRPDPASS\SSQTP*PVPGAEAQ LALSCPPNSCPAKEVGAAGF*APLH LLSPSVGEGGGASGTPKVSSFPLPF GGPLHSP*Y*PGPENWEGGGDEGPL SHPARVPAAQSETECVPTESPFQ
4559	10056	A	4856	3	394	SQAPS/GVAAHTPPLS*AWTQPWNS IHMASTRPNMPLRSGPA/CMPQL QLQELFTRSLVESELRIAPSEYPDES PIEQLEERRQLLEQPISLDVMLEPYI LRRSKLDLLYTDSDSDLQLYKEQGE GQGDR
4560	10057	A	4857	3	666	SLLPKIFIGCLRRASSGPGAGNMLGS PSPQPLVSILGIAESWSTLPQGQPPA NPEAWAGPAGAKTDKSKT*GHFTP ETLPNVPKKDPLQLGA*KPGGSKPS EE/VWSQ/SPGPWLNSGFFPPLNP RWGPFPSTLWERF*NCSQPFRALRN PPVPL*GVLASNPWPPPHPHTHPA NMPPAPPRVRLRSSSTSAPPPWGCT QGPRGARAGA*AGAASS*SRGR
4561	10058	A	4858	3	361	FFFFRKWNIFANYM*KKLILKIYQ QL*KLNHKVQ*LDL*MNKQNFHQK TTQM/AKKHLTGCTKLLICREMKK KTQ*QRNHLTPIRMATYFLKNAN/C W**CNKNETHVGCWWKTKM*SLF
4562	10059	A	4859	3	397	DQPTDIILDEQ*LELFHLRTGIRRG PVSSLFPN/IRAIRQEK*IKGIQLGKEI

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						KLALFADMILYLENPEDS/AQKL/LR LINNFSQVSGYKINAQKLGAFLYTN NVQAE/SQIKNPIPFTVAIKKLKYLKI HLAKE
4563	10060	A	4860	2	328	AHIDAVNEAMRLLHEGFHAPTMSW PVSGTLMVEPIETEDHA*LDRFWDA LINLLQGIADIEDGRICPRVNPLKMS PHSLTCVTSSHWDRA\YSEKGAAFP LPFVKPENK
4564	10061	A	4861	13	410	NKMRRQATDRDKMLAKDTFDK\GT LEIYNQFLKFNNKKMSIPIK*WAKN L\NSHLTREDIQVANKPMKRCSTSY FIKEMQIKAMTRSRCADIKMAKIQT TDDIKC*RTCTRSTNFPFALHLFYQ LTFRKSHISH
4565	10062	A	4862	3	293	DKGLKGFGRGFPTFTSFGQPTWLGLG LDLPEPGN*GPGFGCGP/NSRVGPTL SNLGPGERGPPGPPGLGV*ALKGK RADKKGGASFFPGF*KFPVGLP
4566	10063	A	4863	125	366	GIPGERRLEPPG/PKGPPGLSPQIKGN NGPGPQN*VFFGGFKTKVPFGAQQ GS/GNPGPKPIFPGPMPKGRKYRVGP MAPPLQ
4567	10064	A	4864	79	336	HIATFNALSYVQASKRDKKFFACAP NYSYAVLCECLSSSIHLSSACSHVH C*RHDDALLWQPHGSIRDDMR*HI ATFNALSYVQASKRDKKFFACAPN YSYAVLCEC\HRRVFIYRQPAPMST VFYNRKDCLQ/TVDRMLIHKVASLK TNDPILSIQAPK
4568	10065	A	4865	2	512	KIQIASIRNEIGH/LLTDATYIQRRLR E*CGQLQANKFDNLNGRDKFPGRH KLPKLIQKEMEAGRSGLPLSPRVLG LQA*ATVSGLTGKFKYKTCKEIIPIL TILFQKTEKGTQ\SS*EETSTILIPNQ EGKKNFQNGCLSMPTGKGVPLTK ILVNQIQQSVIHKDNISI
4569	10066	A	4866	466	1451	EVCGLKKARISLFFF*DGVSLLCCPG WSAVAQSRILTATSASRVK*FSCLSL LSSWDYKRPPRPANFLHF**RQGF TMLARLVSI/WIS*SVPPWPPKVLE L*AKAGDSLEPGSSRLQ
4570	10067	A	4867	3	379	NKSCQGPRTSFASAGWALKNPRWQ EQKEGLGKAGRPSGMNSSASSPTPG RKRELGMGSPSLSRSP*CE\GRSDR LG*PP*GGQGGGGHGA PSTPGPGG\ GPGDFHSKPPDPSLVPRPTEARGSP GP
4571	10068	A	4868	2	1718	SEGAPPRRGAWGGPPARSHTLAPT PLPP/GPLSLCFACKWLGV D/HRDG AG*LGSQKAGGRGHPGMGQKGKT PPAHAW*PTGWCTGKP*KLGFLCPF HIPPVSLACFLLSCAASDFSVLTWQ LWGP*EPPTEGGHSPFPSCRC/HRQE EGFLPVWQSPRQRPRMRPDSAPPST SARASKVGPRGLPLL NFG/QRPNL TPYGPAPALALS*PPQRWEELAEGA

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						PGPQPPVASKGPFSS*PKVLRPAVE TSSCASAPLAVFVRGVHTCIGG*AP GLSGGHPLTVSF*JGGIEGLDCLSPQ *AWGPGLGLEVCCGSHQASPPGPG VLGAPCPPPPCPPQGG/PAQPVGPS/P SHHGGERE*RGRPHSKLPLPPGVWG GC*RIHSRGPPGLSQPLFCF*PRRLS\ PAQPA*SKGGSRLVGSFCFLLPGS* GTRASGRGHSPSLKPGPGRAGRQ\G ETRGS\GSPGE*GCWSQNWDRGPA GQPWATSRVSIVRGWRVPGVAGAG FLAVLPWAPPSEARWQEADQNPSA FGPKEWEAAFLPNLPCQGGQQRGSPS PPPPGCRNGDPSQGLGAGAEYSLGP LPYT
4572	10069	A	4869	253	451	RWKA WFGREIKGNNPRCKRGGGK HGTG/EEIKGNNPRWKRGGGKHGT GGK/YKGNNPRWKRGGGKHGTGG K/YKGNNPRWKRGGGKHGTGGKL K/SNNPRW*REGGKHGSGGK/YKGN NPRCKRGGGKHGTGGKLK/SNNPR WKRAGGKHGSGGKFKEIIPDGSVK VESMER
4573	10070	A	4870	2	269	EGGLGLNRFPPPPGPPRRPAAACMS AP*PQR/HWPP/SPREEKASLNEPGG PGRGRGRGSGQLHGEGGPRGGE/R GNWPGGMEGEGGIDAPAS
4574	10071	A	4871	20	312	SVMNGTSICKCRANDETGLSPSPAG PKSRSRRLS*LWRPSAATDSGSPPT* PVPTSPPPAPTARPGSRAPSSPLA PILTGPGG/PLRPPPPPAEEP
4575	10072	A	4872	299	472	KSISVATANPGKCLSCTNSTFTFTTC RILHPSDITQVTPR*/GVPGKSGASLL SSAVFS
4576	10073	A	4873	1	3454	MKHTLIPRIKNAQLQMSSLAVPVNS LVCLGKILEYLDKWL VLDGILPFLQ QIPSKESAVLMGILGIYKCTFTHKLG ITKEQLTGKVLPHLIPLSIENNLNQF NSFISIIKEMLNRLSEHKTLEQLHI MQEQQKSLDIGNQMNVSSEETKVTN IGNQQIDKVFISHIGADLLTGSDSEN KEDGALNVPPAGAKPTQQRPTDMS ALNNLFGPQKPKVSMNQLSQQKPN QWLNQFVPPQVSPATGSSVMGTQM NMIGQSAFDVCSNEDLPEVELVSLL EEQLPQYRLKVDTLFLYENQDWTQ SPHQRQHASDALSPVLAETFRYMI LGTDRVEQMTKTYNDIDMVTHLLA ERDRDLELAARIGQALLKRNVHLSE QNESLEEQLGQAFDQVNQLQHELC KKDELLRIVSIASESEETDSSCSTPLR FNESFSLSQGLLQLEMLQEKLEKE EENMALRSKACHIKTETVTYEEKEQ QLVSDCVKELRETN AQMSRMTEEL SGKSDELIRYQEELSSLLSQIVDLQH KLKEHVIEKEELKLHLQASKDAQR QLTMELHELQDRNMECLGMLHESQ EEIKELRSRSGPTAHL YFSQSYGAFT

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						GESLAAEIEGTMRRKLSLDEESSLF KQKAQQKRVFDTVRIANDTRGRSIS FPALLPIPGSNRSSVIMTAKPFESGL QQTEDKSLLNQSSSEEVAGSSQK MGQPGPSGSDLATALHRLSLRRQ NYLSEKQFFAEWQRKIQLADQK EGVSGCVTPTESLASLCTTQSEITDL SSASCLRGFMPEKLQIVKPLEGSQT LYHWQQLAQPNLGTILDPRPGVITK GFTQLPGDAIYHISDLEEDDEEGITF QVQQPLEVEEKLSTSKPVTGIFLPPI TSAGGPVTVATANPGK\CLSCTNST F/TLFTTCR\IYLHPSDIT\QVTPSSGV PFHLSCG\SSGSSFHNTAVNSPALS YRLSIGESITNRRDSNYNLSVGTME VGPKFLQER\GIS\AKVYHSP\SENPL QPLPK\SL\AIPSTPPNSPSHSPCPSPL PFEPRVHLSENFLASRPAETFLQEM YGLRPSRNPPDVGQLKMNLVDRLK RLGIARVVKNPGAQENGRCQAEIG PQKPDSAVYLSNGSSLLGGLRRNQS LPVIMGSFAAPVCTSSPKMGVLKED
4577	10074	A	4875	1	638	LAWGKGKGASSDSGGLVDSISTL TTPGDTNT/HSDLIVRGGAYGGQW AHGVLAQVQPSVGAEVTP*PQMGE *TDVCGSQSPHICSLTLRVGATML GKAR\WKPLG*TLPR\KIVNSKATC SPGGTAKVSAAIRGLGRCRVVTPTA ASFHSS*\WLVWKTGGSRRKKDSES WVNLTRTPIATAVPDMTTDSLGGIQQ SIPGHPVLQPIDPGESL
4578	10075	A	4876	31	448	PKSLLSLVKINYGYVPK*QATKAK LDNWDYIKLQSFCTTKIMNRVRRQ PAE*ENIFANQTSKGLISKIYKELK QLNSKKANNLIKWNSSDDLNR/HFSN EDIQMASRYMKK\NSTSQIREMQIK TTRYHFMPIRMTT
4579	10076	A	4877	3	286	KFTFKRHHHLQLLKRK*DS*V*T*Q MFMEQIKEDLSKQRDNCS*IGKLSI AKNIYVSNIPG*FDAIPIKIPARFFYA FGLYCRNSVSLSPRLN
4580	10077	A	4878	3	236	ATHSTLPSFQGPVSLASMTVVGIDG KASRPLQTP\VCQLDQHSFLHS/FLV IPTCPVPLLG*GILTKLSASLTIPRLQ P
4581	10078	C	4879	206	262	MVAIGTGYRRPGLRFTLN*
4582	10079	A	4880	2	756	LTSSRGARPAPLRAPAR/LDPAFRAN PLRSYSGSLPTFPYLHCSNMPKAC SPWRPAADMGT\PGARFTSPPDFQ GPARAPPDAAGTATLSKARAPLSGR NPFQGRPCPSQRKENSRRSRTSPG SRRVTD\TGRLAGAPCSATPD\SGI*T RLPFRIGRGAPEAIAPSLRNGARPSL RTD*PMFQLLGYNWNPSVPRPSKV LRLNICYYTP\SHAPAAAPP\GPADFQ GPARAHRTPEPRRFPRHGPLSRGE P
4583	10080	A	4881	3	322	MGSVTGPLYSGYKEEVVCCTLVEV

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						FPSLLQVSRNPRMPFDLGLIFCLG GQGFPRATTVSGHWPE*LSQSSSSP KLRPPTL*SKPAHPGAAEALKAVPR TSAGAR
4584	10081	C	4882	240	500	MQNGLSGAYFPSVWAAKDSQERR RSPATGRNDSPRAPLPRSSARRPSK ANLHTLGQLKSSRCRAPRLRRAA RTRXSXDQXWRRXTT*
4585	10082	A	4883	22	696	CTFGSFPFGLSAWSFRASLPPAPAP GPNERFRSPGAGGFWGVDAAGQPA PAEVLGTALRASAAPGCAD*NPKKI KWHPG/SFCSPGEGMEILQQVCSKQ LPCNLSKEDLLQNPYFSKLLNLS QHVDSEGLSLTLAKEQAQAWKEVR LHKTTWLRSEILHRVIQELLVDYYV KIQDTNVTSEDKKFHETLEQRLLVT ELMRLSPSQEREIPPLGLEKADLL E
4586	10083	A	4884	1	594	AVVHFRLPLPGPFILCLSGPRFPQP AAPGPNERFRSPGAGGFWGVDAAG QPSPAEVLGTALRAPAAPGLQVCF KGSAGGASGRSSGRVIPA/MWPET VVALGNPWTVQTEGKVGAGEPVL HFDSSRAL*GSVSCENNL*NQFNRS SCSV*RQALRI*KTPSEHLKCLGPC SSVFNTSECRVENRSLNCPFTPCNL
4587	10084	A	4885	2	326	VKTAEFVNKWKQNSTKLWNSQAQI DSSSLVNQINDLRQTEIWMGDRIMN LESRIQMCDWNTSDFCVTPQYNE TEH*WKKVKRHLEGREENLTL*IVK LKEQDFEASQ
4588	10085	A	4886	2	373	VLLTPEERTVVIALWRKVNVAALC R*GAWA*L*AYPWTHRFFESFGDI DSSDAVMGKPIVNAHGKNVLGAFS DGQSHLDNLLGTYSQSELHCDKL HVDPENFKLLGNVLVCVLARNFGK EF
4589	10086	A	4887	3	332	HLSIINLVNQLNSPLKAYTLPVWIP SSIRGPTICCLQEIHFASKNTYKLKV KELSSSFQANEKEKHADKTGFKPK L*REKNGHYIMIKRSVQKENIYIM FLIADPDIC
4590	10087	A	4889	1	304	HSCSSMRMPPLPTPPP/IVLCPHPSP LIKALVSSKPP*VPSAETWPVAAL GA*VPAVLGWPLHTENVLPVPLPL EMPRIQWHFMLCSFPQRSRADEST
4591	10088	A	4890	1	254	RPRRQFGIEGSFLNQIKNIYKKSTAN VILYVDRLNAFSLISGSSSSSSSSSS SSSS*LPVNIIRQ/EKVI*GMQIVKEE LNLSL
4592	10089	A	4891	310	415	SQYFGTLRRVDHLRSGVRDQPGQL GKTPS*PQVIHPPQCPKVLGLQYYH FLFFLRRL/DSVAQAGVQWRDLGS LQRPFGFTPFSCSLPSSWDYRRPP PRLANFFVFSVETGFTVSARMVSIS *PRDPPASASQSAGDTGVSQAPV
4593	10090	A	4892	2583	3580	DRVSLLLPRLECNGAILAHCNLCLS

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						GSSDSPASASQVTGITGKCHHTQLIF VFLVEMGFHHIAQAGLELLTSDSPT LASQSAGITGVNHHA WLFFCS/RD TVSLCYPGWSRVA*SRITATSA/PGL K*FACFSLPSSRDYRHVPPHPGNFCI FGRDEVSPCWPGWF*TPDLRYPPA SASQSAEIIIGVSHHTWPQEVFLNL FIYLRWSL/DSVAQARVQRRDLGSL QAPPPRFKPFSCSLSPSSWDYRRPPP HPANFFVFLVETGF/TVLARRVLIS* PRDLPASASQSAGITGVSHHTR/LIF/ NFFETGTHSVTWAAVQWYTI/GSLQ PRTPELK*SSHLILTSNWDYRCTPPC PPNLFIYLFYFHRDEGSLCCPGWS* TPELK
4594	10091	C	4893	40	180	MSFEAEIVLSPDRTTALHPGLQIETL SHIIIIILSTISFHQLLH*
4595	10092	C	4894	4827	5060	MWIFYFWTLNSVPVIYMSTLMSIPHY FDYCCFIVSDIMLPEITFSTFILLMV ALAIRGPLHFRRHFRINLSIATKNA*
4596	10093	A	4895	2	311	FILHVCCLKLILFVSGDTFQTVSPRFL APRTFLAPLQNP*PLSPCAVHISFSRP LPARSPLPP/PRPPPPPTCSTAIPATH NPILTTHSTPPPTLPTINLTSSP
4597	10094	A	4896	2	374	DLTPKV*SRKGKIGKLDFTKTFW SAKDHVKRLKRQTTDWEKIFLNHIS NK/GLLSRIYK*LQTQY*KTPSNPI/K KTAKDVKHEFTEDIQMACNPMKR CSTSLAVRELQIKTTVRYLKIEFNF
4598	10095	A	4897	1	684	
4599	10096	A	4898	1	1349	
4600	10097	A	4899	1	821	MLQTSWGYDNPRVTQKVPPFQLNC LPMTVVLLILYA EVATDWN RVGLT QGQLLHSLRLDPWSGLTQRTFPTGA MEISPDYLPPEFIVENTERIDEREKG REQPPKKT PENKA WPKMLKGKKA KGKKVAPAPAVVKKQEA KKV VNP LFEERPKNFGIGQDIQPKRDLTRFVK WPRYIRLQQRAILYKRLKVPPAIN QFTQALDRQTATQLLKLAKHYRPE TSKRRRLLAQAEKKAAGKG/VRPT KR/PPVL*AGVNTVTTLVENKEAQL DLYCAI
4601	10098	A	4900	1	868	GTRPKMPKGKKAKGKKVAPAPAV VKKQEG\AKKV VNP LFEKRPKNFG IGQDIQPKRDLTRFVK\WPRYIRLQR \QRAILYKRLKVPPAINQFTQALGP RKQATQLA*AWPTKYRPRDKAREG SRDLFGPGPRKKA AWPKGTFPTKRP PVPSKQ\G*TTVTTLGGGPRKASAG WWIAHDVDF\LELGLSFLA\ALCRK NGGSPY\CIKKGQDWGRL\VNKK TCTTGRLSHR*TS ED/NKALLKLVE AIRTNYNDRYDEIRRHWG GNVLGP KSARIAKLEKAKAKELATKLG
4602	10099	A	4901	145	745	RRRGTSQCNLITIVNHISEITVIMFIE CSLCIKVIRLFHILILLDFSSKPAPPPP

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						PCGAPGL*TATLLSRLRTARDLGR L*ASPASPLCAVPSPAAAAFL/SLPLP LCPSSSSARELRSPTPGLSGQPAPAA SPGPG/PAG/PPPPPLAVRPRFAPHL QLCPGPPFSRPSVLPASSRCQPGLSA PSLPSSPRPPPLRGLGRS
4603	10100	A	4902	94	432	TFLFFLIFSSEYWKFKKQYSLEKSL FVAYNHKDG*THFLKGNNQFIFSLA/ LFTLGDIIYCKDIFGRLGLQP/TDISSS DSPFLSFSSSIYILTWGQARWLTPVI PAFWEAKAG
4604	10101	A	4903	109	422	FFEDGVLSRSVAQAGV\QWR\NLSS LQPLPPRFK*FSCFSLRSRWDYRHA PPCPA\FVFLVET\GVTLARMVLIS *PRDPPASASQSAGITGVSHCAPSRH SLS
4605	10102	A	4904	3	364	HEETAYDINILS**TQTFNMARLE*N CCNTIKSISEK/PTANSIR*AKKQEGF FQISGIRQGCLSSFLFIILEVLARGN R*DKN/GIQIGKKKVELSLFSETMRF NIWKRLWKPHITRANK
4606	10103	A	4905	50	394	LSYSWHSIHLMLKIISWHFDGQFSA LVIL*LSVAVDTADYSHFLETASLL DFEFTVLSWFSSYLT/DMFLFTLVFS L\PFISIQLLNIGISQGSVLSPLLYAS ASGYMSLNIMYRH
4607	10104	A	4906	49	366	SGSSLAAVFWGPKGPAQAP\GPWAP WASPSGPDLPRLHPADPQRQLST VPLPLSRPPALSIAPMALSHSCSNIP P*TPPPASLRPESLTPARS/PPTR*SHS PPP
4608	10105	A	4907	119	246	FCFHHLNLPFLIF/NVCLCV*QSHS VTQAGEQWRNLGSLQPPPPRFKPF CLSLPSS*DYRHAPPQLADFCISSRD GVSPCWPGWSQTPDLR
4609	10106	A	4908	1	280	ESRSVAQAGVLWRDLCSLQPPPPVF K*FSCSLPSSWNYRCAPPCPASFFV FLVE\QGFTMLARLVLS*PQ/CDPP TSASQSAGITGMSHCTWP
4610	10107	A	4909	406	661	SQTPDLR*SAHLSLPKCWDYRR/AA TAPGQNISFKLPNPWEKAKHLMKS T*RLKHFTNFALFV*NCIDD/WMEF ALVAQAGMQWHDGLSLQPLPPQFK WFSC\PASPKCWDYRREPPCPANFF FFLYF**RLGFTMLARVVSNS*PQ/C DPPTSASQSAGITGMSHCAWPPFFF LFFSFFETGSHCVAQAGLK/PLCLK RSSCLGLRKCWDYRREPLRLAPSW TFRM
4611	10108	A	4910	3	459	ELRDGEKVLDLCAAPGGKLIALLQC ACPGYLHCNEYDSLRLRWLRQTLE SFIPQPLINVIKVELDGRKMGDAQP EMFDKVLVDAPCSNDRSWLFSSDS QKAS/W*DKSKEEFAFFYRLGC*GL QLRPLRPGGILVYSTCTLSKAENPR CDQ
4612	10109	A	4911	1	95	TPKVHASWQK/MAD*SGQCPVLQIP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LSSLMMQ
4613	10110	A	4912	253	1531	SWKLAEKVWEAQLPGFSPPPQCSV RCGRGQSRQVRCVGNNGDEVSEQ ECASSPPQPPSREACDMGPCTTAWF HSDWSSKCSAECGTGIQRRSVVCLG SGAALGPGQGEAGAGTGQSCPTGS RPPDMRACSLGPCERTWRWYTG WGECSSECCSGTQRRDIICVSKLGT EFNVTSPSNCSHLPRPPALQPCQGG ACQDRWFSTPWSPCSRSCQGGTQT REVQ/CA*APTRPSAPDALLNCGPPG SAPVNSQPC/MPAP**SMARDSSTF APWVGTPGPGFCVLPLLTQPPVCRSL RTCPGSGLPRIPPERGPGLHGFLLCH HRSPIGLGPLWNPLGSSSLFPLGLQ GMSSR*TEGVGKVNGTQSDFSGT GQAHVGGCDGVCCTYCLRCCFWG LHGICVWSNVYHFSKRRRLHRTLEG TRPVFLEDFS
4614	10111	A	4913	131	355	STADTLP**TPKLSPQLMDTILPSQS VAMFHT*DHSAPTG/TGAPPHTTPS RPLNTRGPTEEFSPRPPPQHRPSSC
4615	10112	A	4914	3	420	QQPPTRLD*GPKQLMPHSPHNPHTI* NPAVLSLPPQTKLLGPPVVRGPLLIR *SPQLLPACLPL*STRPGTLKPKAT PAIPPTTVHKPVASLRSHLRADGPG APPHTTSPRLNTRGPTEEFSPRPPP QHRPSPPTK
4616	10113	A	4915	11	375	
4617	10114	A	4916	3	260	
4618	10115	A	4917	3	208	
4619	10116	A	4918	1	422	
4620	10117	A	4919	127	4348	GASISDIQTETTEEDSVLLMHTLLAA TKDSLAMDPPVVNRPKSKTKKAPI KTITKAAPAAPPVPAANEIATNPKPI TWQALNLPVITQISQALPTEVTNT QASSVTAQPKKANKMKRVATAKAA QGSQSPTGHEGGTIQLKSPLQVLKL PVISQNIHAPIANESASSQALITSIKP KKASKAKKAANKAIASATEVSLAA TATHTATTQGQITNETASIHTTAASI RTKKASKARKTIKVINTDTEHIEA LNVTDAAATRQIEASVVAIRPKSKG KKAASRGPNVSEISEAPLATQIVTN QALATLRVKRGSARKAATKARA TESQTPNADQGAQAKIASAQTNVS ALETQVAAAVQALADDYLAQLSLE PTTRTRGKRNRKSKHLNGDERSGS NYRRIPWGRRPAPPRDVAILQERAN KLVKYLKVDQTKPIKRSMDLRDV IQEYDEYFPEIIRASYTLEKMFVN LKEIDKQSSLEILISTQESSAGILGTT KDTPKLGLLMVILSVIFMNGNKASE AVIWEVLRKLGLRPGVRHSLFGEV RKLITDEFVKQKYLEYKRVPNRPP EYEFFWGLRSYHETSKMKVLKFAC RVQKKDPKDWAVQYREAVEMEVQ AAAVAVAEAEARAEARAQMIGIEE

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						AVAGPWNWDDMDIDCLTREELGD DAQAWSRFSFEIARAQENADAST NVNFSRGASTRAGFSDGASISFNGA PSSSGGFSGGPGITFGVAPSTSASF NTASISFGGTLSTSSSFSSAASISFGC AHSTSTSFSSSEASISFGGMPCTSA GGVSSSFSGPLSTSAFSGGASSGFG GTLSTTAGFSGVLSTSTSFSGAPTTS TVFSSALSTSTGFGGILSTSVCFGG PSSSGSFGGTLSTICFGGSPCTSTGF GGTLSTSVFSGSSSTSANFGGTLST SICFDGSPSTGAGFGGALNTSASF VLNTSTGFGGAMSTADFGGTLST VCFGGSPGTSVSFGSALNTNAGYG GAVSTNTDFGGTLSTSVCFGGSPST SAGFGGALNTNASFGCAVSTSASF GAVSTSACFSGAPITNPGFGGAFST AGFGGALSTAADFGGTPSNSIGFGA APSTSVSFGGAHGTSLCFGGAPST LCFGSASNTNLCFGGPPSTACFSG ATSPSFCDPSTSTGFSFGNGLSTNA GFGGGLNTSAGFGGGLGTSAGFSG GLSTSSGFDGGLGTSAGFGGGPGTS TGFGGGLGTSAGFSGGLGTSAGFG GGLVTSDFGGGLGTNASFGSTLGT SAGFSGGLSTSDGFGSRPNASFDRG LSTIIFGSGSNTSTGFTGEPSTSTGF SSGPSSIVGFSGGPSTGVGFCSPST SGFSGGPSTGAGFGGGPNTGAGFG GGPSTSAGFGSGAAISLGACGFSYG
4621	10118	A	4920	3	1380	NMLGKYL*VKDQTKIPKRSHMLR DVIQEYDEYFPKIIERASYTLEKKFR VNLKEIDKHSSSYILISTQESSAGILG TTKDTPKLGLLMVILSVIFMNGNKA SEAVIWEVLRKLGL/RPGV*LGSLSA CCPCCPLAREDPRIASVWWSGGT GWGAGLGRGPRVLTCDVDDQMVL KLSAVSLLNVLCF*A*MLDRPSRIP DKEGIWVLNCLLLVAMCSLLSLH* DCPMC*ERSPSMLGKWPLALNLGQ FLICGSWGLIFPNCQG*GIHSFGGSE GKLITDEFVKQKYLEYKRVPNRSP PEY'EFFWGLALPTTETSKM\KVLK FACRVQKKDPKDWAQYREAVEM EVQAAAVAVAEAEARAEWFQHQH WLYLANPAPSNAGASSGPKFYCWL PAVDPSTGVGFCSPKHQVASSGGP STGAGFGGGP\NTGAGFGGGPEHQC WLWQVEPPVLVPVAF
4622	10119	A	4921	1	412	TRMGLPDASRRRTCRMDEGWQE AMSSA*GRITLQRLSTGPEGQGGRE KVGPEGGSENPPQPKAAGVLSKHL PGAPAPPPQRPSSPPPLAGPLTERV EKVCDFLDAAGDYLN/GTPG*PSPG ESPAAQDPPVPPWPP
4623	10120	A	4922	117	295	
4624	10121	A	4923	1	3564	
4625	10122	A	4924	1	355	LPGIEVLWQGPKVVSKEIPVESIEEV

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						CKSIKRAPVIWDTIHVN/DF*SALTP YQIVTTKFYFRIKKIVHWGPFPHSSQ KILSICEKYQWLSVPLTHNLTKFLSII VNYSRYHCIKPQLV
4626	10123	A	4925	3	3145	AAAEGELGAWRGNSGRPKIIGRAA EAENEDRTLGRLLPGNERSQPRSP MLLAPQLKAEAAADKGLAPVPPPF SSGHSGPCERELEGQRGRGRSRRG AHLELKPSPLRAGAPTDRGRGGP AEVAAAGGRRMVQKESQATLEERE SELSSNPAASAGASLEPPAAPAPGE DNPAGAGGAAVAGAAGGARRFLC GVVEGFYGRPWVMEQRKELFRRLQ KWELNTYLYAPKDDYKHRMFWRE MYSVEEAEQLMTLISAAREYEIEFIY AISPGLDITFSNPKEVSTLKRKLDQV SQFGCRSFALLFDDIDHNMCAADK EVFSSFAHAQVSITNEIYQYLGEPT FLFCPTCYCGTFCYPNVQSPLYRT VGEKLLPGIEVLWTGPKVVSKEIPV ESIEEVSKIHKRAPVIWDNIHANDYD QKRLFLGPYKGRSTELPRLKGVLT NPNCFEFANYVAIHTLATWYKSNM NGVVRKDVMTDSEDSTVSIQIKLE NEGSDEDIETDVLYSPQMALKLALT EWLQEFVPHQYSSRQVAHSGAKA SVVDGTPLVAAPSLNATTVVTTVY QEPIMSQGAALSGETTLTKEEEKK QPDEEPMDMVVEKQEETHKNDN QILSEIVEAKMAEELKPMDDTKESI AESKSPMSMQEDCISDIAPMQTDE QTNKEQFVPGPNEKPLYTAEPVTLE DLQLLADLFYLPYEHGPKGAQMLR EFQWLRANSSVSVNCKGKDSEKI EEWRSRAAKFEEMCGLVMGMFTR LSNCANRTILYDMYSYVWDIKSIMS MVKSFVQWLGCRSHSSAQFLIGDQ EPWAFRGGLAGEFQRLLPIDGANDL FFQPPPLTPTSKVYTIRPYFPKDEAS VYKICREMYDDGVGLPFQSQPDIG DKLVGGLLSLSDYCFVLEDEDGIC GYALGTVDVTPFIKKCKISWIPFMQ EKYTKPNGDKELSEAEKIMLSFHEE QEVLPETFLANFPLIKMDIHKKVT DPSVAKSMMACLLSSLKANGSRGA FCEVRPDDKRILEFYSLKGCIEIAK MEGFPKDVVILGRSL
4627	10124	A	4926	3	251	HERHELQMLVDAPCSDLAQELRQS CATVQRLQHTLQQVLD/Q/REEVRQ SKQLLQYLLALYNEVSLLS*QDIF NVALDVCMCRS
4628	10125	A	4927	1	408	GTSLNSLSKTKAKDLFIGDVIHNA PHRDKKLYYIPEVVYSGLYPPYAG GGVGLYSGHLALRLNHIADSVQF*P R*DPYTVR*LLKPSSAGYDPTFVLLI GTDGIYTYTPSSCENGLGSCEEPHL MSFRSYFHG
4629	10126	A	4928	187	378	LCQKTMSTLFTHSFCFSVGRNMEGV

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						LMDVDCEVYPIV*ASN*GLASAEV GGSFEPRLRPAWAT
4630	10127	A	4929	26	121	PDRTMGG\REQRQSPGAQRTFFQLL LSFFVES
4631	10128	A	4930	3	867	
4632	10129	A	4931	1	558	EVRVKCVKALKGLYGIPDLTACL KLFTGRFKDWMVSMIMDREYSVA VEAVRLILILILK\NMEGVLMVDCE SVYPIV*ASI*GLASAVGEFLYWKL FYPECEIRTMGGREQRQSPGAQRTF FQLLL\SFFVESKSHFVTQGGGSGQF SAHRNLCLPGSGNFHVSASRVAGIA GAPHTWLIYVFFS
4633	10130	B	4932	1	1617	MKNGVQWAEAGHDYVLDLVSDL ELLRDFPRQKSYFIVGTEGPAASRG GPKVVFVGNWSDSDMSTRPQPE HMPKVLDSGYSNNDGTNGETE AQRGTATHQGQPTMAAVSESDSLG EPAVPHKGLDCYLDLFDVLSYGD ADLEKPTAIAYRMKGGGQPGGGSS SGTEDTPRRPPEPKPIGLDASTLAL QQAIFHKQAVLLAREMTLQATALQ QQPLSAALRSLPAEKPPAPEAQPTS VGTGPPAKPVLLRATPKPLRPAPLA KAPRIPIKPVAAAPVLAQDQASPETS HRDAATVTQMHLTGQGRLLSLD DSSLHLWEIVHHNGCAHLEELSFQ LPSRPGFDGASAPLSLTRVTVLLV AAGDIAALGTEGSSVFFLDVTTTL LEGQTLAPGEVLRVSPDDYRCGKA LGPVESLQGHLDPTKILIGYSRGLL VIWNQASQCVDHIFLGNQQLESCL WGRDSSSTVSSHSDGSYAVWSVDA GSFPTLQPTVATTPYGRACTPVAHD HIDELVRGAVFSEKHFCIEDL*
4634	10131	A	4933	1	811	HASAGAGCWHLPGLIEGAAQKGR GRQVIARTADVIMMLDATKGE VQRSLLEKELESVGIRLNKHKPNIFY KPKKGGGISFNSTVTLTQCSEKL LILHEYKIFNAEVLFREDCSPDEFID VIVGNRVYMPCLYVYNKIDQISM EVDRLARKPNSVGSSSCGMKLNLA DYLLAEMLWEYLALTCILHQGRR RDRRARFSQDAILRKASVEHVCH RIHR\SLASQFQVTPWVWGAPAPSY SPQAGGALHTTMEHEDVIQIVKK
4635	10132	A	4934	1	431	QRFPAAFPGVPGARRDAPPHSPAEC RAHAATWRLKPRPHRPHSLTAPLP VHWAGTTEPLPSRPATGTESARRC ISGDTQSFLRLARPCRQPGPS* DRCRPGVVSCLDREKNAGHWLSMAFS LLWVLATQHCLHPEESLTM
4636	10133	A	4935	56	252	GAQERGCPREKHGNAELAEGLVLIL RGRGKPPSASLAGRE*I*SRGPEWK VTVNQTAKAKERTGP
4637	10134	A	4936	81	896	CGLVTPACLDPWVGIAPLPDTLIVL RGGGSALLPAPIPPVTLEEKQTLTRL LAARGATIQLNTIRKALSQNLGGG

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						LAQAAYPEAQVVSILSDVAGDPVE VIASGPTVASSHNVQDCLHLNRYG LRAALPRSVKTVLSRADSDPHGPHT CGHVLNVIIGSNVLALAEAPAAGR TG\YQAVVLSAAMQGWGTPAAHR DDRYQCHGHPPLVPAASVMA*VTF WEFRGGLQGQGMAEQARLADGG FPLPLRMRTSPSASSAFPCFSLGQPL S
4638	10135	A	4937	100	332	NKPQPQLLYRIKLTSTPFHPIQKVGL RQMIDLNIPPRIIKLLEENIK*YLS DLGV\TK*KLTKFNFLKIKHFCSPSSC
4639	10136	A	4938	692	900	NKLLWLGAVTPACNPSTLGG*GGQI MRSGVRDQPVQHGE\TWSLLKIQKL AGHGWPAPGSPSCLAGLRQE
4640	10137	A	4939	87	322	ARLVQNTGAQLKEVQYKLFQGLF FE*/QSHSVAQAGYSAVIIAHCNLSL LGSSDPFFSAS*VAGTTGMCQHAW LIFDR
4641	10138	A	4940	91	356	GHAFLFGGYSSSHWPSTYPPHAPV PPPPSPPPYPSLPPFHSPLPIKPFPLPP /SPSPSPPSL*SPPTPPPTLLIPSPSPPP ASPLQ
4642	10139	A	4941	2	332	CGGPPGSPDTRGGSLIPQGV*AA\GP MEQVPLVAPSSAIPVPGSLSGTPSH QPVLGTHTPSCPGTYIPPPESSELP DCPAPGRQRPCPGQTPPTPCPSFI FSKQPR
4643	10140	A	4942	637	1560	VWQLDKSMRAAQPWAPAGGAAGS EWAGLKR\RPLGWSSFSPAAAQSP ELLGHPQSPWPSEAPWKACQVSF QGT/RVAASYHNAQHGTQHS SSC*GLGS*/CNSPTWARLSTHCPQ/HSR NTPRTQHCHPHYPPRGLAKRWLCGE GPNPYSHPLREGPLRRRVGRGMCK EVHLFYRAWHSGIHFPS/TPSRTSHQ DSPHLEN*TSPLIDLPTWAPPMCK RIL*KCTCNSLPQKPSMALQCI*NEI NKTSTTSPT\CLAPH*APATLACSPF LQPAELLPISGTLHVIFHPRTLFPKS RTGSFLSSPQVSV
4644	10141	A	4943	2	335	ALHPTLTLDLYFTIYTKIHST*IVDL DVKPKTLKLEESIR/VKLCDLRLSK ISWILKAQSIEEQTDWDLKT*NNY SSNGTVKRIKRQVED\WHKV FARRI SDTGLVSRISC
4645	10142	A	4944	2	345	FFFFFFETESRSVAQAGVQWRDLSS LQAPPPG\SRHSLASAS*VAGTTGVC HHARLIFVFLVETGFHHVSQDGLN LLTS*SAGLGLPKCWDSEKLLLLFFFG DKSFRFCCPGWSTMV
4646	10143	A	4945	178	388	RREPLHPANLLLLFFFFFFEMESPSVA QAGVQWRDLSSLQAPPPGSCHSPT SLS*VAGRLRNKNCLNPDAW
4647	10144	A	4946	546	850	FSVLFFFESESCSVLQAGVQWRDL GSLQPPPPGSSHSPTSAS*VAGTTGT CHHTQLIFILVETGFHHIGQASLKL

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						LTS*FAHLGLPKFWDYRCEPPHPA
4648	10145	A	4947	169	358	GNGFLFCTQVEVQGAFL*YLNLLAP GVK\LFSCLTLLKPWDSGTFPTFSFN FFIYLAKEKGFNG
4649	10146	A	4948	1	145	ANSAAMP SLGCSASSGLVFWPQGL YLLGVVSVSPLPPTPTTVTFPEQI*LL SPQVSSSPVSEGSSQH*PA*SLRPFHV PRS/SPVSSLQPFAPAKSPGPSATCAF SAPSL SLLTLLASGDSSFWGPGPIQM SAGGSIVMCS*GLVFWPQGLYLLG VVSVSPLPPTPTTVTFPEQI
4650	10147	A	4949	1	295	GTSSRLRLHRTDELTA PSIYRSTKST LDGSLAANEREPFTLGKKPPFSDKP SIPAGRSLGEHLPKIQKPLPPTTER HDWSRRLAGKKPPVPKHGWVP*/R EDDNE*DELTA PSIYRSTKSTLDGSL AANEREPFTLGKKPPFSDKPSIPAGR SLGEHLPKIQKPLPPTTERHDWSR RLAGKKPPVPKHGWVP
4651	10148	A	4950	119	1036	HASCLKTQALQEC SVGVGGGLPVS PAGPPRCFCPALPAAALALQGT FPA TGG*AWGLSSPDWTFSTKKLV MES ARSHGEGGAQGPATLTGPPGEGAL RASQ/PGTAGSELRRHARGPAQICST RTR/PAPWWT*SLPPPGHSRAVGFD RCGPASP/GVPVNAVALPPSTCGE ESRLPQEEGGIHMA/PGTPLCSGDCI CCED*PQSRSGQFGADSL*RAKGGT LPSGPSARRRSPL*ASESASCCRRAS S\GPPAAQGERADSRALGTAPPGE G LALRPTGGIGTPPAGGSEDISREVD PAKRHGLGA
4652	10149	A	4951	2	1262	GSAAGSTYEPSSMRLEALQVLTLLA RGYFSMTQAYLMELGEVICKCMGE ADPSIQLHGAKLLEELGTGLIQYK PDSTAAPDQRA PVFLVVMFWTMM LNGPFSRFSADSEHPTLQASACDAL SSILPEAFSNLPNDRQMLCITVLLGL NDSKNRLVKAATSRALGVYVLFPC LRQDVIFVADAANAILMSLEDKSLN VRAKAAWSLGNLTD TLIVNMETPD PSFQEEFSGLLLLKMLRSAIEASKDK DKLSTISIYYFNGQENRKEKNWNER EYKLEIPYELCTEVD AINKWTAPWT SQAYNALTSVVTSCKNFKVRIRSA ALSVPKGREQYGSVDQYARIWNAL VTALQKSEDTIDFLEFNTVSSLR TQ ICQALIHLLKLG/RSASDLPLMKET LELSGNMVQSYILQSLKRSRIGR
4653	10150	A	4952	52	730	KSACDALSSILPEAFRNLPNDRQML CITVLLGLNDSKNRLVKAATSR\AL GVYVLFPCLRQDVIFVADAANAMV MSLEDKSLNVRKAAWSLGNLTD T LIVNMETPDPSFQGRVLWSPAENG YDQALEASKDKDKVKRHA VVRAL GNLLHFLQPSHI/GKTPHLQKFI*GSL SRALNLLF*QKLAMKVRWNACYA MGNVFKNPALPLGTAPWTSQAYNA

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						LTSVVTS
4654	10151	A	4953	3	363	HELEFEIKNTIPFILAP/N/NIKYLGIT/LTKYVLYLN/DLYAENYKTLMK*IRDLNGDPLSCKVKNLINKYMKÆILCSRIGKDSNIV*VSLLPQLACRLNAIPIKIPANHFVEVN*LILKFI
4655	10152	A	4954	179	438	ENIMSKTSTENCTKQCHFVHVN*YSIFFFFLRQSL/DSVTQAGVQWRHLGSLQAPPPGFTFSPRSLPSSWDYRCPPTSLANFFCILVETGFTVLARMVSI*PRAPPASAS*SARCKLHLPGSHRSPASASPVAGTTGARQQAWLIFVF
4656	10153	A	4955	1	264	QFPKPSPRGP/TPTKSLFHLSPPNQ*ISPPP*QLPPSLYQIPPTIRLSPLAESPSPLSVGLGGPLGWVGQLLCLSFPGPKHVEV
4657	10154	A	4956	3	369	HERHELVKEFNKVSGYKINAHKSVALLYTN/DDQAENQKSSTPFTIAAKSVK/YLGIYLTKEVKDLYKENYKTLKEIVDNTNKRKHIP*P*MGRINIVKMTTLPKAIYKFNSMPIKISPSHFG
4658	10155	A	4957	2	338	GCWDN*ISTCKRMKLDCSLMLHMKINSM/WIKDVNIKSSSYEK/NIGVNLPDNVLGNGFINMMPKAQASKEKINWDSAKLK/IRK*RQTEWEKLCANPIYSHLIPVLCYLYLV
4659	10156	A	4958	42	447	IELVTVLQFYRAFYLFERYAGFLFYYYFLFFVEIRFHYIFQAGLS/ELLGSSDPPTSGLPKCWDYRR/DHRTWPDMDQDFLMFHIFPKLFSFPDMCFLASE*PSANTWLLL VVQSSFSLLSHTYHPPGKASTLWFSA
4660	10157	A	4959	377	1220	FRKVVP LAESHPAVPG\GKVRTSRSPKSPPRALPT*/PGLFNPQCQRETPSLG/PPGQHP/VPGLNSKRKQIPHNE LVEQTLRSGLTSAQPAHPTGGYSCSKLRPGPLPNPGLCRCSDGRIPGDERPLALSRT*IHLRACTGPDAAAQVLPGLLPCPPHLPPLSGMFD SWLAPLPDPCQRPTPPQAPSSEANNQRSQAPGCGPHSLRDELQGCPCGPAQAFCRGSGLFQLTQLTGPLHGTR*RLSPKNSQALKPHM*AVGRILHWPPAARP GNSGRYPDD
4661	10158	A	4960	3	353	HEVPAKGPRPHLTDCPTTQDFLPGFSPRPASGPPPSLSLRLFQQPG*TVWSPGPPCPVVPDCTSASGQVPFLPPAFRFKNVF*PSRPSPGTRGGP/PP*VCTS R/PLP*TSEPQPPG
4662	10159	A	4961	301	343	TRMAHFWS*STKPSPMGPIQWSHMPGAFSESSSCHSHSAFLPPYFSHGPSNRPPIRALCRNLPLPLPNKPRAPSAADEDNSLNVEWYVPYITRPA*AALIKINQDGTFLVRDSSKK
4663	10160	A	4962	2	319	ARGPGPSGKSGARSGLGNTPRRGAGLGRVPWSLCY*EGVESGRPEGAGPGTSPGVGFIGAYHGRGVTKVGG

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						LPG/GQACGVWSDPKSPGEPVEPIPG GSWPPQREP
4664	10161	C	4963	109	372	MQAWINIRKSVYVIHCVNKIKXXX XXXXXXXXXXXXXXXXXXXXXXXXX XKLRELQPVKGHLQKPMADIPN GKKLKASTTKIMNKTSS*
4665	10162	A	4964	3	990	RTLRECYK/HI*ANELNNDDEMSKL KDA/TLLQLTQEEIETLYNNEIE*I M/NKLPTKKSPGPHGFTG*FYQMFQ EEFTPILSRL**KIKEEGTVPNLLYEV /SIIMIPKPKDITRPVSLMIIGAKIFK QNI*HTQVYAHIRIVYHDHNGFM QAWFNI*KSVYVIHCVNRIKDKNH MIVSIGA/EKAFDKIQHPFMVKTCT QERTF/FILLKGIY/NKPMADIPNGKK LKA\LPLRSGTRRVPDRFWKWQ/CP LPLLFSIVLEVLARAVRQEKEIKGM QIRKVVKLFTDGMILYVEKSKESTI KTSKLINRFNKGSEYKANIKK*VVF L*SSNQQT
4666	10163	A	4965	3	314	HENDSNPETDNRQEGPSQENIGRVS D/MAFVPSAWTASGGVAWGNPGES GSRTGGVRAETLAPRLQV*PAHLIG HPRSNGQGRPPWKAGKLKGCQEV LFRFAAF
4667	10164	A	4966	2	329	ARGECCRKAFCIYDCVIHE/CEEER KAFCIYDCVIHERIHNGEKLIEC*E CETSLSSNSVLIHQHRIHTAEKPYEC NECGKAFHRTSVFLQHQRFTGEQ LYKCNECWKTFRCSSRFIVHQRIHN G*KPYECNECGKAFHRTSVFLQHQ RFHTGEQLYKCNECWKTFRCSSRFI VHQRIHNG
4668	10165	A	4967	61	533	WTEPVRHPDIHSQKREPSLMPPTVT GPGTTNMLFQPHRGPEKSRVPLHSS SSSSSSSSSSSSSSSPKTF/FGAPK/LP PSAPTSPDLAQAS*GLKSWKPWSGE RRFGCSKQRRALPTAS*FQQQSHAA PETPSYVGQDQSPSPGG*RPSTSPG DSCFP
4669	10166	A	4968	22	482	GKGPVPPGGVCKSTLPPAKPWRGPP HLPLPLGL*EKALPRALGQWEGRES FWDQPGKLPLQN/PPRSLGVAMGT QAVEIPDGRLPDLSPTPAHSFSFLAL KPLLGEARVHFRASAWPLPTRAWT LDLPQLGWGFWDCLMALESRSSG ESPSLL
4670	10167	A	4969	146	1299	GAPGPWPTGTTWLPGAAGAVPDGP FLLPSSAALSRTAS*FSQPPVPPAL TVPWPRCGC*TSCPAVPQSP/GLPR TLVPACRGLPLSSVPSSPASRPKLPL HSPSSWSIPPEGSWGPLETTLPWPW L/PRLQSRHKKPALSAAWQGLVVD PSPHLLAFPLLSAQVHF*PGLRSW VGPFGLRKQP*HTGLSSLTTGCCP AWLTSWPRISQSERKAHP*CLPL*Q ALSPPISYFNLTVDLNRNDYHSASSS SSSSSSSSSSSSSRRLSWSPKHHLPL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LPSFILSWPQGIPRGLKNPGKTRGGL GWWKKGFLANWLSKKPRRKKGPS FPPLVL*FQGPRALVPRNPHPKLG ASSQSPSPWWGKRPKPKSPGNGTS WLPPK
4671	10168	A	4970	298	954	QVQGHEDFLGARNTTLCSSFSCPGP GILGAIELETVGWCEKVCMLRAEK GSPHCFVIPGPEPCSPRNPFLAGAGP ESKPWWVEAKQKP*SGLLLPLVVFS VPRS*NCEPGVGERSGRG\HLGFLQP GYP*PHQGFWEILQGQLSRLFPNSSL PPH/MPLKPQKSHSSHKQKGRGKN EEKTLCQVICRQRMGLVP*QHPTPC GAPPSPHHPQTTPPKQVPYL
4672	10169	A	4971	4	410	PIERPHELKHRLPHVQKLVEDVGDG VIPAALEEGQAGWSHGFLVFLVEIK SAEGP/PGPADSRVRGVRPQRSQSA GPA*RAGRQDGVCRSLGQGRGGGR ATSLVLHPPGYPGCWFSVGVPSLPQ YTGIRSSSPRTRG
4673	10170	A	4972	148	268	LQPR*PLTCAPPPCPVQTQTHPISVS QTLLGLEFCCSLSL
4674	10171	A	4973	397	1449	RSHPSGTGRRTSRLESWFLGVSCCK SKVREGPLGPA**AG*RGVRPQRSQ SAGPA*RAGKRQDGG/SPEPRAGVG GEVGTQSP/GPSGASGYPGMLVSKP VGGTSASWLPAGCPIPS*LS*QRSQ SPSSCLIGHLLALWAAFGLGVTSLP QYTGIRSSSPTA*ATVQGD SGHKGG TGGTGLGRGRNTQPDAAACGRGHR SPTR/RPHGNPNGNTGCAEGGQARS LLPKLAPKLPGWPVSPVAVG/PGD FGWRQAQYQSSLWDLSSPRNTLGR SATSAGPAPPALLGAGSGRSSGTSP AAPGCSSRCHCWASAPAGVSGGPG/ GRGAEAPPSTLAQRGSPPGAAIFP PACGIPP
4675	10172	A	4974	2	637	ARAKEV*DLYTERTK/PLLKEIKEDR NKWKHTSCLWIARLNIVKMSILCKL VHRLSAITIKI/PCWLCLAEIDKLILK/ FIWKFK/RSRVAKTVLKKRKRVRRL TLSNFKTYFRVTVIKIEWLWQKD KYIDQWNRIKSLEINSYICGLLIFYK SAKTIS*ENSVSWYLDNWIPTCERM KLAPYIIYKKIK/WIKDLNIRAIVKL IKENIGPGARL
4676	10173	A	4975	254	590	KARYILPDLMIGLDFFFFLGETKFP FAQPQGGHQDGLG*LKLTPPRDFP/C LTPPRSGNYRLGPPPLNFFVF*KKR GGPHVGQTGFELLT*KDPPPLASQR AEITGGTHHA
4677	10174	A	4976	103	378	CFLYSICRGADTQRRFKLSDSLINST ECLHVHCRGLEISLADCAYT*ILTK GNHNPLS*YTFMRN\AKQPVN*YHR CTETFSLTRMELLVSV
4678	10175	A	4977	2	327	RQCLALWPRLECSGVIIAHSLSHLL GSSDPPTSAS*VAGTTGMHHHAQL/ LFWVLIDTG*CYVAQTGLEPLNSGH

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						PPTSASQSAGIIGLRHRAQPCVFQSS QKRGPELF
4679	10176	A	4978	19	1009	KTTQQQONLFFSSAHETFTNTDHIL GHETSFDMF*HIQVI*STFLYHNVIK LEVNSRKISGKCPNMWKLNNTVLS NTKIINFNDNKQNETIKI/RAETNELE NR/RTEKIN*TKM*FFEMINTIDKSL AR*SRGKRHKLLISGMTNVVSHCVS LPTLFLFQSCFDYILTTLHFLINF/QN RFNNLYKMIRGY*QLYKN*FDKLH EMKNFL*/RY*LPILTQEEI/S/HLNSPI YILKIEIVLNLPTNKTW*TLKF/EE MIPIVHRLFQKQETLPNPFYEVSITPI PKI/QD/D*TKENFRPISL\VDKIPSK NLSNYICSRLNNASHPQRSTDPNLQ NF
4680	10177	A	4979	3	358	STSNAYHSNSLHQIKEKKNHTILSI DAEKAFYKIQEPLLAITL*NRNSGN/ FLNMLMTTY**PKVNVILIGNITPY* YFAFLP*KLRTQRSRLSSLFNVILK NPANVTVISINIKRK
4681	10178	A	4980	3	341	FFETESNSVAQAGVQWHDLGSLQP PSPGSSNSPASASRVAGITGACPNV QLISVGFLFFVFWFFETESLSVAQA TGVQWVRSWAYCNRLPGSGRFLC LCLPSSWGLQGV
4682	10179	A	4981	658	1001	LILSARPPKGEKGSFLAEFSSYFHS GLFSSARSFFFFFFFETESHCVQAQA GVQWDLGSLQPPPPGSSNSPASAS QVAGTTGVCHHAQLIFVLLVETGF HHVGQAGLELLTS
4683	10180	A	4982	53	394	PQQSGFWFIYFSKQGCFFVNILNIC SFVLFFFETESCSVAQAGVQWHDL GSLQPPPPGSSDSPASASRVAGITG ACHQTWLFVFLVDMGFRHVQAS LKLLTSGFKKWT
4684	10181	A	4983	66	516	HFYQFFPHFSGRMDLWSSLLCHFF MTSQFVTFVFLYFIFVYILSV*LD F*MRKQT*LISG*ASI*YRYV*LQNL YVLKLYITPLSL*AHVLIYL/CYLKS ESHSVTQAGVQSHNLSSLPPRFK*FP CLSLPNG*DYRNVPPHPANFCIS
4685	10182	A	4984	3	324	HENRMKYEISINMWKLNNIFLNKL WVKEITSRLQKYFECSENKTTTYQK L*DAKIKMNQCQGYLWVFMALSA* ISKRKRLLINYSFYLSKLEK*EPTK PKASSRKVV
4686	10183	A	4985	108	277	ARVIRANFCIFGKDRVSPCCPG/W/ SPELPGLKRSPSLPKCWDYP*AT APGQHPYS
4687	10184	A	4986	29	454	
4688	10185	A	4987	116	424	
4689	10186	A	4988	1	1217	PPTTCTPACQGLSGAAMKSLVLLC LAQLWGWHSAPHGPGLIYRQPNCD DPETEEAALVAIDYINQNLPGWYK HTLNQIDEVKVWPQQPSGELFEIHD TLETTCHVLDPTPVARCSVRQLKEH

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						AVEGDCDFQLLKLDGKFSVVYAKC DSSQDSAEDVRKVCQDCPLLAPLN DTRVAHA EKAALAAFNQNGS\N FQLEEISR\AQLVPL\PPS\TYVIEFTV SG\TDCVAK\EATEAAKCN\LLAEKA IMAFVKATLK*ESLGGGRRRLQLTCT VFQTQPCDLHSPNPEGANEAVPTP VVDPADAPSPPLG\APG\LPPAGSP PELPCFYWAAPP\HQLHRAHYD LR\HTFHGVWVFIGGHPSGRKCSHP PGKHGTVGSSLVFWCCCLGPVVP SIVPG\IRHFKVLG
4690	10187	A	4989	1	443	KKFVIPDFEFTGHVGRIFEDVKELT GGKVAAYIPQLAKSNPDLWGVSLC TVDGQRHSVGHTKIPFCLQSCVKPL TYAISISTLG/DYVHKFVGKEPSGLR YNKLSLNEEGIPHNPMVNAGAIIVS SLIKMDCNKA EKDFVLQHLNKK
4691	10188	A	4990	3	217	ATKRKKKMKDKDKAKLLEAMGTS KTNEEDKRRGLDKRTPDQAAFEKM QEKRD FSRHLDL TEHYDIPKVHH
4692	10189	A	4991	3	475	AATESGMVAYYQVQKGPLKLKG VAKLGVT/KVRPEGPRDSVFIPLKP FLGTPGDPPTRRLLMFFSRKKKKK DKDKAKLLEAMGT\SKKN\EEEEKR RGLADKRTPAQAAFEKMQEKRHME RILMKA\SKTHKQRVEDFNRLGTL VTEHYDIPKVITWTK
4693	10190	A	4992	783	5158	PDKSGRRRDVEGGVCCFLSLLRNSR YLLSTHILERGKKASLCHPGWNAL VPSPLTAASASWVQVILLPLSLPSG WDYSLHLEELTGESPTSERAFNYH PTTCLRRKILQDSEHTASTRGPMTL DRPGEGATMLKTFTVLLFCIRMSLG MTSIVMDPQPELWIESNYPQAPWE NITLWCRSPSRISKFLLKDKTQMT WIRPSHKTQVQVFLIGALTESNAGL YRCCYWKETGWSKPSKVLELEAPG QLPKPIFWQAETPALPGCNVNILCH GWLQDLVFMLFKEGYAEPVDYQV PTGTMAIFSIDNLTPEDGVYICRTH IQILPATLWSEPSNPLKLVVAGLYPK PTLTAHPGPIMAPGESLNLRCOGPIY GMTFALMRVEDLEKSFYHKKTIKN EANFFFQSLKIQDTGHYLCFYDAS YRGSLLSDVLKIWVTDTFPKTWLL ARPSAVVQMGQNVSLRCRGPVDG VGLALYKKGEDKPLQFLDATSIDD NTSFFLNNVTYSDTGIYSCHYLLTW KTSIRMPSHNTVELMVVDKPPKPSL SAWPSTVFKLGKAITLQCRVSHPV EFSLEWEERETFQRFVNGDFIISNV DGKGTGTYSYSRVETHPNMWSHR SEPLKLMGPAGYLTWNYVLNEAIR LSLIMQLVALLLVVLWIRWKCRRRL RIREAWLLGTAQGVMTLFIVTALLC CGLCNGVLIETEIVMPTPKPELWA ETNFPLAPWKNLTLWCRSPSGSTKE

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						FVLLKDG TGWIATRPASEQVRAAFP LGALTQSHTGSYHCHSWEEMAVSE PSEALELVGTDILPKPVISASPTIRGQ ELQLRCKGWL AGMGFALYKEGEQ EPVQQLGAVGREAFFTIQRMEDKD EGNYSCRTHTEKLPFKWSEPSEPLE LVIKEMYPKPFFKTWASPVT PGAR VTFNCSTPHQHMSFILYKDGSEIASS DRSWASPGASAAHFLIISVGIGDGG NYSCRYYDFSIWSESPDPVELVVTE FYPKPTLLAQGPVVFPGKSVILRC QGTFFQGMRFALLQEGAHVPLQFRS VSGNSADFLHTVGAEDSGNYSCIY YETTMSNRGSYLSMPLMIWVTDTF PKPWLFAEPSSVPMGQNVTLWCR GPVHGVGYILHKEGEATSMQLWGS TSNDGAFPITNISGTSMGRYSCCYH PDWTSSIKIQPSNTLELLVTGLLPKP SLLAQPGPMVAPGENMTLQCQGEL PDSTFVLLKEGAQEPLEQQRPSGYR ADFWMPAVRGEDSGIYSCVYYLDS TPFAASNHSDSLEI WVTDKPPKPSLS AWPSTMFKLGKDITLQCRGPLPGVE FVLEHDGEEAPQQFSEDGDFVINNV EGKGIGNYSCSYRLQAYPDIWSEPS DPLELVGAAGPVAQECTVGNIVRSS LIVVVVALGVVLAIEWKKWPRLR TRGSETDGRDQTIALEECNQEGEPG TPANSPSSTSQRISVELPVPI
4694	10191	A	4993	1	369	GTFQLPKPIFWIEAETPALPGCNVNI LC\HGWLQDLVFMLFKEGYAKPVD YQVPTG\TMAIFSIDNL TPE\DEGVYI CRTHIQMLPTLWSEPSNPLKLVVA GGCGLWLLASGNCCPRYHGWLS
4695	10192	A	4994	183	429	ISIKSMKLISDYKYCIYIYRYHRDVI RLGIIDIYSVLHPTSAQYTFSSLHGT LTTRDNILGHKT\LNKFKRIEIRQYL FSDQ
4696	10193	A	4995	2	270	TSGCLOGSCC\TGPPGAVGRASRSR PSTRPPSRARPLGSPGCSARAQDAA DLPLPPPPPPCCSPSAGCRCSLGCF RRCPLRSSRRSRF
4697	10194	A	4996	1	428	NPCLSERQGCCEKLPLERSSTPQDS AGHPVT/HAHCSLPSVDLCPLLAT HRISCWHCQDEVQGGTD\ SADTGD LEALSLLAGHGD TDGHIILDVPDGA PYPQRTKAGIDHLHQILKIHIEQITIE HEARDDNAPDYPKLANN
4698	10195	A	4997	131	412	RKWLKLLPCSFFSSKNIYAETFSPCV CIRVCIHV CVYTCVYTCVCIHVCS PC/VGQASALKSVSLCQLHCILVLTP MLTLRFDKKFFTQDSHFI
4699	10196	A	4998	2	175	KFTWKHKGPRIARNILKRKIKVEGF TLPNFKTY YKAAVTETVWYWHKD SGLDHFVLL
4700	10197	A	4999	2	175	KFTWNHKGPRRIARNNLEKEN\KVEG FTLPNFKSYYKAAVTETVWYWHK DSGLDHFVLL

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4701	10198	A	5000	1	909	MVLEVSVSDRDAVWRLWRAPIGES QQRSLGFWSKVLPSADNYFFFER QLLACYWALLETDRLTVGHQVTLQ PELPIMNWVLSDPSSHKVGHVHQH SHKWKWYIRDQTRAGPEGTTTPVIT Q/WDAHEQSGLSGRDGKQGRFVLT GVDTSYSGYWFAYPAHNASAKTSIY GFTECLIHCHGIPHSIASDQGTLFTA KEVWQWAHAHGIHWSYHIPHPPIA AGLIEWWNGLLKSQLQCQLGDNTL QGWGKDLQKAMYSLNQRLIYSTVS PISRIHGSRNQRVEVEVAPLTITLSD PLAKFFFLP
4702	10199	A	5001	1	1014	
4703	10200	A	5002	349	718	AGPEGTTTAECP/I/CQQQRPILSLRY GTISWG/DQSATWWQVDYIRTLIS WKWQSASAKTTIHGLTKLIHHDIP HSIASD*GTCFMAKEVWQWYCFSH SQDSRVQESRGGIGSCTTHHPCSF PN
4704	10201	A	5003	1	558	
4705	10202	A	5004	1	2205	MGAVFEALWQYSPPELPAKASVMVQ EASKAIGQCQSSAAKLRRSGKESVT EPWARVLGALEMAARLYKVTSGH CHGIHTPSWRCLCFSTGGKERHAH DLPHVTAQSQGHQGGKISRALK EPTVHKVTASLSPVVATSPQPMPLP SDFPPLSEINPMLPEATVIASPEIA RQDNVDSPQEPPTPQFSSRPITRLK SQWAPRGPECVIGIDILSSWQNPHIG SLTGRVRAIMVGKAKWKPLELPLP RKIVNQKQYHILGGTVEISATIKDLK DTEAVTPTTSPFNPIWPVQKTDGS WRMTVDYCKLNQVVTPIAAAVPD V/VSLLEQINTSPGTWFEWSPKKAL QQVQAAVQAALPFGPYDPADPMVL EVSVADRDAIWSLWNAAGESQRR PLGFWSKALLSSADNYSPPERQLLA SYWALVETERLTVGHQVTLRPELPI MNWVLSDPSSHKVSGAQQRSIIKLLK WYIHDWVRAGPEGTTTSTVITQWAH EQSGHGGRDGGHAWAQHGLPLT KADLATATARIHRSRNQGVKVEVA PLTITPSDPLAKFLLISATSTSLEVT VPEGEMLPDRDTTKIATFGTQTGFL ALQLADGLLWDLVIIPGKGKPSRDL VESPSPYSTYEGIDGWPEAPTAT KPPVMPAPALPPDTRSGSKAPTVP PYPQMEHHQVQLASNNSTEALGH LSPQSSWVQTPGQNSGAIPNHLGK DMISPPQMAPAGVKWESQKY
4706	10203	A	5005	155	531	GNLWSVDLRPGTPLRQNFRTIRQQ HSRFTKNHCSQTPLLIPRQTGSGVD LSKLQQTCS*GSCLVCTIDLANAFFS IPVHKA/HQKQFAFSWQIYFTVLP LTWLQPC*VPNLPAETNTEPSNGT
4707	10204	A	5006	1	518	MTVDYCKLNQVVIPIAAAVSDVVS LLEQINTSPGTWYAAIDLANAFFSIP

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						VHKAQQKQFAFSWQGGQYTFTVLP QWYINSPALCHNLIRDLDCFSPL DITLVHYIDIMLIGSTIKWVVHSS/ DSIIKWKWYVHDWARAGPEGTTN GLAG*SGTCKKHEWKTGDKGIRGR G
4708	10205	A	5007	1	2592	MVRKAKWKPLQLPLPRKIVNQKH RIPGGTVEISAITKDLKDAGVVIPTT SPFNSPIWSVQKTDGCWRMTVDYC KLTQVMTPIAAVVPDVVSLKQINT YPGTCK\FLGVQWCGACRDI/PSKV KDKLLHLAPPTTKKEAQHLVGLFG FWREHIPHLGVLLQPMYQVTRKAA SFEWGLEQEKAQQVQAAVQAALP FGPYDSADPTVLEMSVADRVAVWS LWQAPIGESQWRPLGLWSKALPFS ADNYSPFERRLLACYWALMETEGL TMGHQVTMQPELPIMNWVLSDSPR HKVGHAQQHSIIKLKWIYCDQARA VPEGTC*LNKEVAQMP/MGTTRKW TAAALQSLSGISLKDSGEGKSSQWT ELQAVHLVVHFAWKEKWPGTWKK HDWKTGDNEIWGRGIWMDCSEWS KTVKIFVSHAHEPSGHGGRDGGYA WAQEHLSFTKADLATGIVECPICQ QQRPTLSPRYGTIPQGQTFILTGINT YSIYGFAYPAHNASAKITIRGLTECL IHGHPHS/IVSD*GTHFTAKDV\ET RIHRPRNQGVVEVAPLTITRSDTL AKFLLPVPTTFRSANLEVLLLEGGT LPPGDPTTIPLNWKRLRPRGHFGLPL PLSQQAKKGVSVLAGVTDLDYQDE FLLLLHNRVTAAPFSLHSSFAILD NMIEKANKCHVEGVDHVSQPAQRR ECDRHTGSSCHLLRGPQLQSQLVS GPRSPKSDSGESCLAWDPTFKAEVS PLAQGSPRNSVQEPSRGTGSPKSLG ALIALWPSWYLSSDPDPQGSNSRNL EISACQKYLSPAFGNSDYSTAEDFN SDYTLKSPENSIGYARLEKHRRLYG GDGGDGGGDDVRGGKRGDDASR KGVTERV
4709	10206	A	5008	1	942	MVGKAKWKPLELPLPRKIVNQKH HIPEGIAEIAATIKDLKDAGVVIPTTS PFNSPIWPVQKTDGSRMTVDYCK LNQVVTPIAAAVPDVVSFLEEINTSL GTWYAAIDLANAFFSIPVHKVHQKP FAFSWQG/QQYTFTVLPQDYINSLA L*HNLIWRDLDFLLQDITLVHYI DDIMLIGSNDHKVGGAAQQHSIIKWK LYIHDQAQTGPEGTTTSVIAQWAHE QSGPGSRDGGYAWAQQHGLPLTK ADLATTAAECPVCQQQRPTLSPRYG TIPSLPLTKALTQLKKCSSGPMLM EFTGLAMFPIILKQLD
4710	10207	A	5009	1	1795	MRKCGKPQFKLGQTNKANSRIQEE LIHKSLEQEKEKPVQFSAFHRMW QPADSQCIDIADSADIWADPLVRHREI

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						ITGSGGINRRRTRGGRGRGGEAAGG AENCGSREERERAGVGTAVTQLQN LNTIGIIGSRGGRGQVAAINHQRQG GHSYCKGQQKQNSNQNSVTHVEL WHWLNHVSVPREIDRKPTTFLNL YKQKTSRDLWPFTRVTLHRGKRND QTFQGLLDTGSELMLIPEDTKHHCG PPVKVEAYGGQVINGVLAQIQLTV GPVGSNGTHPVVIYPVPECIIGILSS WQNPHGSLTSRKTDGSRMVTVHY HKLNQMVTPIAAAIPDVVSLLEQVN TSPGSWYAAIDLANAFFIPVHKAH QKQFAFSWQGQQYTFTVLPQGETL VNFSLPQDITLFHYIDDIMIGSSDQ EVANTDLLPRKSTTPSG/LYGFWR QHIS/HLGLLTPIY*VTQKAA/SFEW GLEQEALQQVQATVQASPLGVY DPADPMVIEM/SLSDPSSHKVGAQ QHSIIKWKRYVCDQA*ASPEGTS*L YCTSFIMEKEEVC/LSLEQTLTDMG LPILHAMLLWIHLWIHGLPYPSSWY STQQCL
4711	10208	A	5010	3	169	DFQPFTRVTVHWGKGNDQTFRGLL DTGSELTLPDGPKHGYPVKVG AYGAQLL
4712	10209	A	5011	1	562	
4713	10210	A	5012	3	591	DPADPMVLEVSEADRDA\VPISSEQ QRPLGFWSKALPSSANNYSFFKRQL LACYWVLVEIEHLMGHQVTMRPE LPIINCVLSDPCSHKVGHQAQHSIIK WRWYIHDWAEGTSKLHEEVAQIPM VSTPSLPQPAPMASWEVPYDQLTEE EKTRAWFTDGSARHAGATQKQWTA VALQPLSGTSLQDSSEEKSSQWTEI
4714	10211	A	5013	2	586	
4715	10212	A	5014	3	514	
4716	10213	A	5015	1	994	MVRKAKWKPLQLPLPRKIVNQKQH RIPGGTVEISAITKDLKDAGVVIPTT SPFNSPIWSVQKTDGCWRMTVDYC KLTQVMTPIAAVVPDVVSLKQINT YPGTCKFLGVQWCGACRDI/PSKV KDKLLHLAPPTTKKEAQLVGLFG FWREHIPHLGVLLQPMYQVTRKAA SFEWGLEQEALQQVQAAVQAALP FGPYDSADPTVLEMSVADRVAVWS LWQAPIGESQWRPLGLWSKALPFS ADNYSPFERRLLACYWALMETEGL TMGHQVTMQPELPIMNWVLSDP SRHKVGHQAQHSIIKLKWIYCDQARA VPEGTC*LNKEVAQMPM
4717	10214	A	5016	1	643	MVGKAKWKPLELPLPRKIVNQKQH HIPEGIAEIAATIKDLKDAGVVIPTTS PFNSPIWPVQKTDGSRMVTVDYCK LNQVVTPIAAAVPDVVSFLEEINTSL GTWYAAIDLANAFFSIPVHKVHQKP FAFSWQG/QQYTFTVLPQDYNSLA L*HNLIWRDLDF\LLLQDITLVHYI DDIMLIGSNDHKVGGAAQHSIIKWK

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						LYIHDQAQTGPEGT
4718	10215	A	5017	3	1074	VTASLSPVVATSPQPMLPSDFPPLS EEINPMLPEATVIASPKFIARQDNVD SPQEPPPTPQFSSRPITRLKSQWAPR GPECVIGIDILSSWQNPHTGLTGRV RAIMVGKAKWKPLELPLPRKIVNQ KQYHILGGTVEISATIKDLKDTEAV TPTTSPFNSPIWPVQKTDGSRMTV DYCKLNQVVTPIAAAVPDV/VSLLE QINTSPGTWFEWSPKIKALQQVQAA VQAALPFGPYDPADPMVLEVSAD RDAIWSLWNAAGESQRRPLGFWS KALLSSADNYSPPERQLASYWAL VETERLTVGHQVTLRPELPIMNWV LSDPSSHKVSGAQQRSIIKLKWWYH DWVRAGPEGT
4719	10216	A	5018	1	1482	MAPNSRVQELVLGQVAVICQGLLS LQPRTEGYTVGFLTFEVLDLTGSSA CRWPVIGLHVSIIIDKVTKEKDEL RDSNSWLQKQILSLKFSKTALSES SCRQRAEIVENQTQGLIMRPLAFHR GNCIGERGMITLFRGYWTEPTLIPED PKHHCSPPVKVRA YEDGSWKMTV DYHKLNQVMIPVTAAPDVVSLLE KINTSPALFHNLVQRNLDLCSLPQDI TLVHYVDDIMLIGSSEGEVANTLDL LVRRLCAKGWEINLTKIQGPSSLVK FLGVQWCGASQDIPSKVKNKLLHL ALPTTKKEAQCLVGLFGFWKQLIPH LATPIIPQRAHEQSGHGGRRNGGYTW AQQHGLPLTKADLATATAECPICQQ QRENGA/PRYGTIPRGDQPATWWQ VDYVGPLPSWKGGQFVLTRIDTYS AYGFAYPTCNASAKTTIHSLTACLI HRHGIPHSIASDQGSHTAKEVQQW AHAGHIHWSYHVPYYPEATGLIEW
4720	10217	A	5019	1	1494	
4721	10218	A	5020	101	304	
4722	10219	A	5021	1	1912	MTVDYCKLNQVVIPIAAAVSDVVS LLEQINTSPGTWYAAIDLANAFFSIP VHKAQQKQFAFSWQQGQYTFVLP QWYINSPALCHNLIRDLDCFSPL DITLVHYIDDIMLIGAPRQLLACY/W ALVETEHLTISHQVTRPELPIMNW VLFDPSSHKVGCAQQHSIIKWKWY VHDWARAGPEGTTTTVISQWPHEQ CGHGGRDGGYAWAQQCRLPLTKA DLNTATAKRPICQQQRPTLSPQYGT IPQGDQPATWWWVDYMGSLPSWK GQRFVLGTIDTYSYGFAYPACNAS AKTAICGLTECLIHHDIPHHSIASDQ GTHFMAKEVRQWAHDHGIHWSYH VSHHPEAAGLIEWWNGLLKSQQLQC QLGDNTWQGWGKVLQKVYALN QHPIYGTVSPIAKIHRSRNQGLEVAP LTITPRDPLAKFLLPFATLQSAGLE VLVPEEGTLPPGDTMPLNWKLRP PRHFGLLLPLNQQAQKGVTVLAGV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						TDDYKDEITLLLHNGGKEEYAWN TGDPLGLLLILPCPMIKVNGKLOQL KPEALVPKGVVFPPGDTTMLSLSW KLRLPSGHVGLLMPLSQVQKGV VLAGVIDPGHTSAASLVRSCVWS GSDTIVSPGSQDFRLGINDTTGFPV PD
4723	10220	A	5022	3	835	DLWPFTRVTVH/WGKANDQTFQGL LDTGSELTLIPGYPKRHCCPPVKVR VYGGQTDGSRMTVGYHKLNVV TPIAAAVPDVVSLEQINTPPSTWAY GQVAAPPTTKKEAQLVGLFDF GGNTLLIWVYSGPLSSDLKGCQFE WDPEQERLCKAFSAHSQWFGCQGL GRSVDWKIDDKLKGKRRMDLSE LGKNREEYWYPVQQAQKGVKVL VVIDQTIKMKSVYYFTMEKTCQRQ ATTAELEPEKNVIGVDETVEGQSYH SSKQKDIPFQGEK
4724	10221	A	5023	2	1300	DLWPFTRVTLHRGKRNDQTFQGLL DTGSELMIPEDTKHHCGPPVKVEA YGGQVINGVLAQIQLTVGPVSGT HPVVIYPVPECHIGIGILSSWQNP SLTSRKTDGSRMTVHYHKLNV VTPIAAIPDVVSLEQNTSPGSW YAAIDLANAFFIPVHKAHQKQFAF SWQGQYTFVLHQGYNSPALYH NLIWRDLDRFSLPDITLIHYIDMT LIGSSEQDVANTDLL/SDLSRGGF* *SSG*DDPFCGHHSASFSPHCNRP MGP*TK*PWGQGWRLRMGSATCTP THQG*PGYGHC*VPNLPAETNTKP SIWHHSSG*SASYQAAG*LYWTSFI MERA EVRP/TWSTCLLWIWVCLSCT QCFCQDYHLWTHGMPYPLSRYSQA HCL*PRHSLYS*RSVAVGSCSWNSL VLPCSPSS*SSWI
4725	10222	A	5024	2	790	PRGRNRRRKTFQERRMTL NESPEKI GKWIECYGHPASKLVEIYHTVFV EDKLSICIRSFNKKADGSRMTVD YCKLNQVVTAAAAIPDVVSLEQI NTSPDTWYAAIDLANALFSIPVHKG YINSLALCHNVIWRELDLCSLPRDT TLVHYIDIMLIGSSVQEVENKLDL LVKD KLLHLAPPTTKEEVQHMVGL FGFWRQH IPHLGV LHQPIYRVIRKA A/SFEWGPEQE KALQQVQAAVGGK QSENNLGHQRSPGLWFS
4726	10223	A	5025	281	1461	VRVLSPEKELKLWKNTHKLLSYP TVGAAVTQLQNL TAMGVIGSHGAR GQVVALNRQRQGLQPFTRTVH WGKG/NMQIFGGLD TGSELTLIPG DPKHHC GPPVKVGAYGGQVINGVL AQVQITVGPQTHPVVISPVPECHIGID ILSSWQNP HIGSLTGIMVGKAKWK QLELPLPRKIVNQKPYCIPGGTVEIS ATIKDLKDAGVVIFTTSLFNSPIWPV QKTDGSRMTVGYRRLNQQVVTPIA

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						AAVPDVVSLLEQINTSPGTWYAAID MANAFFSIPVHKAHQKQFAFTWQG QQYAFTVLPQGYINSPALCHNLIWR DPDCFLLLQNITLLVHYVDDIMLIGS SEQEVANALDLLVFSHLAIKWVM HSSIASSSGSGICVIRLKKVLKAQ
4727	10224	A	5026	1	3179	MAEDKEEQVPSYTDGSRQRENEED TRVKTPDKTIRSHETYSLPREQYGG NYAHSIIISHQVPPTTCGNYGSTIQD EIWVGHDHSGYVRPVPVPRSLNSDIS YFGVGGKQAVFFVQGSARMISKPA DSQDVHELVLKEDFEKKEKNKEAI YSGYIRNRKDDYDNHTGIDLVTII ATIKGSNEEDTDPLFIGKVRTLEFP FVNGSAEIMLMPSNQQHKTDKGR ANLGVFSVFAPRGEHTLQVKAIYN KSIIEGPIIKLMILPDEKPVRLNVKY DKDASFLAGGLFTAPPLPAQLMSSL SCAWIIESVLNSWRKGCNKLNRQR ALHKKQDRGKLPEDRELQHTKKQT NWAGLLIPAMNNNVDMTARKLQR DLQPFTSVTVHCRKGNDQTFGGPL DAGSELTLPDGPKHHCAPPVKVGA YGGQVINGVLA\HPLIWL VQKT DGS /WRMTVDYCKLNQVVIPIAAVSD VVSLEQINTSPGTWYAAIDLNAF FSIPVHKAQKQKQAFSWGGQYTF TVLPQWYINSPALCHNLRDLDCF SLPLDITLVHYDDIMLIGSSEQEVA NTLDLFVRHLRARGWEINPTKIQGP STSVKFLGFQWCGACQAIPSKMRD KLLHLVPPTTKKEAQLQLLACY/ WALVETEHLTISHQVTMRPELPIMN WVLFDPSSHKVGCAQQHSIIKWKW YVHDWARAGPEGTT/HPCHFPMAP *TMWPWWQGWRLCMGSAM*TST H*G*PEYSHR*APNLPTAETNTEPSI WHHSSG*STSYLVVG*LYGISSIMER AEVCPHWNRYLLWIWVCLSCMQC FCQDCHLWTHGMPYPPS*YPTQHC L*PRHSLYG*RSAAVGS*SWNSLV PCFPSS*SSWIDRMVEWPFEVTITVS TR*QYLAGLGQSSPEGRVCSASNI WYCFSHSQDSQVQESRARS GTTHH HP*GSTSKIFASFSCNITVCWPRGLS SRGRNAATRRHNSIKLEVKIATQT LWAPPTFKSTG*EGSYSVGWGD*PG L*R*NHSPTP*WR*GRVCMERYRSI RASLNITMPYD*GQWETTQAARSS
4728	10225	A	5027	2	1284	CHCGPP/VKVEAYGSQVLKGVLAQ VQLTVGPVGPRTHPVVIFPVPECIIGI DMLSSRQNPHTGSLTGRVWIMVR KAKWKPLELPLPRKIVNQKQYHIPE GIVEISATIKDLKDAGVVIPTTSPFNS PIWPVQKTDGSRMTVGYCKLNQ VVTPIAAAVPDVVSLLEQINTPPGT WYAAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTFVLPQGRWEINMT

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						KIQGPSTSVKFLGVQWCGACQDIPS KVKDKLLHLVPPTIKKEAQCLVGLF GFWRQHIFHLGMPLOPIYRVQMA ASFEWGSVEQEKALQQAG\QAAVQA ALPLGP/HKDPADPLVLEVSVDSDR AVWRLWQASI/GHKVGHAQQHSIIK WKWYIRDWARADPEGTTKGQGQR RWWQLAERQDSRDREAAIGERQET AVGKTARDGEAVCD
4729	10226	A	5028	422	1252	TTLFSVQIFQWRQLENLYFREKKFS VEVHDPRRASVTRRTFGHSGIAVHT WYACPALIKSIWAMAIHQHYLD RKQSKSIHAARSLSEIANDLTRTRT LENSKLANMGSKGKIISGSSGSLSS GSGARRHCILLPGSQESDSSQSACK DMLAALKSRQEALLETLRQRLEEL KKLCLREAELTGKLPVEYPLDPGEE PPIVRRRIGP\AFKLDEQKILPKGEEA ELERLEREF\AIQSQITEADRRLASDP NVSKKLKKQRKTKYINAVKKLQVY
4730	10227	A	5029	1	400	RHEERTTGILTSEGLASDTSLICVIED FFDTALISRSSEGGKIQMLDSFLLSL GFLVTEKTVNHLLQQEERPCMDTL DCG/LQVAISEALCRLTIKKSRLDELV HKWFDDEVIAEAFKEIKDREFETDS RRFLN
4731	10228	A	5030	1	612	
4732	10229	A	5031	64	323	LFPTLWLLDLLGTVEEILPSLSENIS VWGMKDSVPQGVISLKEKL\STSPD EPVPRSHHVVSLLKSTCLYFTSG\T TGMIOFFWKA
4733	10230	A	5032	287	508	YYSIFLIYYYYYFLRWSFALVAQAV VQWCDLGSLLQPLSPGFKRFS\PSALS SWDYRHEQPRPANFIFLVETGFL
4734	10231	A	5033	1	3627	
4735	10232	A	5034	3	3613	
4736	10233	A	5035	353	406	MLHLQGIILMIVLYSCCRELIHSFLK DSKSMPCNWGESDGPVTGARHPSW EEEEDEGGVWNTTGSQGSASSHNSA SWGQGGKKQMK/CSLKKE
4737	10234	A	5036	1	514	ECKDCGKSFTVSSSLTEHARIHTGE KPYECKQCGKFTGRSGLTKHMRT HTGEKPYECKDCGKAYNRVYLLNE HVKTHTEEKPFCTVCRKSFRNSSC LNKHHIHTGIKPYECKDCGKTFTV SSSLTEHIRTHTGEKPYECKVCGKA FTTSSHLIVHIRTHTGEKPYICK
4738	10235	A	5037	1	3222	
4739	10236	A	5038	1	4267	MGPWAWKLRWTVALLAAAGTA VGDR CERNEFQCQDGK CISYKWVC DGS AECQDGSD ESQETCLSVTCKSG DFSCGGRVNR CIPQFWRC DGQVDC DNGSDEQGC PPKTCSQDEF RCHDG KCISRQFVCDSDRDCLDGSDEASCP VLTCPASFCNSSTCIPQLWACDN DPDCEDGSDEWPQRCRGLYVFQGD SSPCSAFEFHCLSGECIHSSWRCDG

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						GPDCKDKSDEENCAVATCRPDEFQ CSDGNCIHGSRQCDREYDCKDMSD EVGCVNVTLCCEGPNKFKCHSGECIT LDKVCNMARDCRDWSDEPIKECGT NECLDNNGGCSHVCNDLKIGYECL CPDGFQLVAQRRCEDIDECQDPDTC SQLCVNLEGGYKCCQCEEGFQLDPH TKACKAVGSIAYLFFTNRHEVRKM TLDREYTSILIPNLRNVVALDTEVA SNRIYWSDLQSRMICSTQLDRAHGV SSYDTVISRDIQAPDGLAVDWIHSNI YWTDVSLGTVSADTKGVKRKTLF RENGSKPRAIVVDPVHGFMYWTD WGTFAKIKKGGLNGVDIYSLVTENI QWPNGITDLLSGRLYWVDSKLHSI SSIDVNGGNRKTILEDKRLAHPFSL AVFEDKVFWDIINEAIFSANRLTGS DVNLLAENLLSPEDMVLFNLTQP RGVNWCERTTSLNGGCQYLCLPAP QINPHSPKFTACPDGMLLARDMRS CLTEAEAAVATQETSTVRLKVVPD KTVRWCAVSEHEATKCQSFRDHM KSVIPSDGPSVACVKKASYLDCIRAI AANEADAVTLDAGLVYDAYLAPN NLKPVVAEFYGSKEDPQTFYYAVA VVKKDSGFQMNQLRGKKSCHTGL GRSAGWNIPIGLLYCDLPEPRKPLE KAVANFFSGSCAPCADGTDFFQLC QLCPGCGCSTLNQYFGYSGAFKCL KDGAGDVAFVKHSTIFENLANKAD RDQYELLCLDNTRKPVDEYKDCHL AQVPSHTVVARSMGGKEDLIWELL NQAQEHFGKDKSKEFQLFSSPHGK DLLFKDSAAGFLKVPQRMDAKMY LGYEYVTAIRNLREGTCPEAPTDEC KPVKWCALSHHERLKCDEWSVNS VGKIECVSAETTEDCIAKIMNGEAD AMSLDGGFVYIAGKCGLVPVLAEN YNKSDNCEDTPEAG\YFAVAVVKK SASDLTWDNLKGKKSCHTAVGRTA GWNIPMGLLYNKINHCRFDEFFSEG CAPGSKKDSSLCKL\CMGSGNLNCE PNNKRGDTTGYTGAF\RCLVEKGD VAFCKHQTVP TGTGGEKNPD PW A\KDLNEKDYELLCLGWVPGKPV\ EEYAN\CHLARAPNHRCSHGKDK EACVHKILRSTASHLFG\SNVTD\CS GNFWLVRSETKDLL\FRDDTVCLW AKLHDRNTYEKYLGEYVKA VGN LRKCTSSLLEACTFRP
4740	10237	A	5039	2	342	LSRVVL SAAATAAPSLRNAA\FLGP GVLQATRTFHTGQPHLVPVPLPEY GGVRYGLIPEEFFQFLYPKTGV TG PYVLGTGLILYALSKEIYVISAETFT ALSCSAFELFRDHF
4741	10238	A	5040	53	940	DCYLDVSLTMSRVVLSAAATAPT IIMKNA AFLGPGVLQATRTFHTGQP HLCPMY\PIPEY\GK VRYG\LIPE\

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						FFQFLY/PLKTGVNTDPNVPPETWG LNLVTVLFQRKYMVEFRRRGPSLA LIKY*GGKWVYGNLKKYGSPLVAG LWLD*TPMEQKLGPT*EE/ARQGGF PSQHIQN\AIDYGRSLYQALVQKRH YLF\DVQRNNIAMALEVTYRERLYR VYK\EVKNRLDYHISVQNHDAVRN GTTNSLLNW\VE\KHVRAKLFPQA RKEDILPKWHCRPIKLLAKEGSKAQ AQLW
4742	10239	A	5041	2	205	APVTSW/IQPKDGSCPFSESTKISLY ISSEQQFHLPRPSESDDFIEDTADMLA VSFSGYSSAPKNQEQ
4743	10240	A	5042	1	360	SPCLSERQFCCEKLPLQRSSRPQDSA GQPVT/HAHCSLASTVDLCPPLLAT HRISCWHCQDEVHGGRD\SVDKGD LEALSLPAGHGD TDGPISLDVPDGA PDPQRTKAAIDHLHHKILKSTE
4744	10241	A	5043	106	396	
4745	10242	A	5044	77	4026	
4746	10243	A	5045	1	344	LDFIQTMLQVVGVSVAVPV/IPWI AIPLVPLGIIFLRRYFLETSRDVKR LESTTRSPVFSHLSSSLQGLWTIRAY KAEERCQELFDAHQDLHSGLSISGN GFKGQDLLFLA
4747	10244	A	5047	3	378	ERDGALTPLTPGLPSPPLPP/HTSS QAHYRLSAFGQQFLFNLTANAGFIA PLFTVTLLGTPGVNQTKFYSEEEAE LKHCFYKGYVNTNSEHTAVISLCSG MLGTRSHDGDYFIEPLQSMDEQE
4748	10245	A	5049	2	278	FVNHGCSQ/TLHFVFKVGNRFQTAR FYRDVLGMKVQAGADRGWRARLE PAPEPALAEGGENGCVVNLSRRVS DLRPCAVFSFRSVASCRWGS
4749	10246	A	5050	1	1539	MRLTPFSLSTGNSFRYSRRLKKNIFG TAPALRVSEMSLRPSSRIFFCFSRNG LDFTIVITLAQPPVPGISFIVAKPRLF PGAGSAGCGLLERLFLSLLGTGLR WCLRGCFPGARFCSTTSPEGHTTFT GLRRSARTQLAQQPKPGPPAATV ARQTSRVSPAPPCSLRPLRHESAPS GIGDVTARGALRGLGCTVRVTAAC GGNHGCSQ/LCLHFVFKVGNRLQT AAFHIGTSMGMKVQQHEEFEEGCK AA\CNGPIYDG\KWSKTMVG/YLGP EDDHFAELTYNYGVGDYKLGND FMG\ITLA\SSQAVSNARK\LEWPLT EVAEGVF\ET\EAPGGYKFYLQNRSL PQSDPVLKVT\LA\VDLQK\SLNYWC NLLGMKIYEKDEEKQRALLGYAGL TSVSLELQGVKGGVDHAAAF\GRI AFSCPQKE\LPDLAEDLMKRENQKIL TPLVSLDTPGKATVQVVILADPDGH EICFVGDEAFRELSKMDPEGSKLLD DAMAADKSDEWFAKHNPKASG
4750	10247	A	5051	21	223	HPGSRGCSEPRSGHCTPAWGTVKVK T/SRLNKNKTKQKKEVKDCMSSTPL

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						AHPPGVWCEWRGLIPSSSP
4751	10248	B	5052	64	543	RGWKRDRDKRDDQDDVSSVRSEG GNIRGSFRGRGRGRGRGRGRGN PRLNFDYSYGYQEHGERTDQPFQTE LNTSMYYYYDDGTGVQVYPVEEA LLKEYIKRQIEYYFSVENLERDFFLR GKMDEQGFLPISLIAGFQRVQALTT NLNLILPPLKDSTE*
4752	10249	A	5053	1	567	AAATSAGA/PGRAVAGAGAGTQRA PGGCPREAPGAAPG\HKARGPGGPF GGEPPPPPP/LVAVAAVAAGSAGR GRPGR\VAAGPAEKRPPLPPKGN PWTKKPPQHLSPDTTGPPPPLETLE AEFGSLKIIKAGKLKTKKSNKASDF SDMENWPTPSELVNTGFQSVLSQG NKKPPNRKEKEEKGEREEQ
4753	10250	A	5054	3	763	SGRPHPVIRESSPSSSLALGGQLGRG RPSGRAAPGRANPSAPAGGPAREGP EFGSLKIIKAGKLKTKKSNKASDFS DMENWPTPSELVNTWISERPQPRK\ KKPQNRKEKEEKVEKRSNSDSKEN RETKLNGPGENRQ/STDEAQSSNQR KRANKHKWVPLHLDVVRSESQERP GSRNSSRCQPEANKPTHNNRRNDT RSW/ESEIEKKE/HDQDDVSSVRSEG GN\SRGSFRGRGRGRGRGRGRGRG NPRLNFDYSSC
4754	10251	A	5055	1	372	RHEQGISFLETESTFMTDQLVDALT TWQNKTKVGLLWSAIAHIRFKPTLS QQQKSPEQHETVLDGNLIIRYDVDR AISGGSIQTREALIKILDDLIPRDQFN LIVFSTEATQWRPSLVPASAEN
4755	10252	A	5056	1	1021	AQAQYSAAVAKGKSAGLVKATGR NMEQFQVSVSVAPNAKITFELVYEE LLKRRLGVYELLLKVRPQQLVKHL QMDIHIFEPQGISFLETESTFMTNQL VDALTTWQNKTKAHIRFKPTLSQQ QKSPEQGETVLDGNLIIRYDVDRSIS GGSIQIENGYFVHYFAPEGLTTPK NVVFVIDKSGSMSGRKIQTREALI KILDDLSPRDQFNLIVFSTEATQWR PSLVPASAENVNKARSFAAGIQALG GTNINDAMLMAVQLLDSSNQEERL PEGSVSLIILLTDGDPTVGETNPRSI QNNVREAVSGRYSFLCLGFGFDVS YAFLEKLALDNGGLGRG
4756	10253	A	5057	570	831	HGNYRNVICILLGLFYPHFVGEKKIH IGFFLFFPAIDLKSGSGKVYQGPAGK AADTTILSDEYFMEVVLGKLDPOK AFFSGRLKAEG
4757	10254	A	5058	1	2229	MGSPFRDGRVVLVTGAGAGLGRA YALAFARGALVVVNDLGGDFKG VGKGSALADKVVEEIRRRGGKAVA NYDSVEEGEKVVKTALDAFGRIDV VVNNAGILRDRSFARISDEDWDIIH RVHLRGSFQVTRAAWEHMKKQKY GRIIMTSSASGIYGNFGQANYSAAK LGLLGLANSLAIEGRKSNHCNTIAP

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						NAGSRMTQTVMPEDLVEALKPEYV APLVLWLCHESCEENGGLFEVGAG WIGKLRWERTLGAIVRQKNHPMT EAVKANWKKICDFENASKPQSIQES TGSIIEVLSKIDSEGGVSANHTSRAT STATSGFAGAIGQKLPPFSYAYTELE AIMYALGVGASIKDPKDLKFIYEGS SDFSCLPFTGVIIGQKSMGGGLAEI PGLSINFQVLHGEQYLELYKPLPR AGKLCCEAVVADVLDKSGSVVIIM DVYSYSEKELICHNQFSLFLVSGGG FGGKRTSDKVKVAVAIPIRPPDAV LTDTSNLQAALYRLSGDWNPLHID PNFASLAGFDKPIHLGLCTFGFSARR VLQQFADNDVSRFKAIKARFAKPV YPGQTLQTEMWKEGNRIHFQTKIV QETGDIVISNAYVDLAPTSGTQAKT PSEGGK\QITVFEEVIGPRLKDIGP VVVVK\KVNAVFEWHITKGGNIGAK WTIDLKSGSGKVYQGP\AKGAADT TIH\ILSDEDF/LWEVVLGQA*PSRKA FFSGRLEGQEGNIMLS\QKLQMIL\K DYAKL
4758	10255	A	5059	1	7449	
4759	10256	A	5060	1	7458	MTDSKPITKSKSEANLIPSQEPFPAS DNSGETPQRNGEGHTL/HQDTQPGR ASLPQRPQ\SGRRRNSLPPSHQKPP RNPLSSSDAAPSPELQANGTGTOGL EATDTNGLSSSARPQGGQAGSPSKE DKKQANIKRQLMTNFILGSFDDYSS DEDSVAGSSRESTRKGSRASLGALS LEAYLTTELLALDFGIFGIRGSLVFA GYPLTLLHTYRQGSNTSSLVFTGLG SGFIELLGCPRLPQQKAAVQRPMS GLHLVKRGREHKKLDLHRDFTVAS PAEFVTRFGGDRVIEKVLIANNIA AVKCMRSIRRWAYEMFRNERAIRF VVMVTPEDLKANA EYIKMADHYV PVPGGPNNNNYANVELIVDIKRIP VQAVWAGWGHASENPKLPELLCK NGVAFLGPPSEAMWALGDKIASTV VAQTLQVPTLPWSGSGLTVEWTE DLQQGKRISVPEDVYDKGCVKDVD EGLEAAERIGFPLMIKASEGGGGKG IRKAESAEDFPILFRQVQSEIPGSPF LMKLAQHARHLEVQILADQYGNA VSLFGRDCSIQRRHQKIVEEAPATIA PLAIFEFMEQCAIRLAKTVGYVSAG TVEYLYSQDGSFHFLELNPRLQVEH PCTEMIADVNLPAALQOGFKPSSGT VQELNFRSSKNVWGYFSVAATGGL HEFADSQFGHCFWGENREEAISN MVVALKELSIRGDFRTTVEYLINLL ETESFQNNIDITGWL DYLIAEKVQA EKPDI MLGVVCGALNVADAMFRTC MTDFLHSLERGQVLPADSLNLVD VELIYGGVKYILKVARQSLTMFVLI MNGCHIEIDAHRLNDGGLLLSYNG

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						NSYTTYMKEEVDSYRITIGNKTCVF EKENDPTVLRSPSAGKLTQYTVEDG GHVEAGSSYAEMEVMKMITLNV QERGRVKYIKRPGAVLEAGCVVAR LELDDPSKVHPAEPFTGELPAQOTL PILGEKLHQVFHSLVLENTNVMMSGF CLPEPVFSIKLKEWVQKLMMLTRH PSLPLELQEIMTSVAGRIPAPVEKS VRRVMAQYASNITSVLCQFPSQQA TILDCHAATLQRKADREFFINTQSI VQLVQSLGTEQDLVFYEKEKRNQSI LGFEPVNSRHVSHVPETHRYKESHY DKCVINLREQFKPDMSQVLDICFSH AQVAKKNQLVIMLIDELCGPDPSLS DELISILNELTQLSKSECHKVALRAR QILIASHLPSYELRHNQVESIFLSAID MYGHQFCPENLKKLILSETTIFDVL TFFYHANKVVCMALEVVYRRGYI AYELNSLQHRQLPDGTCVVEFQFM LPSSHPNRMTVPISITNPDLLRHSTE LFMDSGFSPLCQRMGAMVAFRRFE DFTRNFDEVISCFANVPKDTPLFSEA RTSLYSEDDCKSLREEPIHILNVSQ CADHLEDEALVPILRTFVQSKKNIL VDYGLRRITFLIAQEFAEDRIYRHLE PALAFQLELNRMRNFDLTAVPCAN HKMHLYLGAACKVKEGVEVTDHFRF FIRAIIRHSDLITKEASFYELQNEGER LLEAMDELEVAFNNTSVRTDCNHI FLNFVPTVIMDPFKIESVRVMVMR YGSRLWKLRLQAEVKINIRQTTTG SAVPIRLFITNESGYLDISLYKEVT DSRSGNIMFHSFGNKQGPQHGMILN TPYVTKDLLQAKRFQAQTLGTTYIY DFPEMFRQASPAQTRVHVHNVQA LFLWLGSPDKYPKDILTYTELVLDS QGQLVEMNRLPGGNEVGMVAFKM RFKTQEYPEGRDVIVIGNDITFRIGS FGPEDLLYLRASEMARAEIPKIY VAANSGARIGMAEEIKHMFHVAW VDPEDPHKKKKTVAFSAGNWIRSL TKVFFKGFKYLYLTPQDYTRISLN SVHCKHIEEGGESRYMITDIIGKDD GLGVENLRGSGMIAGESSLAYEEIV TISLVTCAIGIGAYLRLGQRVIQV ENSHIILTGASALNKVVEPCTVQDIA NHVVSQVVLGREVYTSNNQLGGV QIMHYNGVSHITVPDDFEGVYTILE WLSYMPKDNHSPVPIITPTDPIDREI EFLPSRAPYDPRWMLAGRPHPTLK GTWQSGFFDHGSFKEIMAPWAQTV VTGRARLGGIPVGVIAVETRTVEVA VPADPANLDSEAKIIQQAGQVWFPD SAYKTAQAVKDFNREKLPLMIFAN WRGFSGGMKDMDYQVLKFGAYIV DGLRQYKQPIIYIPPYAELRGGSW VVIDATINPLCIEMYADKESRGGVL EPEGTVIEIKFRKKDLIKSMRRIDPAY

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						KKLMEQLGEPDLSKDRKDLEGR KAREDLLPIYHQVAVQFADFHDTP GRMLEKGVISDILEWKTARTFLYW RLRRLLEDQVKQEILQASGELSHV HIQSMRLRRWFVETEGAVKAYLWD NNQVVVQWLEQHWQAGDGPRSTI RENITYLKHDSVLKTIRGLVEENPE VAVDCVIYLSQHISPAERAQVVHLL STMDSPAST
4760	10257	A	5061	6	906	EQPALLPRYRSGIRGYMKTVVLDLL RRYLRVEITFSKARDADANTSGMV GGVRSLSFTSVWVLSPPAHYDKCV INLREQFKPDMSQVLDICFSHAQVA KKNQLVIMLIDELCGPDPSLDELISI LNETQLSKSEHCKVALRARQILIAS HLPSYELRHNQVESIFLSAIDMYGH QFCPENLKKLILSETTIFDVLPTFFY HANKVVCMALEVVYRRGYIAYEL NSLQHRQLPDGTCVVEFQFMLPSSH PNRMTVPISITNPDLRLHSTELFMD GFSPLCQRMGAMVAFRRFEDFT
4761	10258	A	5062	2	560	APRLDVSFSQIIHRDIKPENILVSQSG ITKLCDFGFARTLAAPGDIYTDYVA TR*PVDI WALGCMIIEMATGNPYLP SSSDLDLLHKIVLKVGNLSPHLQNI SKSPIFAGVVLQVQHPKNARKKYP KLNGLLADIVHAWLQIDPADRISS DLLHHEYFTRDGF*KFMP ELKA*L LQEAKSQF
4762	10259	A	5063	1	573	
4763	10260	A	5064	2	791	NLVNLIIEVFRQKKKIHLVFEDHTV LDELQHYCHGLESKRRLKYLFQILR AIDYLHSNNTVVDI WALGCMIIEMA TGNPYLPSSSDLDLLHKIVLKVGNL SPHLQNI FSKSPIFAGVVLQVQHPK NARKKYPKLNGLLADIVHEIEKEKK PKEIKVRVIKVGGRGDISEPKKKE YEGGLGQQDANENVHPTSPDTKL TIEPPNPINPSTNCNGLKENPHCGGS VTMPPINLTNSNLMAANLSSNLFSP QCEVSCNREEP
4764	10261	A	5065	3	524	TYGPASRGICRVSLGRPRWENAAT WKLAAMASIRLQGLHKPVYHALSD CGDHVVIMNTRHIAFSGNKWEQKV YSSHTGYPGGFRQVTAAQLHLRDP VAIVKLA IYGMLQ/NNLHRRRTMME RLHLFPDEYIPEDILKNLVEELPQPR KIPKRLDEYTQEEIDAFRLWTPPED YRL
4765	10262	A	5066	1	250	YSSHTGYPGGFRQVTAAQLHLRDP VAIVKLA IYGMLPKNLHRRRTMMER LHLFPDET*RLSAIRE*ELQKITVK*L KLSSDEFL
4766	10263	A	5067	129	796	MGKCSHLANFAAIASIRLQGLHKPV YHAP E*L/CGDHVVIMNTRHICIF/H GNKWGTSILFRILAYPGWSLDKVT SLAPFTLRRSQW/CNL*NLA IYGIP AKKTFTRRTIDWKGLHLFPDELYS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RKIFLKKFS*EELPSTTEKYLNVLDE YTTRNRRLFKIVDSTLKIIGYKRIRI AENNSEVIETFLMSFSNLQDGVKQ LLQFEHLFLCAESLWGVKRVK
4767	10264	A	5068	15	350	GPGSAITVGPQPL/RAQRNHLRPVPS PGLSIVMGLRPVPSPGPTGLPGHRQ SSEMRPREAGSLRSSGEKGLPAPVP RPQQSDMTKRTLPRDTPDTPRCPPQ HCPWSRVRGQPQ
4768	10265	A	5069	1	2175	
4769	10266	A	5070	3	86	KNYRGTM/STTKNGITCQKWSSTSP RRPR
4770	10267	A	5071	2	583	LLLLFLKSGHGEPLDYVYVAQGA SLFSVTNKLHLAGSTEECASQCVED KEFTCGAFQYHSKEQQCAIMAENK KSSIIIRMRDVVLFEK*MYLSECQTG NGKNYRGTMSTKNGITCSKMGPV LFPHRPRFSPATHPSEGLRNPNDNA QGPWCYTDDPEQRYDYCDIPECEG QEWALGKCFHFCSSPVKINLL
4771	10268	A	5072	844	4515	TVKAPGYSHSHPGALLDLEVGDPN GTNAQLIKCFLLPLCPSFPLCPEECM HCSGENYDGKISKTMGLECQAWD SQSPHAHGYIPSKFPNKNLKNYCR NPDRELRPWCFTTDPNKRWELCDIP RCTTPPPSSGPTYQCLKGTGENYRG NVAVTVSGHTCQHWSAQTPHHTN RTPENFPCKNLDENYCRNPDGKRA PWCHTTNSQVRWEYCKIPSCDSSPV STEQLAPTAPPELTPVVQDCYHGDG QSYRGTSSTTTTGKKCQSWSSMTP HRHQKTPENYPNAGLTMNYCRNPD ADKGPWCFTTDPNKRWELCDIP SGTEASVVAPPPVLLPDVETPSEE DCMFGNGKGYRGKRATTVTGTPC QDWAAQEPHRHSIFTPETNPAGLE KNATECGGASTELCSTSLCAFTML MDYEGQGEPLDDYVNTQGASLFSV TKKQLGAGSIEECAAKCEE\EEFTC RAFIQYHSKEQQCVIMAENRKSS\III RMRDVVLFEKKVYLSECKTGNGK NYRGTMSTKNGITCQKWSSTSPH RPRFSPATHPSEGLEENYCRNPDND PQGPWCYTDDPEKRYDYCDILEC *RRECMAFAVGKLLTGKIFPRTMS WDWECQAWGLFRSPHGHGYIPSK FPNKNLKNYCRNPDRELRPWCFT TDPNKRWELCDIPRCTTPPPSSGPTY QCLKGTGENYRGNAVTVSGHTCQ HWSAQTPHHTNRTPENFPCKNLDE NYCRNPDGKRAPWCHTTNSQVRW EYCKIPSCDSSPVSTEQLAPTAPPEL TPVVQDCYHGDGQSYRGTSSTTTT GKKCQSWSSMTPHRHQKTPENYPN AGLTMNYCRNPADKGPWCFTTDP SVRWEYCNLKKCSGTEASVVAPPP VLLPDVETPSEEDCMFGNGKGYR GKRATTVTGTPCQDWAAQEPHRHS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						IFTPETNPRAGLEKNYCRNPDGDVG GPWCYTTNPRKLYDYCDVPQCAAP SFDCGKQPVEPKKCPGRVVGCV HPHSWPWQVSLRTRFGMHFCGGTL ISPEWVLTAAHCLEKSPRPSSYKVL GAHQEVNLEPHVQEIEVSRLFLEPT RKDIALKLSSPAVITDKVIPACLPS PNYVVADRTECFVTGWGETQGTFG AGLLKEAQLPVIENTKVCNRYEFLNG RVQSTELCAGHLAGGTDSCQGDG GPLVCFEKDKYILQGVTSWGLGCA RPNKPGVYVRVSRFVTWIEGVMRN N
4772	10269	A	5073	9	141	FYRLSLGFKCDWFTMEKRVKLEER YRDMAEENLKDISISLKL
4773	10270	A	5074	3	360	QTKPKESRKRIIMFRTEFNETENRI ESSSSSSSSSFSSSSSSYKCLARLT/ RKK/EKIQIIVRSEKEIITNYRIKRIT KGYIELLYANQLYHLMKCPKFLER HKLLKLTQEETKSGV
4774	10271	A	5076	1	245	AAAYYYYTAARRRQKGERRKKRK EER/KEEKKKKRKKKEKKKRRRRG GRRTKKEEKKKEKKRRRTKKEKKK KKKKKKKVSM
4775	10272	A	5077	68	246	SMAFLTIEDTALKFIQNHKRPQIA/ KPILSKNRAESITLFNSKIHMYPTVI KPLRVST
4776	10273	A	5078	3	364	TSIVAAQMFNVITVMQVRISPQHMT SMWPIMVCELSQTFTQLEEDVKDK VESLRSTNKVNRTKVSVDANGPS VGYIPQSEL\IMYLSACKFLDAALSIP HYKIPLFKIYRWAFIPEVDTE
4777	10274	A	5079	2	1315	GKDAKILCSNPNTGEVLVELPTNTQ RCFDIQWCPRNPVLSAASFAGRIS VYSIMGGSTDGLRQKQVDKLSSSFG NLDPFGTGQPLPPLQIPQQTQHSIV LPLKKPPKWIRRPVGASFSGGKLV TFENVRMPSHQGAEQQQQHHVFI SQVTEKEFLSRDQLQQAQVSQGF INRQKKIDASQTELEKNVWPFLPV TFEDDSRGKYLELLGYRKEDLGK/K DCFGL/GTKWMEPMWLLKTLTKYH ITNHEPAG*PPVTNAAATASSSSTA KPVFIPTDTSSRWTALPWRTATSW NRHAPIFFTAQY*RCPRGSYWKYLP ACAVFGNKKNYQETYSR*APHSKD HI*GSYSALPFFSNRPSNQEEAR*CQ QTFGVSV**T*GTDFTNNHQWFTQ HCKEH*NSKLLRRIDHAYPHS*HQQ LQ*DLCFHASSQSCL
4778	10275	A	5080	18	3600	
4779	10276	A	5081	238	480	SIQFYFFSFQDSKGKHSLSVSVIGPQN GWNDDPALNRVPKKKKMPENFMPP VPITSPIMNPLGDPQSQMLQQQPSA/ PVPLS
4780	10277	A	5082	352	4060	DYSRRYILRMKLKEVDRTAMQAW SPAQNHPIYLATGTSAQQQLDATFST

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						NASLEIFELDLSDPSLDMKSCATFSS SHRYHKLIWGPYKMDSKGDVSGVL IAGGENGNILYDPSKIIAGDKEVVI AQNDKHTGPVRALDVNIFQTNLVA SGANESEIYIWDLNNFATPMTPGAK TQPPEDISCIAWNRQVQHILASASPS GRATVWDLRKNEPIIKVSDHSNRM HCSGLAWHPDVATQMVLA SEDDR LPVIQMWDLRFASSPLRVLENHAR GILAIASWMA DPELLLSCGKDAKIL CSNPNTGEVLYELPTNTQWCFDIQ WCPRNPAVLSAASF DGRISVYSIMG GSTDGLRQKQVDKLSSSFGNLD PFG TGQPLPPLQIPQQT AQHSIVLPLKKP PKWIRRPVGASF SFGGKLVTFENVR MPSHQGAEQQQQHHVFISQVVTE KEFLSRSDQLQQA VQSQGFNYCQK KIDASQTEFEKNVWSFLKVN FEDDS RGKYLELLGYRKEDLGKKIALALN KVDGANVALKDS DQVAQSDGEESP AAEEQLLGEHIKEEKEESEFLPSSGG TFNISVSGDIDGLITQALLTGNFESA VDLCLHDNRMA DAILAIAGGQELL ARTQKKYFAKSQSKITRLITAVVMK NWKEIVESC DLKNWREALAAVLTY AKPDEFSALCDLLGTRLENEGD SLL QTQACLCYICAGNVEKLVACWTKA QDGSHP LSLQDLIEKVILRKAVQL TQAMDTSTVG VLLAAKMSQYANL LAAQGSIAAALAF LPDNTNQPNIMQ LRDRLCRAQGE PVAGHESPKIPYEK QQLPKGRPGPVAGHHQMPRVQTQ QYYPHGENPPPPGFIMHGNVNPNA AGQLPTSPGHMHTQVPPYPQPQPY QPAQPYPF GTGGSAMYRPQQPVAP PTSNAYPNTPYISSASSYTGQSQLYA AQHQASSPTSSPATSFPPPPSSGASF QHGGPGAPPSSSAYALPPGTTGTL P AASELPASQRTGPQNG\WNDPPALD KVPKKKKKMPENFMPPVPITSPIMN RLGDPQSQMLQQQPASAPVPLSSQSS FPQPHLPGG\QFPFWGYSKPF GFKQ GMATIFFQSPNIEGAPGAPIG\NTFQ HVQS\LP TKKITKKPIPD\ EHLILKTT FEDLIQRCLSSATDPQTKRKLDDAS KRLEFLYDKLR\DR TFSPTITSGLHNI ARSIETRNYSEGLTMHTHIVSTSNFS ETSAFMPVLKV VLTQANKLGV
4781	10278	A	5084	121	419	DLCFTTPKAGRRQEITKIRAE LNKV EVQETIQKISEKRSWLFNIINKIARLL TRLIQKKD\QINTVRNDKGDITTYPT EIQKTLRDYYEHL YACRVENLQ
4782	10279	A	5085	1	279	TMDSNNTVDQLDL\TDIYRTLHLTS AAYTFFSSAHLRCSR\DLRLSHKTS LNKFKKIVII PGIFCDQNGIQPEINSG RKMRRVSNVWKLNNIL
4783	10280	A	5086	1	279	TMDSNNTVDQLDL\TDIYRTLHLTS AAYTFFSSAHLRCSR\DLRLSHKTS

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						LNKFKKIVIIIPGIFCDQNGIQPEINSG RKMRRVSNVWKLNNIL
4784	10281	A	5087	1	1915	MAILPLLCLLPLAPASSPPQSATPS PCPRRCRCQTQSLPLSVLCPGAGLL FVPPSLDRRAELRLADNFIASVRR RDLANMTGLLHLSLSRNTIRHVAA GAFADLRALRALHLDGNRLTSLGE GQLRGLVNLRLHLSNNQLAALAA GALDDCAETLEDLDLSYNNLEQLP WEALGRLGVNNTLGLDHNLLASV PAGAFSPHLKLARLDMTSNRLTTIP PDPLFSRLPLLARPRGSPASALVLAF GGNPLHCNCELVWLRLAREDDLE ACASPPALGGRYFWAVGEEEFVCE PPVVTHRSPLAVPAGRPAALRCRA VGDPPEPRVRWVSPQGRLLGNSSRA RAFPNGTLELLVTEPGDGGIFTICIAA NAAGEATAAVELTVGPPPPQLANS TSCDPP/PGRGLPDALTPPSAASASA KVADTGPTDRGVQVTEHGATAA LVQWPDQRPIPGIRMYQIQYNSSA DDILVYRMIPAESRSFLLTDLASGRT YDLCVLAVYEDSATGLTATRPVGC ARFSTEP\SLRPCGAPHAPFLGGTMII ALGGVIVASVLVFIFVLLMRYKVHVG GQPPGKAKIPAPVSSVCSQTN\GAL GPTPTPAPPAPPAALRAHTVVQLD CRALGARPRTCGTLARRPPL
4785	10282	A	5088	1387	1567	GKNLLPLFFFFFFFETVSQSVAQAG VQWRHLGSPKPLPPGSSDSPASVSQ AAETTGTCHH
4786	10283	A	5089	96	408	SPRKRKTRHSTNPPLECHVGWVMD SRDHGPGTSSVSTSNASPSGAPLA GRYGCTPH\SFPKFQNPSELLKEN GFTQQVYHKYRRRCLSERKRLGIG QSQEMNT
4787	10284	A	5090	390	665	PLNIHYCFLGGKYLVFQFSVAANKT SGAP\GNSPVSAIRAFGDAHPDLVT PGTFIPYCSMAHAQLCFHGHRAV KFFVAVPGQVISPOSSSS
4788	10285	A	5091	185	386	WEASKKKPRGAQISNAITTYKYLPK VG\KNYQTEALYKPIQTGKIGHPV FFQKPPLLGDGQNYDTPP
4789	10286	A	5093	3	330	GTGLKARKSASSLPETFPTRTRHGE AALPLSPTWKMTGPVGNMIPRQR SMSLLTAVSGQPHFQDSALSQASSS PDLL/LHLSPR\SCPGRVQETLKATD RPPRCPAGCG
4790	10287	A	5094	2	349	PRVRKSPGPNGFTANFYQTFKELISI LLKLFSSSSSLKKGNNPPNSFYGAIIP RIPNPNMDLPSSSPT/RPVSGRNMEA KIFTKFLAGHFKQSFGREIHHDQREF IPGIQGGFNIGN
4791	10288	A	5095	2	353	PRVRKSPGPNGFTANFYQTFKELISI LLKLFSSSSSLASSSSSSSSSSSSSSS SSPPNMDLPSSSPT/RPVSGRNIEAKI FTKFLPGHFQQSFGRVTHLDQRELI LGNQGGSTICKS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
4792	10289	A	5096	1	262	RGRAGGEPLPATTGAAPPPGRRLLH/ RQLPDRRGLASMPREEKASLNEPG GPGRGRRRGSVQLHGEGGPRGEE GTGREEWNEKAEFTL
4793	10290	A	5097	116	177	LGEHGVYSGVGTGGRLLS*KKGKP WFK*KKLKGGPIPI*RDPRGFSRFSV
4794	10291	C	5098	231	347	MGLGPLHKFFYLKHGLPFFKELNPL KVKIWPRNPWIKKI*
4795	10292	A	5099	518	931	ATRHSMLSCHYTYIYIKHTHTHVFI YIYTYTYIHTHIYTYTYICHTHIHIYI YIYIHTHFFFFFFFETESRSVTQAGV QWHDLGSLQAASWGHA/DSPASTS QAAGTTGAHHHAQ/LIFFFFVFLVET GPHRASQDS
4796	10293	A	5100	2	1109	DAEMLVMAPRTVLLLLSAALALTE TWAGSHSMRYFDTAMSRPGRGEPR FISVGYVDDTQFVRFDSDAASPREE PRAPWIEQEGPEYWRNTQIFKTNT QTDRESLRNLRGYYNQSEAGSHTL QSMYGCDVGPDGRLLRGHNQYAY DGKDYIALNEDLRSWTAADTAAQI TQRKWEAARVAEQDRAYLEGTCV EWLRRYLENGKDTLERADPPKTHV THHPISDHEATLRCWALGFYPAEIT LTWQRDGEDQTQDTEL VETRPAGD RTFQKWA AVVVPSGEEQRYTCHVQ HEGLPKPLTLRWPSSQSTVPVIGIV AGLAVLVTVAVVAVVAVMCRR KSSGGKGGSYSQAASSDSAQGS DV SLTA*KA
4797	10294	A	5101	3	1145	SDSPQTPRMRVMAPRTLILLSGAL ALTETWACSHSMRYFYTAVSRPGR GEPRFIAVGYVDDTQFVRFDSDAAS PRGEPRAPWVEQEGPEYWDRETQ KYKRQAQTDRVSLRNLRGYYNQSE AGSHTLQWMYGCDLGPDRLLRG YDQSA YDGKDYIALNEHLRSCTAA DTAAQITQRKWEAARAAEQRAYL EGTCVEWLRRYLENGKETLQRAEH PKTHVTHHLVSDHEATLRCWALGF YPAEITLTWQRDGEDQTQDTEL VET RPAGDGTTFQKWA AVVVPSGEEQRY TCHVQHEGLPEPLTLRWPSSQPTIP IVGIVSGPAVLAVLAVLAVLGA VVA AVIHRKSSGGKGGSCSQAAS SNSAQGSDES LIACKA
4798	10295	A	5102	3	242	GFWAPRVCKDIDKWHLSEPEALWF GEGGSPGGCRWGGWLCQGNRA AGGVGAEGACGLLSATGLLWMT GLQEPREPQV
4799	10296	A	5103	1	138	FPLIPKPGKDPFN/ENFRPIFLMAKN AKILKKILANLIFQPLKKIL
4800	10297	A	5104	59	337	IPYPALPFTSVEAPNSHVKA VMKTS VLLSWEIPENYNSAMPFKILYDDGK MVEEVDGRATQKLIVILNPEKSYSF ELTYRGNCAGGLELMVT
4801	10298	A	5105	54	226	TKAETENLRPVT/EIKSVI/NSLPTK

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						KSPGLDGFIAKFFQTYKREIPTLLK LLQKLKW
4802	10299	A	5106	2	265	ETVKLLEENI/GQKLFDIGLGSDFLDI TPKAQETKINKWDFIKLSFCTVKE TIKMKRQSVWEKILVSHVSDKWFI SKIQGIYITQYQ
4803	10300	A	5107	1	296	GREKEEGESGEDWGRVGREKEGG EGREEEGEGGREEEGEGGRKEEGE GGREEEGEGGREEEGEGGREEEGE/ GREEEGEGGRQEEGEGGRREGRG GRS
4804	10301	A	5108	1	253	
4805	10302	A	5109	190	472	
4806	10303	A	5110	1	314	HNVPVPHVFMLOKEITKKNSTFRVHI KAVFYN/HDIYCMPLLNYRKTDFV IVIDPPWQSKSVKRSNRYSLPLQI KQIPIPKLAAPNCLLVTLTNTQKH LRFIK
4807	10304	A	5111	3	362	FFFFFFESLSVPQAGVQ*HDLSSLQ PP/PPGFTPFSCSLSPSSWDYRCPPPR PA/NIFFVFLVETGFHHVSQDGLDLL T/S/GDPPASASQSAGITGVSHRARPP PPQFFIQLPLNYHTLEGR
4808	10305	A	5112	3	385	FFFETESRSVAQAGGQWHDLSLQ APTPGFTPFSCSLSPSSWDYRCPPPC PANFFVFLVETGFHHVSRDGLDFT S\DPPTSASQSVGITGVSHCARARPF FKKKKKKKTSILSSSSLSFSHKQRSFG F
4809	10306	A	5113	1	390	SKAVKV/YRLITRNSYEREMFDKAS LKLGLDKAVLQSMGRDGNITGIG QFSKKEIEDVLRKGAYAAIMEEDDE GSKFCEEDIDQILLRRTTTITIESEK GSTFAKASFVAGNRTDISLDDPNF WQKWA
4810	10307	A	5114	2	214	GRVDIERAILVQTGQQALEPAVRL RRAPYPCHTSDLFLNNVGGFFPLIM MLTWMVSVASMRPLVSQQE
4811	10308	A	5115	30	379	KRSVNSPGRALSELVSTELGFLRC VSVVCSLSQEYFLFTTLLYFGL/LPF ACLLSSSPVFFVFRCSVPLFFCFLFC VSLCLPFLGFFHVLFFHRLLPVFSF MEGFYWAWCLVFFCL
4812	10309	A	5116	1	304	GTRETVGLGDTNLAHQCSRLTMVN NDNHSEAYNNLAVLEMKGHVQQ ARALLQTASALSPHMYETDFNFATI CDMTGYLHRSYVDAQKSEAALSEH VDTQH
4813	10310	A	5117	119	264	
4814	10311	A	5118	720	2798	VYWPHSFLGCPSNYPLYLGAETRO GGRARPPFLPLSFPPRFRPNSPFQN VLETQRISYSFLLADTSNTRATSGH AQQPAPILPLREVAGAEDIIRVHVPF SLSDLSQIAKRLGSFSSDPDTYIKEF KYLTQSYELTWHDLIYILSSTLLPEK KERVWLAAQAHANDLHRQDPTKPI GAAAVPLEPPWKYQPTDPGRASR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion)
						NHMITCLIAGLNKAAHKAVNFEKL KEISQRADENPAEFLSRFTEALQKY TRVDPTSREETIVLNNHFISQSAPNI QHKLKKAEDGPQTPQQDLLNLTfK VFNNREEQIKLDKAQRDCAKYQLL AVAIHQPSHSTQGHKKPNGSNPPGP CFKCSKEVTYLGVLSPGAQAMTP AQATLINSPLPSSKNEILSFLRLEGF FRIWIPNFALLAQPLYEAAKGPLNE PLSPIHNILPSFCKLQTALITAPALS PDLSQPFVLYTTKNQGIALGVLGQQ KGNPPSFDPAVYLCKQLDNTVKGG PTCLKASSAVAVLPLESKLTFGQS TTHSPHNLDLLSSWALSSLSPSQI QSLYALFIKNPEFSLAKSAPLNLASL LPISSSPPTHSCDILDHLQPQFPNISS KPLTNPDDQLFIDDSSSRAPGSPKIV GYAVVTLNHVIEAKPLPETSSQKA EL\ALTRALTL SKDKQHWLISEPVQ RPPSSVHST
4815	10312	A	5119	2	697	HGRLLLLLLLLLLPCCEKTTEGEAM KEITAGLPVKVVVDVLRQASKACV VKREFKKAELIKHAVYLARDHFG SKHPKYSDDL DYGFYLLNVDNICQ SVAIYQAALDIRQSVFGGKNIHVAT AHEDLAYSSYVHQYSSGKFDNALF HAERAIGIITHILPEDHLLLAASSKRV KALILEEIAIDCHNKETEQRLLQEAH DVHLSSLHLASKSYGDLAVVVLVH MSLLKSY
4816	10313	A	5120	3	277	EEEEAPPPGRERARGKGGDRPRGG NPEHQCGGTPRAEGSSTA/A/PPTCT SSSRTPASTVGPEPCGAGSAATAPG PELSGQNQMGRGPPVEDTE
4817	10314	A	5121	1	337	GTSSCVREVQAMGKKKVLVKVH LKDKFVIDVDKNISISDVTPSSLVVL RNDSTYTLHKILPNKVHSLVSLMMV NTVPY/STNETIVSLDGPMVTILFSD KLSFTAPQLYIFTG
4818	10315	A	5122	2	302	ARGLPFFTRNDFS VWTIA/RNKCVG LELSKITMPIAFIQPLIFLHRITEYME HVYLIHRAFCQPQPLERMQVGLKG ARQEFVMKVMPLACLATQSWGPR HL
4819	10316	A	5123	3	346	HENWKLLPCSSKAGLSVLLKADR LFHTSYHSQAVHIRPVCNRARCTSS WELRQTL SVVFDAFITGQGKDW LF/RMFSRTLTEPCPLASESRVYVDI TTYNQDNETLEVHPPP
4820	10317	A	5124	213	425	QNSQGLFSSGCLPFCGSNTKGILK YIQNH/KKPQIAKATLSKKNKAGSIT LPDFKIYYKALKPKITWYWH
4821	10318	A	5125	1	356	GTSTRIIFYRDGVSEGQRQQLHHE MLAIREACIKLQKDYQPGITFIVVH NIHHTRLCSDKNHPLGKRGNSPTG SNCGTKITHPTFEFDYLRRHAGIQG TSRPSYYHVLWD\DNRRFFS
4822	10319	A	5126	1	238	HMSSHMHSHSTPHA/HHTHHMHS

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						HHMHSHTHHMHSHHMHSAPHAL TPHACTHTHHMHSHHMHSHHMHA LTPHACTHTPH
4823	10320	A	5127	180	405	IWGEQDTFHSMAKWIIHLNVNHKT VKLLDDNIG/IKRGDLG/VDNEFLGT TPKAQSMEETIDKLDFIKMKNFCSV KDG
4824	10321	A	5128	61	85	PS*NYPP*KGITFGPLNKK
4825	10322	A	5129	3	2004	RRRRRPASPPAGLALAPRSPSASPEP REGETLSPSMQREEGFNTKMADGP DEYDTEAGCVPLHPEEIKPQSHYN HGYGEPLGRKTHIDDYSTWDIVKA TQYGIYERCRELVEAGYDVRQPDK ENVTLHWAANNRIDLKYYISKG AIVDQLGGDLNSTPLHWATRQGH SMVVQLMKYGADPSLIDGEGCSCI HLAAQFGHTSIVAYLIAKGQDVDM MDQNGMTPLMWAAAYRTHSVDPTR LLTFNVSVNLGDKYHKNTALHWA VLGNTTVISLLEAGANVDAQNI KGESAPDLAKQRKIVWIINHLQEAR PAKGYDNPSLPRKLKADKEFRQKV MLGTPFLVIWLVGFIADLNIDSWLI KGLMYGGVWATVQFLSKSFFDHS MHSALPLGIYLATKFWMYVTWFF WFNDLNLFLIHLPLANSVALFYN FGKSWKSDPGIHKATEEQKKKTIVE LAETGSLDLSIFCSTCLIRKPVRSKH CGVCNRCIAKFDHHCPCWVGNCVG AGNHRYFMGYLFFLLFMICWMIYG CISYWGLHCETTYTKDGFWTYITQI ATCSPWMFWMFLNSVFHFMWVAV LLMCQMYQISCLGITTNERMNARR YKHFKVTTTSIESPFNHGCVRNIDF FEFRCCGLFRPVIVDWTRQYTIEYD QISGSGYQLV
4826	10323	A	5130	3	144	HEKYHKN TALHWAVLAGNTTVIS LLEAGANVDAQNIKAILRCHMAL
4827	10324	A	5131	148	325	RQGKECKIHCKKKLSPGIRSYPVEN/ F/VDTMYDYLQPAYYKLNLDLTNAD PCAVRYLLFDQN
4828	10325	A	5132	175	405	NILNSQFSTFLNDYVEFFVVFKIFNFI IIIF*DRVSICCPGWSIMVQSWLTAA LTFGRR*SSNLSLPSSWDYRRVP
4829	10326	A	5133	14	26	YSPHEVGWKGRNREKMFCSEINVV FPDSVCQEMGFHHVAPAGLELMSS SDSPASASQSAGITSVSHHSCLYTSK GVE*FTGIIFSS
4830	10327	A	5134	177	454	PLLERAKIGPRPEKPMETROGWGPF SPKVPGQKKFWG*LAPIPSGPMHPN PILGPMV*EGGP*PPGILGPP*PYGKP LF*RKRGSNGGPYLQ
4831	10328	A	5135	3	92	NAWRTATEEWWTEDWNEDCSEP* HFTYVI
4832	10329	A	5136	1	442	PLIMNSIKSFSDDHAQCGRÆFDRQED DIHLVTLCTELNDREENENHFPVI YGIAVNIKTAEIYRASFDQDRGPEEQ

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						RAARTLAGGPMISYDAETEQLRIG PYSWTPPHVDFWLHQDDKQIFEN LSTSPLEPPHFVEHIRSYLD
4833	10330	A	5137	177	566	EPFWSLSYLSLRGGRNVRLCRLSA LVFCQFKAMLLTLTAGNNKTAIEY RASQDRGPPEQLRAARTLAGGPMI SIYDAKTEQLRIGPYSWTPPHVDF WLHQNDKQILKGRVYRLGKS*ISAP WPHL
4834	10331	A	5138	1	981	PLLVEGR*VRLPQSAGDLVRAHPPL EERARLLRGQSVQQVGPQGLLYVQ QRELAVTSPKDGSIILGSDDATTCH IVVLRHTGNGATCLTHCDGTDTKA EVPLIMNSIKSFSDDHAQCGRLEVHL VGGFSDDRQLSQKSTHHFLIEFDR QEDDIHLVTLCTELNDREENEN\H FPVIYGI/AVILLSLTAVNIKTAEIYR\ ASFQSRSGVREEQA/LRAARKL*AGG PMIS\YDAETETTS**DPYFLGHPFP HVGFWL\HQD\DKQILDESFRPL AE\PPHF\VEHIRSTLMVF*KNTPSPA \NTLFPGNKALLYKKNEDGLWEKIS SPGS
4835	10332	A	5139	1	405	AYVTVCNQCGRESKLLSKFYEL NIQGHKQLTDCISEFLKEEKL*GDN RYFCENCQSKQNAIRKLLSLPCT LNLQLMRFVDRQTGHTKKLNTYI GFSEILDMEPYVEHKVW*PTSLNSM LSLKLGGMCMLT
4836	10333	A	5142	2	204	ETGFCHVVQAGLKLGGSDLPASAP QSAGITGMCHCAQPTKVSASKVF KGSHKD*ILT*GYANKGA
4837	10334	A	5143	1	360	QQLTVLVAHLGVTLMDQRGYHWL LKSLMTQYQGLLYENP*ITLIVNTL NPGTLLPNESVPGSALHCRVDVVE MLSIQRDLTDHTLRDSDIEYFIDRS FILGGDPLSGVCSSDFGLST
4838	10335	A	5144	36	380	FVALMGHKMSHNKFKIEIRSMFSN HNRSQ*SK*IKEIYKCGN*HTSK**M H*GKKSALKENNEMNENESTT*Q NLWDAAKTALNEQFML*MPILKKG *MSQINKPTFHLKTIK
4839	10336	A	5145	1	362	ELNLPAPLPRKRTENLFLQLAEYV AHSLNVT*YVCEGTTMGD*WPWE TQELEPTDPVPDIIPVQKAQTSNFW VLKTSINGQYCIPRKGKDFITPVGRL N*LGQKLYKSITGTQGQSPG
4840	10337	A	5146	2	428	MFLLVVINLHILFVF*FKLFSWS*AI L*FLF*FMSESENIYYAEIGIITIVT LKSLIATYCINPSSHCHYKVYLVL LYCIIVNFDIYFLLLCVPFCYFSLI SPLFLIYMIFLYIHFILLFVIFYTFIP FSFY
4841	10338	A	5147	3	361	TLFQL*DLRKQRLEDLSTLIPRIY PGWKCRTHFLMKKSQIVIAWYRRY AQHKRNQPTKSTVLVLSYIRGRK ARKILRELKHQKRCTEAVTTIAAY

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						WHGTHALTETERLKKEARRKH
4842	10339	A	5148	1	424	VHLTADDKVIIAGLWSIVNAQDAV GETLGRLLQGVYPWQIRFFGSFGNLS SASAI VVNPKVTAHGKNVLTSLVD AITHLV DLMGTFAQLRELH*DKLYE DPENLHTLGHVLT VLVVIHFGT*FT AEVQASWLMMDTERANAL
4843	10340	A	5149	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFDFSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLT VLVLAHFGKEFTP EVQASWQKMTGVASALSSRYH
4844	10341	A	5150	38	501	APSPDAMGHFTEEDKATITSLWGK \VNVE/DAGGETLGRLLVVYPWTQR FFD\SFGNLSSASAIMGNPKVKAH GKKVLTSLGDAIKHLD\DLKG\TFA QA*SELH\CDK\LVDPENFKAPGG NVAGDPFLAIPFSAKEFHPLKVARL SWAERWVTW
4845	10342	A	5151	2	198	KVRPPPLKKTDFSVDYRVLSEVDFE ERFAELPEFRPEDDLSSFS*PFLSPPP CMSTALAHGDFSL
4846	10343	A	5152	1	119	DIMTGPHEVA AKNIQLTNEIQTLE TE*HEATKEFQVLS
4847	10344	A	5153	3	83	RMVLRMLPLSTDEALCFHAMFQPF LDMIHEAQQAMDIFHSPDFQHPPPT EFIREGDDDRTVLREMHII*TG*LR VKWRCEEWR*J
4848	10345	A	5154	2	370	GAARLDERTKEGSDDDEDSG*GARA ELEGNKEGESEGQYKAKGERSAWS KLRTEIRQKAEESIDGIKVDDPS*IS MKATYTTMKIS*RQIRKIRQREKKN TAKGEGQERQKNLSHKRHDISC
4849	10346	A	5155	106	344	RPCQQMQINVIHPINRMDKKHVIPI DTSDKI*HPFMIQTLNTLCI**MYLSI IKAIYDPYTADIILTG*TFNAFFSTI
4850	10347	A	5156	198	474	
4851	10348	A	5157	1	131	PQEV PQSFGPPGDKAGC*GAGKMS PRERGGFLKCAEGGHPAPA
4852	10349	A	5158	104	440	FSKIYHFLCCCFVLSKNCPILLHFL KIYLLALGNINISYFYSYHSKTLATG LKLTDSDQHISHGTSGSRFKCLLS KAVLMSSLPVYS*LLKLLDVREVS NMVHDTLGIL
4853	10350	A	5159	2	393	EVWPRGLMGYVTVTEPSAVLVVRG VRDRLVITYPHEHHALTSSRYLLM LFVGDPSSGSGSNGSPDS*GLLLFRN DQAHIDLFCFSVILSCFFLFLSLCEL LWNAKQAMDQRQEQRRLQEMTK MARRPF
4854	10351	A	5160	2	154	FRDGVSLHCSGWS*TPGLK*SSCLS LPKCWDYRHEPPLLFLWRAIGNIY
4855	10352	A	5161	142	399	HLLTYSEMFLGGVRYFLQSTLPADL SKHAYLYAP*LRLFA*RYTSAFTEW THSANKTVCLMPKLYELTYVGIDTL ATPVIKRYYS

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4856	10353	A	5162	3	410	HEG*PTFSSILHHPGAWAQLQ*PSQ ATTALFTLISVA*QQAGCSPQPGAG NTPPPPPNSGTLTPSPACAHWAQC* ANKDEFSVPGPQCLWPR*GPSYTAS LPQALRARPSQMTRVPQAPPTGPG PVVSPCANTN
4857	10354	A	5163	168	435	IIAQ*N*FLKNNFQ*TI*K*NKILFTT RSK**I*QKQKKNLYLEKYKTLLKEI KDLNKWKNISCSWIGTLSIDKLVT SKLNYRVNVI
4858	10355	A	5164	2	427	QIFRYLIMEKEQEHTYRGFKTVNR WTDAYDYAQHYSEASVASKDVS W*FHDYLGMSRHPDVLQA*QETLQ RHGAGSGGSRNLSGTRNCHVELEH ELADLHLKDSSLIFSFCFIANDCTLF TLAKILPGREIHS DACQHAFM
4859	10356	A	5165	11	1232	MAGAAATGSRTPGRSELVEGCGWRC PEHGDRVAELFCRRRCRCVLCALCP VLGAHRGHPVGLALEAAVHVQKLS QECLKQLAIKKQQHIDNITQIEDATE KLKANAESSKTWLKGFTELRLLL DEEEALAKKFIDKNTQLTLQVYREQ ADSCREQLDIMNDLSNRVWSISQEP DPVQRLQAYTATEQEMQQQMSLG ELCHPVPLSFEPVKSFFKGLVEAVES TLQTPLDIRLKESINCQLSDPSSTKP GTLLKTSPSPERSLLLKYARTPTLDP DTMHARLR\MSADRLTVRCGLLGS\ LGPVPVLRFDALWQVLARDCFATG RHY\WEVDVQEAGAGWWVGAAAY ASLRRRGASAAARLGCNRQSWCLK RYDLEYWAFHDGQRSACGPATTST GSASSWTRPASSPTT
4860	10357	A	5166	115	447	MSSWARLCESPVVWYF*HVLVCL HKLRALISQQFLTGINCQLSDPSSTK PGTLLKTSPSPERSLLLKCKTPGSGD RVETVEMVGCWVEEDHGNGGPSFF LIRIYLFYLF
4861	10358	A	5167	1	423	ADMKAHLLHSGGMGFSCECSTGF VKHS*LIEHIRTHTGEKPFQCPKCDK SFRLKAQLLSHHGLLTGDRPFHCPE CDKNLRERGHMLRHQRHRRPERPF ACGYCGKGFYKSKLAHIRVHTKS CPAANELDIKKMLHPLV
4862	10359	A	5168	481	908	EGSQWEAQKALAIQPVPCGAVRVP WTTSSIPASIPKQSVGKGCDCLR*L GDFAPARGEEACECHTEPFRNSRGV GGAWARPGYLVLSSLQCPDSAC NQDLLAYLQRIALYCHQLNICKVK AEVQNLGGELVVS GVSIS
4863	10360	A	5169	2	2799	EMTAVHAGNINFKWDPKSLEIRTLA VERLLEPLVTQVTTLVNTNSKGPSN KKRGRSCKAHVLAASVEQATENFL EKGDKIAKESQFLKEELVVAVEDV RKQGDLMKAAAGEFADDPCCSSVKR GNMVRAAPALLSAVTRLLILADMA DVYKLLVQLKVVEDGILKLRNAGN EQDLGNQYKALKPEVDKLNIMAAK

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						RQQELKDVGHRDQMAAARGILQSN VPILYTASQACLQHPDVAAYKANR DLIYKQLQQA VTGISNAAQATASD DASQHQQGGGGGELAYALNNFDKQI IVDPLSFSEERFRPSLEERLESIIISGA ALMADSSCTRDDRRERIVAECNAV RQACRTC VSEYMGNAGRKERSDAL NSAIDKMTKKTRDLRRQLRKAVMD HVSDFSLETNVPLLVLIEAAKNGNE KEVKEYAQVFREHANKLIEVANLA CSISNNEEGVKLVRMSASQLEAGCP QVINAATWALAPKPQSKLAQENMD LFKEQWEKQVRVLTDAVDDITSIDD FLAVSENHILEDVNKCVIALQEKDV DGLDRTAGAIRGRAARVIHVVTSE MDNYEPGVYTEKVLEATKLLSNTV MPRFTEQVEAAVEALSSDPAQPM ENEFIDASRLVYDGIRDIRKAVLMIR TPEELDDSDFETEDFDVRSETSVQT EDDQLIAGQSARAIMAQLPQEQKA KIREQVASFQEEKSKLDAEVSKWD DSGNDIIVLAKQ\MCMIMMEMTDF RGKGPLKNTSDVISAACKIAEAGSR MDKLGR TIADHCPDSACKQGLVA YLQGIALYCHQLNICKSKVKA EVQNL GGELVVS GNC DTCGALQGLKGWPP PLCLATHWVDSAMSLIQA AKNL MN AVVQTVKASYVASTKYQKSQGM SLNLPVSMKMKAPKPLVKREK QDETQTKIKRASQKKHVNVPVQALS EFKAMDSI
4864	10361	A	5170	25	458	
4865	10362	A	5171	3	764	GPLCIALALQEFGTRRRWACRSLSS SGRRSLFRRMGSVKAVKNKA YFKR YQVKFRRR/RKGKTDYYAR*RLVIQ DKNKYNTPRYRMIVRV TNRDII CQI AYARIEGDMIVCATYAH*LPKYGV KVGLTNYAAAYCTGLLLARRLLNR FGMDKIYEGQVEVTGDEYNVESID GQPGAFTCYLDAGLARTTTGNKVF GALKGAVDGGLSIPRSTKRFPGYDS ESKEFNAEVHRKHIMGQNVADYM RYLMQEDEDAS
4866	10363	A	5172	8	400	PLASFD TGDVECALCMRLFYEPDTT PCGHTLCLRCL*RCLYHNAKCP LCK DGLSQ**ASIKYSYNVIVEELIAKFL PEELKEREKLYE*EMEELYNLNNNV PILMCTMAYANVTCP LHMFEPCYR LMIRIW
4867	10364	A	5173	2	400	SLPLASFNTCNVECALCMRLFYEPV TTPCGHTFCLKCLERCLDHNAKCP L CKDGLSQCLASRKYIKNVIMEELIA KFLPE*LNERMKLYEYEMEELS NLN NNVPFVCTMAYPTDPCPLHIFPCY RLMIRIC
4868	10365	A	5174	1	216	AGRTGRPEERAPESKSGSGSESEPS RGGSLRRGGEACGTSDGGPSPF*GS SVVSFTLLSYLGYYSYLLSTV

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4869	10366	A	5175	301	446	SYFSYIILIIRGNESEGGFFEN*YFCL LINGGSWSGEPPIRRNSHTFNC
4870	10367	A	5176	155	404	AAVPSRILKQYSHPNIVRLIGVCTQK QPIYIVMELVQGERGALSSR*GAQP GQVAALPQEAQQGSSPPAGGDFLT LRTEGAR
4871	10368	A	5177	172	443	TGMIRGPWTKVGPAGAEKPPVGDGK VPNGCPKSLGNRQPCF*VLEVNEPY VPKKFKAEPFPFHANICPLSEKERQF RKQTALVDL*KPKPR
4872	10369	A	5178	3	428	PDQTLCCCAEMGSHCVAQAGLEL LGLSDLPIASQSAAITGVGHHACP VLGS*RPSQMLCPFPWWLLSATFY LAVPHLLPCLLFQPHSLRCSRSSSSA NLPVVFSPGAGCLSLSCMECSFP AKVLVIPFSPERPPCS
4873	10370	A	5179	2	432	NIVSQNDLPQTVIWMGDCIISLETR IQMQCDWNTSDFCVTPHS*NETEH HWEIKCHLVGREENLTLDIVKVE QVFEASQAHLTLLPGTDIFSEAANG LSAINSLKWIKTTGNSTLVNFVLIIC LFLAAAFSPEAASASVD
4874	10371	A	5180	163	585	VEVRAHPKKRQKKKEKKKSDRYSD SSSSSSSDSSSSSSDSEDEKDKKENR RKKKKNRSHKSSSESSMSETESDSKD SLKKKKKSKDGTETEKKDIKGLSKK RKMYSEDKPLSSESLSESEYIEEVQA KKKKSSSEEREKATEK
4875	10372	A	5181	18	566	AEQSGEAARGPVAGPLRPSLWPGFP RRATVCSVQHHGEAGQSGWPYMN PNSNGEIKGSQSQSSGPTIQDYLNRP RPTWEEVKEQLEKKKKKSKALAEF EEKNE*ELEERTGKTQGEIVKWK*E LIQKKDRERKKRRNLVGSSSDSED EDKKQGKRRKKKKNRSHKSSSESSM SETESDSKDSL
4876	10373	A	5182	27	382	SVILSFFFFFFYIAWATVRLCLKQTN ENNDKRDLTSLKVVRK*TLNLHPSI KAMIIRLYFEQLYDNRLANLDEMDI FLATQKLPKLAQEEVKNFRCVTM DYVNNQNL*TNKGPEPDD
4877	10374	A	5183	2	342	GRSCDPKSVGQTLCVALLSVPLPGD PGQRKLPSQNSEEL*SQKCGPNPM CCSFPVPLAGGPGHSRRSTQSRTR*L KPQLPGWRTEKGAPEEIGKMMLQV IDERPGSALSCRC
4878	10375	A	5184	2	147	AETGFHHASQDGLDLLTS*STRLGL PKCWDYRREPQRPADTWFLKSTT
4879	10376	A	5185	8780	9035	LALQVHTMTPSKFFIFLVETGFHH VSQDGLDLLTF*STRLGLPKCWDYR SEPPRPAYFYIFLRRSLSLSPRAGVA VSRDHATAL
4880	10377	A	5186	75	355	SNKNPSISCPRTWGECVCQATSRST WFLYPMPYSAPIKPTPGDVPGTAPS GRPDSTPS**HRLQGTLPKPAPPLLG VFPKPLLAPLFPEGPGP
4881	10378	A	5187	262	354	VWSPPLTWCLVCQCRYYPGLLM

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						MCFILPT
4882	10379	A	5188	1	104	ESETLPGGVAHACNPITLGG*GGRIT RSGV*DQP
4883	10380	A	5189	1	144	RDKVFALSHRLECSGAIHAHYNLQL LG*NNHRVSDSPVAGMAGVCHHT
4884	10381	A	5190	99	241	CFPGA WVRLQLTQASDGPWQCSSS QRLHHAPHVVTLYLCCAFSPCSPVK LRDFESAVNNFEKALERAKLVHNN EAQQAISALDDANKGIIRELRKNTY VENLKEKSEGEASLYEDRIITREKD MRRVRDEPEKVVKQWDHSEDEKE TDEDDEAFGEALQSPASGKQSV GKARSDLGAVAKGLSGELGTRSGE TGRKLEAGRRESREIYRRPSGELE QRLSGEFSRQEPEELKKLSEVGRRE PEELGKTQFGEIGETKKTGNEMEKE YE*SHR*R*GSSVLVLDGDIAQEHG GKDGAELSDASLGP GSDYSSHKL LMGPGSARVARGSIMHHTLSHSTC VVPSPALQ
4885	10382	A	5191	303	427	IVLFEKKIFFFFETGSCSVPKAGVQ WCGHSSLQP*PTGLM
4886	10383	A	5192	82	352	RVPERVLPRIPPASCPVSPASRPL* GTPRAAPETRRRPRTARDPRGLRW QTQPAAPLLASPGPGVAPVASGAPI SRNDFQLCKARMLL
4887	10384	A	5193	1	248	QKLKLLARHGGACACGHKLLGWL RW*DHMSLRGQGCSSES*SCRCTPA WTTE*DPVYQHKILSL*DFLI*KASS NRSSVIYEL
4888	10385	A	5194	3	370	AQWRVDS DGAPKRIADSATSPKLL YVDRVVQEILETERTYVQDLKSIV* DYLD CIRDQTKLPLGTEERSALFGNI QDIYHFNSELLQDLENCENDPVAIA ECFVSKSEEFHIYTQYCTNYPR
4889	10386	A	5195	28	183	YDRKRPVGKEKIGKLDCKMT*NFC ASKNTIKEMKRQRTVWEKIFAHYIS ERK
4890	10387	A	5196	1	681	MHPIGIALSKVPVESKEGDIMSHTG GSVPYLDNLNKASVCRGQSCR VFQ VKEMVTQVESENQEEQKQVRLPE SRLTPWEVWFIGEKEERDRLQLK ALEFKEDWKLLKRRVTKSGSVSV SISSQGNLTVCDCCESFLLTKPVSC KHLIKSHSCPALAVAS/CQRPEGYW SDCGTRSHSDYADEEDSFVSDSSDQ VSSRRTVTHSYAPPQSQPHHRHTQT GTTATYL
4891	10388	A	5197	1	2862	MPGPLGLLCFLALGLLGSAGPSGAA PPLCAAPCSCD GDRRVDCSGKGLT AVPEGLSAFTQALDISMNNITQLPE DAFKNFPFLEELQLAGNDLSFIHPK ALSGLKELKVLTLQNNQLKTPSEA IRGLSALQSLRLDANHITSVPEDSFE GLVQLRHLWDDNSLTEVPVHPLS NLPTLQALTLALNKISSIPDFAFTNL SSLVVLHLHNNKIRSLSQHCFDGLD

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						NLETLDLNYYNNLGEFPQAIALPSL KELGFHSNSISVIPDGAFDGNPLLRT IHLVDNPLSFVGNFAHNLSDLHSL VIRGASMVQQFPNLTGTVHLESLTL TGTKISSIPNNLCQEQKMLRTLDS YNNIRDLPFNGCHALEEISLQRNQI YQIKEGTFQGLISLRILDVSRNLIHEI HSRAFATLGPITNLDVSFNETSFPT EGLNGLNQLKLVGNFKLKEALAAK DFVNLRLSLVPPYA YQCCAFWGCDS YANLNTENNSLQDHSVAQEKGTD AANVTSTLENEEHSQIIHCTPSTGA FKPCEYLLGWSMIRLTVWFIFLVAL FFNLLVILTTFASCTSLPSSKFLGLIS VSNLFMGIYTGILTFLDVSWGRFA EFGIWWETGSGCKVAGFLAVFSSES AIFLLMLATVERSLSAKDIMKNGKS NHLKQFRVAALLAFLGATVAGCFP LFHRGEYSASPLCLPFTGETPSLGF TVTLVLLNSLAFLLMAYIYTKLYC NLEKEDLENSQSSMIKHVAWLIFT NCIFFCPVAFFSFAPLITAISSPEIMK SVTLIFFPLPACLPVLYVFFNPKFK EDWKLKRRVTKKSGSVSVSISSQG GCLEQDFYYDCGMYSHLQGNLTVC DCCESFLLTKPVCKHLIKSHSCPA LAVASCQRPEGYWSDCGTQSAHSD YADEE\DSFVSDSSDQ\VQACGRAC FYQ\SRGFPLVRYAYNLPRVKD
4892	10389	A	5198	2	413	VDFFFFLRRSLATVAQAGVQWRDL GSLQAPPPGFTPFCSLPSWDYRR PPRPANFFVFFFF**RWGFTVLAR MISIS*PRDPPTSASQSAGITGVSDRT RLDFKKKKKYCGKKDIMYRKVYTS LIQLTKKSLIH
4893	10390	A	5199	1	142	RKMFGNGRARS GVIVLPCGKGYQS **GGQAVGSGSASCLPLSLCTFP
4894	10391	A	5200	1	375	GEATMNPSHEAEVVCVPTWWPP VSTR*MGGRE*RKERAEGRGKGG MEKEGAGERRGKEKNGDSRERGRE GKSVTDNST*GAAAGLPQSPCPIQA RGVQSPRPQAMSRGEPEYSGIGGW GSGEA
4895	10392	A	5201	109	331	PLYCSPGASYMTLTALGPTQTQVPE QRLFVTCILCQEEQEVKVESRAMVL AAFVQRSSVLSKNRCKFI*DPGKS
4896	10393	A	5203	2	168	FFLDSTLKA*AIKAKINKWNDVKLK SFFKTKETINKM*QPMVWENIFANH LSDKG
4897	10394	A	5204	107	357	DLRWYSSFLWMCCIPGAKWHPING SSCVMGMGIKYDFTGHWIVKHIGL AADLDSFYEYLLKSYILFGE*DDL* MFNAAYQSIQ
4898	10395	A	5205	3	376	CQSQVPTDHGGQPPGSHPGWKPGP DLPPRFDPPEPSRPGN*GLLGPALCP SDLYAFGPQGISVNGLPQWRPGW GHPWRLPEPDS*APAIQPLAEPVL WGWGGQRPRVPQQLPTAERCCSDF

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						S
4899	10396	A	5206	1	262	QNIFLHLFFCSFTAQKYPMVHLLQK SDNSFNQELLKSMVKSIMNDVYG PMSQILETLNKCPhFKRQR*VLLLD EYIVLLGRFILFA
4900	10397	A	5207	2	296	NGTHASYGAFYLEYSLAEFTLVV KHKLPGVYVQPSYRSALMWVGVL SMWEGG*RQGLVRSTVGLGGAVLS SEDRSWGVGSLLSRASAPRLPLAHL RC
4901	10398	A	5208	30	280	FYYAFKEEIPVLYSLFQKIETGGILL NSALLIPKST*YRRPYKKGKLNRYR PKSFVNINVKILNRLANQIQKCIKRI TYYS
4902	10399	A	5209	1	277	NFSSLLIHGRMHTGEKPYECKNCGK AFTSAKSLQNHGRTHTG*KPCECKQ CGKAFICSSSCQRHEETHSVNMHSV ILIPKHKRVRVGKGPLR
4903	10400	A	5210	220	585	EILVRSRLRQDPLRSRRGKRHTGRRW DGSGWRATGARE*RRESRGWEME AREAGRRKPASERRKSGRRAGDF LEPATRSRSEKEVRTLARNGRP*AS PGSHRSSQ*LQPRVACGGRAATKSS
4904	10401	A	5211	1	291	SFLETLLPRLGCSDAIMAHCSLELLG YMRSCHLSLPS*DYRPTPSRLANSFF LIHGGFFTLSWADLQLLGLKQSFRR SWGLTGVSHHAQPPFPYYLY
4905	10402	A	5212	228	379	
4906	10403	A	5213	317	534	ATKEN*INWDLIK*NKQKPFASKDT TKQAKRQHIEWEKKVVNPIYDKAP VSRIKNLLKLNNKNTNNLIVKKK
4907	10404	A	5214	3	366	IGY/NPDTVACV/PILGWNGDNMLE QSANMPWFKGWK VTRKDGNASGT TLLEALDCILPPTRPTDKPLRLPLQD VYKIGGIGTVPVGRVETGVLKPGM VVTFAVNVTTTEVKSVEMHHEAQK AK
4908	10405	A	5215	1	1254	
4909	10406	A	5216	33	1472	KLPLKAKMGKEKTHINIVVIGHVDS GKSTTTGHLIYKCGGIDKRTIEKF EAAEMGKGSFKYAWVLDKLAER ERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQAD\CAVLIVAA GFVEFEAGISKNGQTRHALLAYT LGVKQLIVGVNKMDSPEPPYSQKR YEEIVKEGSTYIKKIGYYPDTLAFEP ISGWNGDDMLEPSANMPWFKGWK VTRKDGNASG\TTLEALDCILPPTR PTDKALRLPLQDVYKIGGIGTVPVGR VETGVLKPG\MGVTFAP\NVVYN GK*KSVEMHHE/AL*SEALSWGTVN GLQLSRNVSVKDVARRGNFAGDSK\ NDPPMEA\AGFTAQVILNHPISQKN ARHMPLELDCHTAHIACKFAELKE KIDRRSGKKLEDGPKFLKSGDAAIV DIVSGKPMCVESFSDYPPLGRFAVR DMRQTVAVGVKAVDKKAAGAGK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VTKSAQKAQKAK
4910	10407	A	5217	178	566	KGGATCPESPQDRKRRGNLDMKEL YSENEGMA SNHGKMENE*QPQDQR KPQVTLYSGRQEVVRKRGKDRKQGQ NRR*GNV*RIKGKPESEGEAKEGKS EREGESEMEGGSEREGKPEIEGKPE SEGEPL
4911	10408	A	5218	27	336	TNPVQQTLPVIWTSTRLPDTHEDKA FSAPQIEDRGTPGLGSRGPALGPSPT PDCAG*VVAAGPGPAESHPRAPKPT AGMSPGVARLSSPGSGSQGSWQNNQ ERP
4912	10409	A	5219	2	454	HFNM RDPLTDCPYNKVYKNLKEFS QNGENFCKQVTSVLQQRANLEISY AKGLQKLASKLSKALQNRKSCVS SAWAWASEGMKSTADLHQKLGKA IELEAIKPTYQVLNVQEKKRKSLDN EVEKTANLVISNWNQIKAKKKLM VSTQET*STADLHQKLGKAELEAIK PTYQVLNVQEKKRKSLDNEVEKTA NLVISNWNQIKAKKKLMVSTQET
4913	10410	A	5220	26	130	TTWKYQYKNLERNQKEITELKSTIA EENITRGI*R*FEQTKE*INELEDKI MEIFKDKR*KKGEKSLRGLWPPSRD KEACMPWKLQTEKKKGAERLSEE IMAESFSNLLADMNINS*ELKSTIAEI ENITRGI
4914	10411	A	5221	48	394	SPSMCGSLDPPTLPQTWLQVPSMLT HPCPPPPHCPPLAHPPSSLLPSTHIY H**HLSPYPNPGTQEGHSGVRLRA TDVASPSVLGQFPSYSISVPREGHA ATVAAKGPLECRA
4915	10412	A	5222	3	726	EQEVDYDPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCKKADD EMPADLPSLAADFVESKDVCCKNYA EAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLKQNCCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLRKVGSKCKKHPEA KRMPCAEDYLSVVLNQLCVLH/EK TPVSDRVTCKCTESLVNRRPCFSAL EVDETYVPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCKKADD EMPADLPSLAADFVESKDVCCKNYA EAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLKQNCCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLRKVGSKCKKHPEA KRMPCAEDYLSRGPEPVMCVA
4916	10413	A	5223	4274	5256	HTLFGDKLCTVATLRETYGEMADC CAKQEPERNECFLOHKDDNPNLPR LVRPEVDVMCTAFHDNGETFLKK* VIRCL*FKIKKHGVTP*ANTL*KLP* QKYFQH*DLEVLL**FFKEVVFDTT

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						KFYTAKNMIKDILKFIETGYNLSQK FKIDKFFNVFRRYVYMVVIDFVLV SNIILPKFNHLCCTHTHTHTLTLFST YLKNDRDKTIMCKLSLIG*L/ESLEF GGSGENV DYNFCNIVCYRK/ADCF SFLKFRYLYEIARRHPYFYAPELLFF AKRYKAAFTECCQAADKAACLLPK VLCTRIEKKSLLSNLILSILWDLGT LSV
4917	10414	A	5224	1	332	RMPCAEDYLSVVLTLQCLVLDKTP VSDIVAKCCSESLVNSQACLSDL*V KDAYVPKEFNTETFTFHADICALSE TERRIMKQTGLDEFVKHKP*ASDER LSAVMDDFAAF
4918	10415	A	5225	7	564	TTRAAGREALSPGQGAGGGEGGAE PRHTATGHAAGREGRGGRGADQG* GWPRGARALHDQAEGRGGLPAGLP VQAERPQREPCSGQVGSEPPCHPA TAGGRKVRPAWPAAGEAGGHSG TGRAGAAGGAAGVTGGGAAGPGG LPMSGGAGPGGSGAAAPHAAS*VQ PAAGAASAATRNRMPTT
4919	10416	A	5226	132	917	PGLFYLGEEQPGQPAGGPAAGQG ATAGAEAAAGCPGGAAPAVLAG GRAGGRSAGWCAGAPGA*PGLFYL GEEQPGQPAGGPAAGQGATAGAE EAAGCPGGAAPAVLAGGRAGGRS AGWCAGAPGA*AQP*TTGAAGREA LSPGQGAGGGEGGAEPHTATGHA AGREGRGGRGADQG*SLSQATDLW TSGPSHKWTDLSLWPYPCCSGCSW GQCL*LRAEGRGGLPAGLPVQAERP QREPCSGQVGSEPPCHPVSHTPKGP VPHCLGASPLLWLATAGGRKVRP AGPAAAGEAGGHSGTGRAGAAGG AAVGTGGCQQRWIR
4920	10417	A	5227	3	1245	AWEFVWHPGGFDRSCPGPQGGE EGGEGT*EGSGSLALRPLSCPR GPGGPRLA*ASVYPWNQKRVGGL WRPQRTPARLCDPHAPEHAWAL*G KPGPAGHPAEAA*RQRE*AAGPRGT AAAPAGQDRQHHAGPRGRPARGA AAAERQRAPEKGEEQPGQPAGGP AAGQGAAGAEAAAGCPGGAAP AVLAGGRAGGRSAGWCAGAPGA* AQP*TTGAAGREALSPGQGAGGGE GGAEPHTATGHAAGREGRGGRG ADQG*SLSQTDLWTSGPSHKWTD LSLWPYPCCSGCSWGQCL*LRAE RGGLPAGLPVQAERPQREPCSGQV GSEPPCHPVSHTPKGPVPHCLGAS PLLWLATAGGRKVRPAGPAAAGE AGGHSGTGRAGAAGGAAGVTGGG AAGPGGLPM
4921	10418	A	5228	612	795	PGFISAIGGLVGLSSYDFYKEYED KPTSPPIAEMNPGYNI*HDLIKSFKM LAFICSISS
4922	10419	A	5229	1	345	SSWSFTLVTQAGVQWHDLSLQPL

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						PSEFKRFSCLSLPSSWDCRRLPPRPA NFLYF**RWGFTILTSLVLSY*PCVS PTSASQSAGITGVSDHARLIVGDFN TPLLITERSSTQKI
4923	10420	A	5230	1	1212	MPKKRQALVEFEDVLGACNAVNY AADNQIYIAGHPAFVNYSTSQKISRP GSDSDSRVNSVLLFTILNPIYSITTP TRLNVFKNDQDTWDYTNPNLGQGG DPGSNPNKRQRQPPLGDPHPAEYG GPHGGYHSHYHDEGYGPPPPHYEG RRMGPPVGEYGPHADSPVIMVYGL DQSKMNCDRVFNVFCLYGNVEKV KISLKKQSPGGRPMGEWL/DGYAV DRAITHLNNFMFGQKLN/CVGA QAREGSRGTGERKGGEGWPAEEHS EAEVLTHTEMGCGSVSKQPAIMPG QSYGLEDGSCSYKDFSESNNRNFST PEQAAKNRIQHPSNVLHFFNAPLEV TEENFFEICDELGVKRPSSVKVFSGK SERSSSGLLEWESKSDAETLGFLN HYQMKNPSINLVT
4924	10421	A	5231	1	421	FDPPGCFFTPIGNPFGPFQGNFHRK NGVQAMVEFDSVQSRQAASLN GADIYSGCCTLKIEYAKPTRLNVFK NDQDTWDYTNPNLGQGGDPGSNPN KRQRGTVISQD*PSLLKNYCTCDF FSCSYICAAHVLCGTFQ
4925	10422	A	5232	2	1883	DEQRRRSAMVKMAAAGGGGGG GRYYGGGSEGGAPKRLKTDNAG DQHGGGGGGGGGAGAAGGGGGG ENYDDPHKTPASPVVHIRGLIDGVV EADLVEALQEFGPISYVVVMPKKR QALVEFEDVLGACNAVNYAADNQI YIAGHPAFVNYSTSQKISRIDE*ND YR\SVNSVLLFTIVNTINWITTDVLY TMCNPGPVQRIVIFRKNQVQAMV VFDSVQSAQRAKASLNGGDIYSGC CTLKIGYAKPTRLNVFKNDQDTWD YTNP\NLGQGGDPGSNPNKRQRQP LLGDHPAEYGGPHGGYHSHYHDEG YGPPPPHYEGRRMGPPVGGHRQCP SRYGPQYGHPPPPPPPEYGPHADSP VLMVYGLDQSKMNGDRVFNVFCL YGNVE\VKFKMSKPGAAMVEMA DGYAVDRAITHLNNFMFGQKLN CVSKQPAIMPGQSYGLEDGSCSYK DFSESNNRNFSTPEQAAKNRIQHPS NVLHFFNAPLEVTEENFFEICDELG VKRPSSVKVFSGKSERSSSGLLEWE SKSDAETLGFLNHYQMKNPNNGPY PYTLKLCFSPAQHAFLIRCLGRVPFE QENISLSFMPFFGFCFCYLQKILGSP FFFFFFFFLKARVEEGFPPP
4926	10423	A	5233	2	337	DMILAERGGVCVMMKTQCCTFIPN TSTTDGSITRALQGLTALSNEANN SGVNDPFTGWLEK*FSKWKGIIASIL TSLAAVMGVILVRCCVIPCLQRLM QRLIKMALTQTS

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4927	10424	A	5234	62	343	RQLNRNDPNNRNGKGVGIKQCLRF WNNFILTCLIGVSEIEEKNGAE*IF EEIMSKNFPKLIKYNPQIQEA**TPS KINTEKTTFRH*IKGR
4928	10425	A	5235	1	359	TDDDLNWLDSRTFREQGVDETET CLLRKFSYSQNVDSRDPVQLNLL YVQARDDILNGSHPVSEKACEFGG FQAQIQFGPHVEHKHKPGFLE*MTF CFSFSSFLSSFSFSLFLS
4929	10426	A	5236	2	264	SYYPGEISVPFFNICHFLLSCFYNLS RFFCKKSPASPLCFSIKKSPFVKIHL VFSLVTSSFLK*FFFYL*FFPESVISF GSFSNSD
4930	10427	A	5237	3	246	LIPRGQGSTVVLPPYNPATSIIFGNDLN EIKMYGHAKTCIWMFMTSSFIIDRT RKRQ*CSSVREWINKQ*CIQTMELV FGRN
4931	10428	A	5238	78	411	VLNSPICNCLYPILCSFLFLIHYFVVC FYTFIPVFYLVYHQEIVI*SLTLVFFV CVVKINRLMVHIFILYICL*LSICNS VYLLHVHIYLEHFL*HILMVVFFKR SDQSS
4932	10429	A	5239	2	175	TKLDFIGIKGFSSVKDNVKGMRQA TDWEKIFAKETSDKGLLSKIY*KPF KLSKQPN
4933	10430	A	5240	1	335	VTIRGAGIPDESRNVNYSLASFLKR WLTLMDRGFIFNLINDYISGFSPKDP KVLAEYKFEFLQTICNHEHYIPLNLP MAFAKPKLQRV*DSDLEYSLSDEY CKHHFLGGLL
4934	10431	A	5241	139	354	SPCLPYCCLLCYRYGDGRIMIGFSC GH*VVISTHTGELGQEIQARNHKD NLTSIAVSQTHIKVATCENNLP
4935	10432	A	5242	2	332	ILAGAH*DNEIKLM*IEKEVVKLFLF TDDMILCVENSKEHTHSHTQLGLI NEFSRASG*KINVQKLFYTNVQS KNEIKEPSLCTKASKRIGYLGHLTK EV*DLYSERTKPH*KKNRILRNFTN KRSVRLVQ
4936	10433	A	5243	137	290	GSSDINQTKHVRS*VNRQICSRTTQ QSPEDCDFKKGDLVKRCMGTQTRQ SL
4937	10434	A	5244	1	363	LTCSGDKEQIKDKSHVLKGGKGNFE RETS*KKK*SLPPFDDNVEPNLDYV EENICKSDSERPRSASSSSRSSSFT PSQTRQQGPLKSMMDLHSDDYEE ESDEMEDNGPDFEMGKPVNIR
4938	10435	A	5245	2	376	VHLGWCMLPLRTHTEYVKALSYA* DKQLGA*AGLDRQIFLWDANTLSA LTASNNTVTSSLSGNTDSIYRLAM NQLVTIIVSGSNDKALRVWDPLTCA TLVNLKGHTDNGKALVFNRDGTQC LSR
4939	10436	A	5246	60	185	
4940	10437	A	5247	1	146	RWRDLGSPQAGFR*FCCLSLSSW DYRHAPLF*QFYLFILFCKKYF
4941	10438	A	5248	2	298	TFFTPFPVAKPNPRGPKTPAPYFSPQ

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						GPQKIYPPKFLGPPFNFPPLLGKVF RAPNPRV*LPPGARPPSSSSLLPGF* KIPKPLFY*KKIFTPQKTKK
4942	10439	A	5249	77	370	EYS*SVVFLDLMRQEELRRMEELH NQE
4943	10440	A	5250	83	467	YSEKSAGLWLNMLEKSLPGHRDTA TQIQHVSPMCQVEPPAKKAATLAE GDKDNDI*PCFVQRQLREGROGRA ARLWEKWLRWYVEKKAKKTALV VKSSIPLDIKPWDNETNIAQLEACM RFIQLDGLV
4944	10441	A	5251	1	359	KYTL SRLATVPPTLNPAEYNISPDTR RAQVEQLAIRAGLK*EYLLQYNNP NRRGLIEDPALIRWTYARSANVYPN FRPTPKNSLLGALCAFGPLFFWYCV FKTMDMRNQKLIREGKLDQ
4945	10442	A	5252	3	349	SSLATVPANLNPAEYISPDNRRAQ VEQLAIRAGLK**YLLQYNNPTRIGI IKDPALIRWTYARSANVYPNFRPIPK NSLLGDLCAYGPLFFWYCVFKPDM DRKETLIPEGKLDQ
4946	10443	A	5254	1	415	NAVIQVAHPLVQKQ*VDYIHNGFL VPVMGPALHKTSVEEMIASTAYLEL FLRSISEPALLRTLRLFLLLHRHDT TILDTLVARIGSNSRLCMVSLSLFKT LLNLSCEDVLLQLGLRYLVPCNHV MLSQKPAVRDVL
4947	10444	A	5255	34	394	YRHYTICCIIGFLNTITMTVSFHKY GEYFPGT*DLRDIDAGKC*YYAVNF PMRDGIDDES YGHIFKPIISKV MEM YQPIAVVLQCDAYS LYGDSLDCFNL TIIRHSTRLYLI*SYHFTS
4948	10445	A	5256	178	417	ILVPPAGGKGNLI*WNP GPPGARG FPGLTPPRGGKKGRAQPPENLVF* EKTGFPIVQRGGLKPPPGPKGGE*R GGPP
4949	10446	A	5257	749	1049	DGSSLLGPRPGGKGNQTKGNRPP G*RESPPHPPRRGKKRMAQPPQLI WDFSSSSGFPL*QGGGINPHDPKKG GKKRGEPEPTTGPSKRGKKQGF
4950	10447	A	5258	1	359	LFPKVNLSPVTPAKDTGLTAAPQEP KAPKASPVQHALPSSLSVPHTAILV TGAQLCGPAVNLSQIKDTACKSLLG LEEKKHAEAPAAENPHGGPGDSSA PY**GDAPKGHAIRAVEVPD
4951	10448	A	5259	1	441	FFFLNRVLT LITQAGVQWCDHGS LQ PRSLGLK*PSHFSLPSS*DYRCAPPH LANFYIFYKDRWGFTMLPRLVWEL LGSSDLSILDSQSAGITGVRHHTWA NFFNFLCVSGIN*RNFYNKFTSWGS HPNSQYYSGISWGQSTNILLGY
4952	10449	A	5260	1	553	FYFYFFFFPLFFFFKPQDDFLVPGDQ NQRPGGSMP LGTAFILFQMKTL SLV RRGINQDN*HWRQEDPLIPISPGFPS RIPPLKSEMSLPLSTDGSETRTQSP FDEIYMAHDASGLRLPDSPPPPAAP GRDPAPSGQRAPGKLRGQCQLKSE

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						RESRKEERQRSKPGEAAALGGVAC TFHLKSRS
4953	10450	A	5261	1486	1695	GKSCRPNVNIYFILFSSFLRRSFALVA QAGVQWCDLGSLLQPPPPGFK*FSC SLPSSWDYRYPPLCPANFC
4954	10451	A	5262	1	334	RRFVSQETGNLYIAKVE*SDVGN CVVTNTVTNHKVLGPPTPLILRNDG VMGEYEPKIEVQFPETVPTAKGATV KLECFALGNPVPTIWRRADGKPIA RKARRHEGCEM
4955	10452	A	5263	78	313	KVTYIQKNVYSKCTAGWVFTQRRAR VGSREFFPAAPSPGPHGGDPPSPQ G*PLSPLQPAPVRLPSPVMMSERIL PF
4956	10453	A	5264	3	320	IFSQENL*YSDGSDILGLLALQAEEN LGMVMIFTLVTAVQEKLEIVDQIK TSSSSSSSSSSSAEEAEKQLFHGTP VTIENVLNWESQGWRRQTFLGKILE KEKG
4957	10454	A	5265	3	941	APPRCLGDLWARARATMTDYGEE QRNELEALESIYPDSFTVDCTLIQPS *QLVFQNINGLS*YHILLQ*CFT*QG PC*VLSNPPTSFTITVTSEAGVENDES IHIKLLSCVLA VQTTLKFTYSEKYP EAPLYEIFLPGKILEDNVDSDILKLL \ALQAEENLGMVMIFTLVTAVHERI NVLV DHIITRCEVEMKL*DKEAEE AVKQLFHGTPVTIENFLNWKAR/SF DAELLEIKKKRMKEEEHAGLDKK\S GKQLFETDHNLDTSIQFLEDAGNN VVEVDESLFQEMDDLEDEDDDPD YNPADPESDSAD
4958	10455	A	5266	1	332	LKKHKSTRVP*NVKSGK*NFSPPFKI RPWAQKRAKKKGAREKKAD*EKG EFGKLSSSSRFRPGKKV*G*PKGFQR NFEKKPVKSQGPVNMGVIPAFEKKP RIPPVAKIPI
4959	10456	A	5267	3	375	SASPQTLQQSLPRSIAPKPLTVRLPM NQIVTSVTIAANMPSNIGAPLISSMG TTMDGSAPSTQVSPSVQTQQHQM LSSSSSSSSSQMQMQQQQLQQHQ MHQQIQQMQQQHFQHHMQ*HLQ Q
4960	10457	A	5268	1	360	KGAPKHGQAPLGDPPRAVGGQEH* GPARGRGPGPREPGSGQTSSPWVH VRPGGGKNDGKARP*ILDPKSVSC IPAPSSHRPLSSPTNPFP*SSYEGSP RSPQPWTLQPQGPWPPSRQA
4961	10458	A	5269	1	181	KKKPTWEKLV*GLF*KKRNPWG QRPVPTPLWGVKKRGGVFRGL KPPLKPRENPF
4962	10459	A	5270	10	108	SHINVPMNQ*VVSLLGPGQVTKGW DQGLLMCE
4963	10460	A	5271	1	336	EFLGAVGFCRLWIPNFAVLAKPLYG VTK*GDTELFKWSQQQ*AFHELK EKLMSAPALGLPDLTKPFTLYVSR EKMAIGVLIQMVGPWPRPVAYLSK

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						ELDGVSKARSEGCE
4964	10461	A	5272	1	118	TEVRHGKLDSSKWIPIRGN*NIYNP HCLSYKLEHGSDQEIPSDWYPFATV QFSVPDLC
4965	10462	A	5274	2	327	SCLVLVLLCVEYLFYPYLHFQSICVFT GEVSFLQAAYSWVMGFFVFLFILIH SYFL*LLWGLFISLHLWLSLTCEDLF LLFFSRCLIIYIICFVLLFMSFLILWR LLVF
4966	10463	A	5275	171	331	LKTSFRTKTCT*MLTASLFVIAKTW KQPRCPSVGE*LSNL*YVQTMECYS VLK
4967	10464	B	5276	83	332	MGKRDNRVAYMNPAMARSRGPIQ SSGPTIQDYLNRPRPTWEEVKEQLE KKKKGSKALAEFEKMNENWKKE LEKHREKLLSGX*
4968	10465	A	5277	76	138	
4969	10466	A	5278	1	1050	
4970	10467	C	5279	146	433	MKKKSNERWDQVYKILKGKSLRPG FPRCATVRAIQHHGEAGQSGGLYEP NSNGEIKGSPVFRANNTGLSESTK AYLGRSKRATRKEKERLQGGF*
4971	10468	A	5280	27	264	NPNHQSLLCRAFCGVLILPVLALL TRLSFGELTYNNHFIYIFKAFFKFI* VFKWTGDNMFFIKGDMDSLAFGGG G
4972	10469	A	5281	135	358	VHSPVL*LISTIPTSRLKFLKETGHGT PMEEIPEEELSEDVEQIDHADRELRR GQNLRCCKGIHRLPTHIQVGQN
4973	10470	A	5282	15	196	KGKIVKLDIFIKI*NFFSAKDPVNY*K DNYRLRKMTANHISDKEFVSKTYK ECLKNLNKKF
4974	10471	A	5283	307	383	YF*VSLATLCVYFLLDEGNILTATK VFTSMSLFNILRIPLFELPTVISAVVQ TKISLGR
4975	10472	A	5284	3	267	TIVRPYLLKKKTGTIVEERVNAPGW NEDDDVSVSDESELPSTTLKAFEK STMEQLVEKACFRDYHRLGL*TLSG SCCRS*P*SRRVQ
4976	10473	A	5285	1	260	TAVPSAASMTSTRAASASSVHVPVS ALGAGSAATAASEEMQTIPQATAA KYPRTIHPESSTSASRSLGT/TISSHP VSHKCSFHKSG
4977	10474	A	5286	60	292	VTNFLIFHMRJISKYISIFLTVFFFVSQ IVLLFKHSYFSYLELWKMQRKDSK NAT*KRAL*RFHEKSFHEGCMCIKS
4978	10475	A	5287	738	1152	KGRVWSWCSRKRFTCSFGSFSSSDA LTSYITTAIPTTAVGGASATAVPS AASMTSTRAASASSVHVPVSALGA GSAATAASEEMSDKELITCTRQLKR DGCFCGQYTNQPGTGNMGKKQPRIT LCPLNKRKVAVKPN
4979	10476	A	5288	3	555	RKRTFCFSFGSFSSSDALTSYITHCCQ SPPAAV*LASATAVPSAASMTSTRA ASASSVHVPVSALGAGSAATAASEE MYVPRVVTSAQQKAGRTITARITGR CDFASKNRISSSLAIMGVSPPHLSC

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						CGKTSSQSTVQTHSLKQLPAKYPRTHSIPESSTLSLPRSLGTQISSHPVSHKCSFP
4980	10477	A	5289	94	323	VIGYRNIRCTILTSTITSSLSIL*LNH*PETRLSE*AGV*DKGLVVAQMMWLMDHIFKYTNFGIVSLVHGDFIRQ
4981	10478	A	5290	2	319	MVLVTLDDKYAVAALWGKVKVDEVDGEALGRLMVVYPWTQRFWES*GDLSPPDADMGNPKVKVHGNKVLGAVSNGQAHVDNLKGTATVSEMHCCKLHVAAQEPEVL
4982	10479	A	5291	1	159	RDLQHFPSSVAM*DQTQNDIASTSNHESILQGIKGGSQL*EEVQLME*APVDC
4983	10480	A	5292	187	282	LRSY*CLLLMISFTRNANLFR LHGTHTDTFKCLEYEKCFNCNSDLIVHHRINMDHNPHQTSA*DSGLLLGMHF
4984	10481	A	5293	1	156	SGGVDEQMMREKEELMLWLQDYEKIKKAEREL*EQIKREMKNQKRKREKK
4985	10482	A	5294	179	322	NKVGGLTLPNCKTYKATIKTVWYWRKKRQIGQ*NRIESPEIDPHKY
4986	10483	A	5295	2	395	RDRESDRDQRRERERRTRKWSRSRSHYRSPSRCRTKSKSSSFGRIDRDSYSPR*KGRWANDGWRCPRGNDRYRKNDPEKQENARKEKNDIHLADDPNSADKHRNDPCPNWITEPINCGRPRTNRNPEKL
4987	10484	A	5296	3	228	HELPHPGGLKRGCVWLEVAEHVV LGKALLILLPYRFKRNILAMDDKTGMTRNPHFSHNNWIPTFFSTQYFWIIFKVRWPRLKDTTDLRILAPNCLADRLSRHRCNIWQFMQGIPLVLFNGSCT*PSFQPQQLYTNLFQHPVFLDHL
4988	10485	A	5297	61	360	YVSNSKCSNHRK*SLSSSSSERESSFVPQVELHGRDLG*LQLWLPFGFKFPGLTPLRNGDDGPRPQPANLGLLVKTGFSPVAHLGVNLGTLGDCPALP
4989	10486	A	5298	124	351	EREFRFVPQVELHDRDLGSLHPGTPGLRKFSGLTLPKSGDNGPGPPPVNLGFLEETGFSHVAHFGLNFGT*GDCP
4990	10487	A	5300	3	388	HERHERHEGALSQDALLRISIPLDSNMRPEKCRRFVHPQRQLLHLNGTFPNTSDADMEPCVDGWVHDIISFSSTIVTE*DLVCDSQSLTSVAKCAFMTG*TADGFLGAHLSHRVRASSNVCMSGGSIVC
4991	10488	C	5301	47	269	MPPLIQSGMSSRTKTRTSSPCWNVHPAPEQYEAPDKDFMIVALDCSAAPRAWVVTWSSWCPQQHHDIAVPVHA*
4992	10489	A	5302	1	253	MYTQ/HPEQYEAPDKDFMIVAL/DL LSGLAEGLGGHVEQL/VARSNIMTL LFQCM/QAEFMPI LGTNLNEP/ISVC NNATWAI GEICMQW

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4993	10490	A	5304	229	2984	PCPCQNFLRCSTSFNFSLPCAMDWQ PDEQGLQQVLQQLKDSQSPNTATH RIVRDKLKQLNQFPDFNNYLIFVLT RLKSEDEPTRSLSGLLKNNVKAHY QSFPPPVADFIKQECLNNIGDASSLI RATIGILITTIASKGELQMWPPELLPQ LCNLLNSEDYNTCEGAFGALQKICE DSSELDSALNRPLNIMIPKFLQFF KHCSPKIRSHAIGCVNQFIMDRAQA LMDNIDTFIEHLFALAVDDDPEVRK NVCRALVMLEVRIDRLIPMHHSIIQ YMLQRTQDHDENVALEACEFWLTL AEQPICKEVLASHLVQLIPILVNGM KYSEIDIILLKGDVEEDEAVPDSEQD IKPRFHKSRVTPLPHEAERPDSSED AEDDDDDDALSDWNLRKCSAAL DVLANVFEELLPHLLPLLKGLLFH PEWVVKESGILVLGAIAEGCMQGM VPYLPHELPHLIQCLSDKKALVRSIA CWTLSTRYAHWVVSQPPDMHLKPL MTELLKRILDGNKKVQEAACIAFAT LEEKACTELVPYLSYILDTLVFAFG KYQHKNLLILYDAIGTLADSVGHHL NQPEYIQKLMPLIQKWNEKDED KDLFPLLECLSSVATALQSGFLPYC EPVYQCCVTLVQK\TLAQAMMYTQ HPEQYEAPDKDFMIVALDLFSGLA GLGGHVEQLVARSNIMTLFQCMQ DSMPEVRQSSFAFLGDFTKACSSHV KPCIAEFMPILGTNLNPEFISVCNNA TWAIGEICMQMGAEMQPYVQMV NNLVEIINRPNTPKTLLENTGRLTSP SAIPAITIGRLGYVCPQEVAPMLQQF IRPWCTSLRNIQDNEEKDSAFRGIC MMIGVNPGGVVQDFILFCDAVASW VSPKDDL RDMFYKILHGFKDQVGE DNWQQFSEQFPPLKERLAIFYGV
4994	10491	A	5305	47	411	
4995	10492	A	5306	20	1020	LSLTSRMEEAELVKGRLOAITDKRK IQEEISQKR\RLKGEDKPKA\QPLKT KAL\REKW\LPWNPASGKEQEEM KKQNQQDPAPRSQVPRTKYPSGLR KRSQDLEKAEQISTKEEAILKKLKS IERTTEDIRSVKVEREERAEESIEDI YANIPDLPKSYIPSRLRKEINEEKED DEQNRKALYAMEIKVEKDLKTGES TVLSSIPLPSDYFNVTGIKVYDEGQK SVYAVSSNHSAA YNGTDGLAPVEV EELLRQALERNKSPTEYHEPVYAN PFYRPTTPQRETVTPGPNFQERITIK TNGLGIGVNESIHNMGNGLSEERGN NFNHISPI
4996	10493	A	5307	1	95	GTRTFLRITYLSEIARRHPEFYAPELL *FAKR
4997	10494	A	5308	1	338	GTSLSA*GLNIDGQLGLGHTEDIPY YTPCRSLFG*PIQQVACGWHVVTIML TEHGQALLCGCNSIVQLAGPHGHL RRVGT*TIELRRENAVHIGAALMPH

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						VALTTSRSIFQCR
4998	10495	A	5309	3	472	VTEFAKTCVADESAENCDSLHTLF GDKLCTVATLRETYGEMADCCAK QEPERNECFLQHKDDNPNLPRLVRP EVDVMCTAFHDNEETFLKKYLYEI ARRHPYFYAPELLFFAK/RLDELRD EGKASSAKQRLKCAASLQKFGERAF KA\VARLSQRFP
4999	10496	A	5310	12835	13995	TIPIESDIFPSIFYLYLSSLAYADTYE ALSRFY*KKKLINLLLSLN*ATHFPK IMPVVQVELKAKFN*LFRKCFLPST NPLLCRWR*YDEWNIATS*LIPAKC SLFYLLC*TVSCLAENT*LLFFRLLV RYTKKVPQVSTPTLVEVSRNLGKVS SKCCKHPEAKRMPCAEDYVSL*KHI IN***KNFPFRYC*CYLS*AEGSNVC VCMFCACVCACTCVYV*YWQSRPR G**FFFF*DGVSLLCCPGWSA VVPSR LTATSASQVQAILLPQPPK*LGLQV HATMPG*FFVFLVENFQLHLF*ISAL LPVL*LSVVNLQCLVLEKTPVSDR VTKCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQI KKQT
5000	10497	A	5311	1	349	GTSKKLANKVVYVNVGLCICLFDITK LEDAYVFPDGDASHTKVHFRCEVC HPFLHEILTGKIKGCSPEGAHHPLR* HPDFPLFSRPPAFLSPSQYILSPREIL VHPSILKFRTRRPY
5001	10498	A	5312	1	410	IEHGIVTNWDDMEKIWHHTFYNEL RVAPEEHPVLLTEAPLNPKANREK MT/QGSVPLPAFP*SLQIMFETFNTP AMYVAIQAVLSLYASGRITGIVMD SGDGVTHTVPIYEGYALPHAILRMD LAGRDLTDYLMKIL
5002	10499	A	5313	216	390	GSADARAPPVLSPVIFCPS*FLTGRP LQGVMMVGMGQKDSYVGDEAQSQR GILTLKYPHIEHGIVTNWDDMEKIWH HTFYNELRVAPEEHPVLLTEAPLN KANREKMTQVRLGRRPCSSRPFP FLPILISDGSSPAGRHGGHGPGLLR GRRGPEQAWHPDPEVPH
5003	10500	A	5314	4	1254	HAHAKLGTRAASSRTLFFRQLRRR VSLPVAMEEEIAALVIDNGSGMCK AGFAGGDA\PRA\VFPSIVGRPRHQG VMVG\MGQ\DSYVGDEAQSQRGI LTLKYPHIEHGIVTNWDDMEKIWH TFYNELRVAPEEHPVLLTEAPLEP QGQTREKMTQIMFETFNTPAMYR GPSRAVLSL*ASGR\TGHCCHGTG DGVTHTVPIYGGPLPHCSTPFLRLGP GLARDLTDYLMKILT*SEGYSFTTH GPSGKFVRDI\KEKLCYVALDFEQE MATAASSSSLEKSYELPDGQVITIG NERFRCPEALFQPSFLGMESCGIHET TFNSIMKCDVDIRKDLANTVLSGG TTMYPGIADRMQKEITALAPSTMKI KIIAPPERKYSVWIGGSILASLSTFQ

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5004	10501	A	5315	279	418	QMWISKQEYDESGPSIVHRKCF VEHSISNKENFLGQGTGCHACNLNT LGGRGGRITWRSGV*DQLDQH
5005	10502	C	5316	274	530	MPCAEDYLSVVLNQLCVLHEKTPV SDRVTKCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKE XQIXKQTALV*
5006	10503	A	5317	2	736	RLAKTYETTLEKCCAAADPHECYA KVFDEFKPLVEEPQNLIKQNCSELF QLGEYKFQNALLVRYTKKVP/SVVL LLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNCCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLGKVGSKCKHPEA KRMPCAEDYLSVVLNQLCVLHEKT PVSDRVTKCTESLVNRRPCFSALEVD DETYVPKEFNAETFTFHADICTLS
5007	10504	B	5318	120	1070	MPADLPSLAADFVESKDVCKNYAE AKDVFLGMFLYEYARRHPDYSVVL LLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNFHT ECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLEKSHCIAEV ENDEMPADLPSLAADFVESKDVCK NYAEAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTLEKCCAAADP HECYAKVFDEFKPLVEEPQNLIKQNC CELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRKPRKSGQQML*
5008	10505	A	5319	2	668	
5009	10506	C	5320	246	365	MDDFAAFXXXCCXXDXKGDLLXR RKVKNLLLQVQLPLGF*
5010	10507	C	5321	261	656	MPCAEDYLSVVLNQLCVLHEKTPV SDRVTKCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKE RQIKKQTALVELVKHKPKATKEQL KAVXDDFXAFVEKCKGDXXKGELL XRRXVXNLL*
5011	10508	C	5322	158	607	MLCQSVGSKCKHPEAKRMPCAED YLSVVLNQLCVLHEKTPVSDRVTK CTESLVNRRPCFSALEVDETYVPK EFNAETFTFHADICTLSEKERQIKKQ TALVELVKHKPKATKEQLKAVXDD FXAFVEKCKGDXXKGELLXRRXVX NLL*
5012	10509	C	5323	158	532	MLCQSVPCAEDYLSVVLNQLCVLH EKTPTVSDRVTKCTESLVNRRPCFS ALEVDETYVPKEFNAETFTFHADIC TLSEKERQIKKQTALVELVKHKPKA TKEQLKAVMDDFAAFVEKCKKAD XKG*
5013	10510	A	5324	2	740	PADLPSLAADFVESKDVCKNYAEA KDVFLGMFLYEYARRHPDYSVLL LRLAKTYETTLEKCCAAADPHECY AKVFDEFKPLVEEPQNLIKQNCSELF EQLGEYKFQNALLVRYTKKVPQVS TPTLVEVSRNLGK/VCTESLVNRR

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						PCFSALEVDETYVPKEFNAETTFH ADICTLSEKERQIKKQTALVELVKH KPKATKEQLKAVMDDFAAFVEKCC KADDKETCFAEEG*KLGAASQAAL GLY
5014	10511	A	5325	1	588	
5015	10512	A	5326	364	1356	TGDHAFQLWKSMKHTFQVSTPTLV EVSRLGKVGSKCKHPEAKRMPC AEDYLSVVLNQLCVLHEKTPVSDR VTKCTESLVNRRPCFSALEVDETY VPKEFNAETTFHADICTLSEKERQI KKQTALVELVKHKPKATKEQLKAV MDDFAAFVEKCKADDEMPADLPS LAADFVESKDVCKNYAEAKDVFLG MFLYEYARRHPDYSVVLRLAKT YETTLEKCCAAADPHECYAKVFDE FKPLVEEPQNLIKQNCLEFEQLGEY KFQNALLVRYTKKVPQVSTPTLVE VSRNLGKVGSKCKHPEAKRMPCA EDYLSVVLNQLCVLHEKTPVSDRV TKCTESLVNRRPCFSALEVDETYV PSVNSNSCRGLKKPRKSGQQL*TS *SKKNALSEDYLSVVLNQLCVLHE KTPVSDRVTKCTESLVKGDHAFQ LWKSMKHTFPKSL/YAETTFHADI CTLSEKERQIKKQTALVELVKHKPK ATKEQLKAVMDDFAAFVEKCKA DDEMPADLPSLAADFVESKDVCKN YAEAKDVFLGMFLYEYARRHPDYS VVLRLAKTYETTLEKCCAAADP HECYAKVFDEFKPLVEEPQNLIKQ NCLEFEQLGEYKFQNALLVRYTKK VPQVSTPTLVE/VLKKPRKSGQQL* TS*SKKNALCRRLSIPWS*TSYVCC MRKRQ*VTESPISRNLGKVGSKCK HPEAKRMPCAEDYLSVVLNQLCVL HEKTPVSDRVTKCTESLVNRRPCF SALEVDETYVPKEFNAETTFHADI CTLSEKERQIKKQTALVELVKHKPK ATKEQLKAVMDDFAAFVEKCKA DDEMPADLPSLAADFVESKDVCKN YAEAKDVFLGMFLYEYARRHPDYS VVLRLAKTYETTLEKCCAAADP HECYAKVFDEFKPLVEEPQNLIKQ NCLEFEQLGEYKFQNALLVRYTKK VPQVSTPTLVEVSRNLGKVGSKCK HPEAKRMPCAEDYLSRGPEPVMCV A
5016	10513	A	5327	1468	1946	LHISWEGEPIDYSVVLRLAKTYE TTLEKCCAAADPHECYAKVFDEFK PLVEEPQNLIKQNCLEFEQLGEYKF QNALLVRYTKKVPQVSTPTLVEVS RNLKVGSKCKHPEAKRMPCAED YLSVVLNQLCVLHEKRQ*VTESNA AQNPW*TGDHAFQLWKSMKHTFP KSLMLKHSPSMQIYENQDSISSKLK ECCEKPLEKSHCIAEVENDEMPAD LPSLAADFVESKDVCKNYAEAKDV

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						FLGMFLYEYARRHPDYSVVLRLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLKQNCLEFQNGEYKQFNALLVRYTKKVPQVSTPTLVEVSRN/LRKSGQLR*J*TSCGRASEFNQTKL*AF*AAWRVQIPECAISSLHQESTPSVNSNSCRGLKKPRKSGQHTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLGGTGRPCFSSSGKSMETYVPKGFNAETFTFPGSFCT/LSWEGEPIDYSVVLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLKQNCLEFQNGEYKQFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPVC
5017	10514	A	5328	1	2063	MKKVKERDSFIMEDLGAEGLKSSAYSRGVFRDAHKSEVAHRFKDLGEENFKALVLIFAQYLQCPFEDHVKLVNEVTEFAKTCVADESAENCCKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFQHKDDNPVNLRLVRPEVDVMCTAFHDNEETFLKLYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTQVHTECHGDLLECADDRA DLAKYICENQDSISSKLKECKEPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLKQNCLEFQNGEYKQFNALAISSVTPKKVPQVSTQLLPTLVEVSK/NTLGKVGSKCKHPESKKKCPVAENYLSVVLNQLCVLHEKTPVSDRVTKIAAQEPLVNRRP/CFSALEVR*NIPFPKEVNAIETFTFHADICTLSIEKERQIRKQTALVELVETQAPRQKQKQLKA/VLWDDFAAFVKKIAAKADDKETCFAETISGNGAKKAIFLVNDEFILMSLTLIQNHRTYSSLPPCLYDSKLLFHYLASIYPFVPPQDACKGVSE L
5018	10515	A	5329	1	339	RRRRKKNEKRKRQRKIKDEKSRKNSLRVEMRETWRQREKQKEEDREKRGQQEKERRKREIEEKEST*CEQMEIGKTKKVNIHCRWQTQLKLKFLHLSLFSIKMSLSFSTRA
5019	10516	A	5330	2	189	ARGGDAGDAFDGFGFGDDPSD*LSCHIDVHRYLFSA LCDCYTFYFVHIRVFLLSMRLADTA
5020	10517	A	5331	3	346	HELETFP*CHNMPLLFYRDRLSASDMLQVRKVMHDVYESIITLNNESQSTSSSNNEHPGGQERSLARA

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5021	10518	A	5332	2	442	VFMDADTLVLANIDDLDFREELSA APDPGWPDCFNSGVFVYQPSVETY NQLLHLASEQGGDQGILNTFFSSWA TTDIRKHLPIFYNLSSISYSLPAI*S EDVSGAISHLVPLGGDSQAMAQAV LVFLGKEPGRGTEWGNKGPR
5022	10519	A	5333	1	292	VLANIDDLTREEMSAAQTQGWPD C/FNSGVFVYQPSVET/YNQLLHLAS EQGSFDGGDQGILNTFFSSWATTDI RKHLPIFYNLSSISYSLPVLPE
5023	10520	A	5334	81	1163	VTNLRPRPPAHFVITMTDQAFVTL TTNDAYAKGALVLGSSLKQHRTR RLVVLATPQVSDSMRKVLETVFDE VIMVDVLDGSDSAHLTLMKRPELG VTLTKLHCWSLTQYSKCVFMDAD TL/VLANIDDLDFREELSAAPDPG G/PDCFNSGVFVYQPSVETYNQLL HLAS/EQGSFDGGDQGILNTFF*QL GQQQDIRKHLAFIYNLSNISIYSYLP AFKVFGASAKVVHFLGRVKPWN TYDPKTKSVK\SEAHDPNMTHPEFL ILWVGTSFTTNVLPLLQQFGPWSK DTCSYV\N\VGRC\QGAISHLSLGEI PA\MAQPFV\SSSEERKERWEQGGAD YMGADSF\DNIRKLD\TYLQ
5024	10521	A	5335	1	241	GTSNSEHALDDRSTAQCRVQMQVV QQL*LQLAKDKERLQAMMTHLHV KSTEPKAAPQPLNLVSSVTLSKSAL EAYALELT
5025	10522	A	5336	13	229	ACPRSPPPDRLGCCFPPPAVC*AP AGPHPDGTTSLECTPAPHPSCPEVS VQQKPEPSALYGTGFPGFGLQS
5026	10523	A	5337	1	341	GLGSGTSSSSSVKSSISPKRVARWSFS SRVCPVCPSALSV*DSRSP*ASKSS SNASGSPFCRVKKLSCELOSKADS FSSSSAVSRDRLSSSSMLSRGQL*Q ETSKEAQMPR
5027	10524	A	5338	3	168	
5028	10525	B	5339	978	1502	MSNLTLCISTKHTPGISRakeKKK GTSRLPTSLCQRRVGLTEEKSCSPEL QQKFRSETITEELVGLMNKFVEDT KKGVHQEGWPSSAYGVTKIGTV LSRIHARKLSEQRKGDKILLNACCP GWVRTDMAGPKATKSPEEGAETPV YLALLPPDAEGPHGQFVSEKRVEQ W*
5029	10526	A	5340	3	239	HEAKSSPNLVKAILQIQEATQIPRRI NKNKSTLRHRIEFLKTKDKEKSLRT PREIYYL*GNKISITVNLESESMGT
5030	10527	A	5341	3	322	HEAKSSPNLVKAILQIQEATQIPRRI NKNKSTLRHRIEFLKTKDKEKSLRT PREIYYL*GNKISITVNLSETMEAR KKWHNYQMIEKNCQPTILHPAKLS FK
5031	10528	A	5342	4	351	VGRGRQSHLSHSPPTDPKGQOASP GWNPGVRMLPGLKWLPQPPAASLS *VPSSPTQOTSAGHLLSMSHEALTW

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						VDRATGLAGNGEACVSGTQRHPGL SLAPPGCAPSPSSRAARA
5032	10529	A	5343	3	163	HEEQPEGLSPNLDRFLGDRHCNQFS SRD*PIFLARCSHEYSGRHPRLADSI LL
5033	10530	A	5344	112	362	EREQRFTGLNDVHYLPIMYIVVGC AIFIT*V*RGWSSPTKCRSTDYCVNP STRLHAYMAPRHLHSHCAERDPD QFTLLRHC
5034	10531	B	5345	85	206	XFSDPEVKKETRPALGSTVLLAPFL HEHEPPSAEVLPGSWRX*
5035	10532	A	5346	142	653	GFWHQRILGASDQAHLLPHKQDG SADGARRVLACARGQGDRLRLRLH LAAVPLQLPGGLRRRAVHVHGGGC QQDGGAESWS/PSPPSRGPRTLHR VEKVPGAPVTPLPVAFSCNPDHIE DPAFP*PAAGPR*LQEGPCGGRAS RAPPTSTRSCCTECLRNLSILIC
5036	10533	A	5347	261	538	GSRSRLLFSPRGPRTPAWKRSTGA PVTSPPIAFSCNPDHIEDPAFP*PAA GPR*LQEGPCGGRASRAPPTSTRS CCTKCLRNFLILIC
5037	10534	A	5348	7	264	FQKISALPQRSDYTHNTPHTDPARV SYKHAGANHITHIHPMTNVSTTIYP PHAYLHTHTQKTPPHIYSTHAP*I*L FISTYAHTKN
5038	10535	A	5349	208	713	SVKMVRYSLDPENPTKCKSRGS\N LRVHFKNTRETAQAIGMHARKAT KYLKDVTLQKQCVFRRYNGGIGR CAQAKHWGWTQGR\WP*RVLNSL VIEHIQVNKAPKMRRRTYRAHGRIN PYMSSPCHIEMILTEKEQIVPKPEE VAQKKKISQKLLKKQKLMARE
5039	10536	C	5350	286	591	MVRLFNLNPEKRQRKSWQIRGFQS SCFTLGLTVKLAQAIGMHARKATE VSERWSLYRNSVYHSDGNNGGVG RRAQAKQWGLGHKVGPKKECLN FLLHML*
5040	10537	A	5351	1	305	GTSIYNVLYEVPLPPPGRSLKFSGVY GPICQRPSTNELPLDFDPVKEVFELL GVDNVYQLFTWALLQKYILLVYQR *CNVTKALELSNLLLFHICDIKL
5041	10538	A	5352	15	234	LSCPDQVHPHSLVPYPEPRRATASV PETSGPPFPHPRRPYATTPALGHNP HA*LSSSFAGSRYKLGEMLHI
5042	10539	A	5353	3	257	HEVKYKNPAQ*QWHLGPDHVP EFRYHKQLIQSQLFLHYHLSQTFTL QESADLQNAFLNSGQCILNKPLKFA DLHSDFMKTI
5043	10540	A	5354	3	334	IIKFIWNPKRA*IAEAILSKKNIAGGI TLPDFRLYNKAIVI*TAWYWHKNR HIDQWNRILNPEIKSHTYSQRIFDKI DKNIH*GKDTLFNKWCWERWIAIC RRIKLDLSLV
5044	10541	A	5355	1	119	QKSRW*TPPNSYMKVNVPEKSRNG ETSLRTKIAVCQYYM
5045	10542	A	5356	3	349	HEPANADFAFRFYLIASETPGKNIF

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						FSPPRFPAA YAMLSLGACSHSRSQL EGLGFNLTELSSEDARRRCRQ*VGT LDLTQHGLQTRGGQGPWPRARPSR GGDAAAGSARLPPR
5046	10543	A	5357	1	499	
5047	10544	B	5358	66	641	MASKINTKALQSPKRPRSPGSNSKV PEIEVTVEGPNNNNPQTSVRTPTQ TNGSNVPFKPRGREFSFEAWNAKIT DLKQKVENLFNEKCGEALGLKQAV KVPFALFESFPEDFYVEGLPEGVPFR RPSTFGIPRLEKILRNKAKIKFIKKP EMFETAIKESTSSKSPRKINSSPNV NTTASGVEDLNIIQ*
5048	10545	A	5359	2	306	ARGVCGGCRCCLGFCGSVVGDLMY* NSFDCFKKVLRY*GFFGLYWGLIP* LIWFAPEQAIYLTDNVVFVRDKFT*R DGSDSLSAEVLAGGCALGSLVIVTN SL
5049	10546	A	5360	3	120	HEGKEPDIPLYETVQTVGPSHARTY TVASHSEGR*TIC
5050	10547	A	5361	2	366	SLPASDRPPISSPLATSGTIFSAISCF WDLPAFLWLAPSCQPTMSSQIRQN YSTDVEAAVNSLVNLYLQASYTYL SLQDIKKPAEDEWGKTPDAMKAA MALEKKLNQALLDLHALGSART
5051	10548	A	5362	1	108	
5052	10549	A	5363	2	536	ARAARDWKNYSTDVEAAVNSLVN LYLQASYTYLSLGFYFDRDDVALE GVSHFFRELAEEKREGYERLLKMQ NQRGGRA\LFQDIKKPAEDEWGKTP DAMK\AAMALEKKLNQALLDLHAL GSARTDPHL\CDFLEPHFIDEVVKLI KKMGDHLNLHRAGWPRRLGLGE YLFERLTLKHD
5053	10550	A	5364	3	331	HEQYPGSISISLTDLGCPDMPVIIAR* TAAADESLVPTRLMLQLADYGPVI YSLVI*VCLTAAFTLAQQHSMKIY ADIIGSEDTTNEDYRSIALYFEREMR YLQAAKF
5054	10551	A	5365	3	52	HEQSWKAENEFTLADLKQLPELN PPVLMPRGNVGTPLRVFLELIRACR LPPRIITQLHFQIPKIGYSLRYCNVPF EYEDSDTAVQE*LT
5055	10552	A	5366	3	323	STFFFFFLRQSLALVAQAGLRTQW RNLGSLQAPPPGFTPFSCSLPSSWD YRRPPRLA\NFFFFFFFVFLAETGFH CVLARMVISIS*PRDQPASASQSAGIT GVSD
5056	10553	A	5367	3	337	HERHEDTLTLKERNRGNGILDDID DHNIIYHLPDA*SEEYEFKEQTTL LRASIPFSVGGSNQLIEAIGKMVRGR LYPWSVDKVENPQHNDFMKLITML ITHMHDLDQDV
5057	10554	A	5368	16	313	SHSVTQAGVQCWHLHAQLIFLYF LVETGFHRVSQDGLYLLTS*SARLG LPKCWDYRRDDHAWPVQFFKCS PRPQAILDFAFTSHELCLGSMRLKKS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
5058	10555	A	5369	1665	1787	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5059	10556	A	5370	1431	1553	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5060	10557	A	5371	1740	1862	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5061	10558	A	5372	1173	1295	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5062	10559	A	5373	1027	1149	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5063	10560	A	5374	2250	2372	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5064	10561	A	5375	934	1092	FFVFLVETGFHRVSQDGLDLLTS*S ARLSLPKCWDYRREPPCPRIYILTR SR
5065	10562	A	5376	2588	2824	VAGTIGACHHAQLIFVFLVETGFHH VGQDGLDLLTS*STHLGLPKCWDS RREPLRPASPVVVFQRTSAPVMADLT PTVS
5066	10563	A	5377	935	1138	RRGFTMFHHVSQGGDLLTS*SARL GLPKCWDYRREPLCPAWKDY*CKL QDEVISQQGLKVSVLIH
5067	10564	B	5378	79	1551	MSEVTKNSLEKILPQKCHFTWNLF KEDSVSRDLEDRCVNCQIEFLNTEFK ATMYNLLAYIKHLDGNNEAALECL RQAEELIQEHADQAEIRSLVTWGN YAWVYYHLGRLSAQIYVDKVKQ TCKKFSNPYSIEYSELDCEEGWTQL KCGRNERAKVCFEKALEEKPNPPE FSSGLAIAMYHLDNHPEKQFSTDVL KQAIELSPDNQYVKVLLGLKLQKM NKEAEGEQFVEEALEKSPCQTDVLR SAAKFYRRKGDLDAIELFQRVLES TPNNGYL YHQGCCYKAKVRQMQ NTGESEASGNKEMIEALKQYAMDY SNKALEKGLNPLNAYSDLAEFLETE CYQTPFNKEVPDAEKQQSHQRYCN LQKYNGKSED TAVQHGLEGLSISK KSTDKEEIKDQPQNVSENLLPQNAP NYWYLQGLIHKQNGDLLQAAKCY EKELGRLLRDAPSGIGSIFLSASELE DGSEEMGQGA VSSSPRELLSNSEQL N*
5068	10565	A	5379	925	1127	FFVFLVETGFHRVSQDGLDLLTL*S THLGLPKCWDYRREPLRPATFSSYQ RNNPDILNDTIMPNIK
5069	10566	A	5380	438	815	TRPSFSFNPLTLFFFLLRRSLALSPRL ECSGAISAHCKLRLLGSSHSPTSASR VAGTTSARHHA WLMFFVFLVETG FHLVSQDSL DLLTS*SAPLGLPKCW DYRHEPPRPAHLHFLNFFLFSYT
5070	10567	A	5381	7944	10115	KQCNYGHNLTCSNFFFFWRWSLA PSPRLECNGAISAHCKLRPPGFTFPS CLSLPSSWDYRRSPRAANFFVFLV ETGFHQVSQDGLDLLTL*SARLGLP KCWDYRREPPCPESALIF
5071	10568	A	5382	1	211	LKTSEKWRNRQDKSNKGSKKAERK

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						RATHADRNREAAIRRKTYTNERK HYEHHRTAGKDQDERATEDSRE* RE
5072	10569	A	5383	2	373	ARECHHLCKINYMDLVKEFMTLNA SAPLRSSFSDTMIRLPALTYPLFPAL ATCAGYSDKA*SSISYVLHNSALWR ASGPTDHRDAPA*A*LESRRSTLRIC ELRTLYSLIKSTASNFDPIKLFS
5073	10570	A	5384	112	913	DFLSMPNRRGGVSLPPTPP*PPFSVT HTIFSVSFSFHWLKGSLRRQFSYCF YGMVLVPFPSPHPLSLSAPSKCLRIP PLPWGWVTAPRLRSHPSVTGRAVL ERKPSVRG*AGSLNTQARDTPPQLP ERPPEG*ALFPPFPYSMAPPSQLKPT LKITAVRS*ASGGATGLGGWSPLGL P*EQGLRPTATLTQTSGIALNPRSLT PAPQLRLSCPPHFALTTRA VPGGPQ PLAWGPEPGTPPAQPRPSPDSAQSH TVYRRESILFFIL
5074	10571	A	5385	2	345	SFWLLCGSSCSDLRSCQVLKCTRNI PYSLVPTASCEHLHGPCIYRPSVQS VLTCTAAQATNILSAQSLLSGPTTQ* WGLTYPCLLVGAADLTPTTPPPPT PAPPHLPSTPPP
5075	10572	B	5386	36	340	MFLDEYARRHPDYSVVLRLAKT YETTLEKCCAAADPHECYAKVFDE FKPLVEEPQNLKQNCLEFEQLGEY KFQNALLVRYTKKNALCRRLSIRGP EPVI*
5076	10573	A	5387	3	182	
5077	10574	C	5388	602	877	METTLRRKCCARLQILHGMAMPKV FRWNFKPLVGRSLRNLNPNKIVEAF WSQLGRSYKFGPMRYLVSFTPKES YPKCSNFPTLCRRVFKET*
5078	10575	A	5389	1	404	GTRNDKMEPGLEQGTIPRLDSVTSS ECFASSGFHEDRSLSDVEEQEDSDG FYKEPITMEDLISYSFQVAIGMESLS SRLCIHRDLEARNFHLSGNYCDTSL EF*IENYDIYL**FNIYSPTKLKPEDT RLKET
5079	10576	A	5390	110	424	LSSLQREREGHLNGSPSFMKCSGF YRLA*GVCV*VSFVL*Y*HILIYSML TVLILCIYFFNMLISGIYTDYAFYIC YIYYCYIF*FILLCFYTLMTIFFGLI
5080	10577	A	5391	2	361	ARETVKRIQYPIPLEGRGLKPLIES LI*DGLLELCMSPTYTPILLVK*SDW *Y*LVEDLQAINQTVQTTTHPVVNP YTILSKIPYDHQWFTEIDLKDAFWA CPLAEDS*DIFTFEWARA
5081	10578	A	5392	3	335	QSQSWWRQKGVSRAGAGPIHPQGL LFGFS*GDLGPLGTLGEQGLIGQRG EPGLEGDSGPMGPDGLKGVRGDPG PDGEHGEKGQEGLMGEDGPPGPPG AAGVRGLHGKSGY
5082	10579	A	5393	61	497	
5083	10580	A	5394	16	951	RRPKIRDKFWGVS/KKLAHSEASPVI SGASKRAKKQINVVYVGKSS/QGK

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						MVVVWKKLDRDTVFALVNYIFFKG KWERPFVKDTEEDFHVDQATTV KVPMMKRLGMFNIQHCKKLSSWV LLMKYLGNAITAIFFLPDEGKLQHLE N\ELTHD\IVTKFLE\NEDRRSASLHL PKLSITGTYDLK\TVLGQ\LGITKVFS NGAD\LSGVTEEAPLKLSKAVH*GC A*PSTEERGLKLAGGHVF*EGHYPC FIPPRGSSFNKPFVFLNGFEQN/SPSF PLFMGEKWVNPTPKITGLSLLNPSP PSLGPLPGMTLKKGLSWK
5084	10581	A	5395	2	306	GFDHVAQAGLEPLGSSDLPPSASQS AGITGMSHHTQPA YILKISFITL PFIIR SLS*VPFVFSIMYKSSFNFSPCGESVF STNLLNNEYLLIDWWLHFIY
5085	10582	A	5396	1	375	
5086	10583	A	5397	162	426	
5087	10584	A	5398	140	426	
5088	10585	A	5399	158	705	PSEKNKNLLLGVVYVRHLPNLLD ETQIFSYSQFG\PVTRFRLSR\NKRT GN\SKGYAFLEFESEDVCQNSCLKQ WNNYLFGGKTG/QCHFMPPEKVH K\NSFKDWDFPFKQPSYPSVKRV*S ESDTNTKA/DGMEERFKK\ERLLRK KLAKKGIDYDFPSLILQKTESISKTN RQTSTKGQVFT
5089	10586	A	5400	2	388	FLFFFEMESRSVAQAGVQWCDLG SLQPPPPGLSDSPALASSVSWITDV RHHLWLIFVFLVETGFRHVGQASLK LPTSGDLPTLASQSAGITGVSHYAW LIFVFLVETEFHHVGQAGLELLAPS DPPA
5090	10587	C	5401	197	415	MLLYVGLEPHHHTMLSLWPRLMF PSVFFFFFFFFFLRQGLALLPRLECS GAILAHCNLHLLGSGDSLASF*
5091	10588	A	5402	671	986	KGVLLLLFFFKTESHSVAQAGVQW CTLGSLQPP/PSRGSSDSPASASRVA GIRGVHHHARLIFVFLVETGFHYVG QAGLELPTSGDSPASASQSAGVTGV SHQCPA
5092	10589	A	5403	65	921	
5093	10590	A	5404	213	442	
5094	10591	A	5405	1	1506	
5095	10592	A	5406	1	286	DRLIYIPFPDEKSLVPILKANLGKSP VPKDLLEFLDLVPWGCGRLPRRG NQGCAHSLHSPAGHACYSLTLDR GFLQKSKPKAVKLPRFSFG
5096	10593	A	5407	2	158	
5097	10594	A	5408	1	9064	MLARAARGTGALLRGSLLASGRA PRRASSGLPRNTVVLFVPQQEA WV VERMGRFHRILEPGLNILIPVLDRI YVQSLKEIVINVPEQSAVTLDNVTL QIDGVLYLRI MPYKASYGVEDPEY AVTQLAQTMRSELGKLSLDKVFR ERESLNASIVDAINQAADCWGIRCL RYEIKDIHVPPRVKESMQMQVEAE RRKRATVLESEGTRESAINVAEGKK

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me thod	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QAQILASEAEKAEQINQAAGEASAV LAKAKAKAEAIRILAAALTQHNGD AAASLTVAEQYVSFAFSKLAKDSNTI LLPSNPGDVTSMVAQAMGVYGALT KAPVPGTPDSLSSGSSRDVQGTAS LDEELDRVKMTWSPVPNFQLLNIPS NWGQPHAPGQTSTEV PADGDGATD GPLCLAHASLCCQVAGAAAAALPG AIAGGAVGWARIPLRLRLSLSTGMQ KASVLLFLAWVCFLFYAGIALFTSG FLLTRLELTNHSSCQEPFPGPSLPW GSQGKPGACWMA SRFSRVVLVID ALRFDFAQPQHSHVPREPPVSLPFL GKLSSLQRILEIQPHHARLYRSQVDP PTTMQRLKALTTGSLPTFIDAGSN FASHAIVEDNLIKQLTSAGRRVVF GDDTWKDLFPGA FSKAFFPSFNVR DLDTVDN GILEHLYPTMDSGEWDV LIAHFLGVDHCGHKHGHHPPEMAK KLSQMDQVIQGLVERLENDTLLVV AGDHGMMTNGDHGGDSELEVSAA LFLYSPTAVFPSTPPEEPEVIPQVSLV PTLALLLGLPIFGNIGEVMAELFSG GEDSQPHSSALAQASALHLNAQQV SRFLHTYSAATQDLQAKELHQLQN LFSKASADYQWLLQSPKGAEATLP TVIAELQQFLRGARAMCIESWARFS LVRMAGGTALLAASCFICLLASQW AISPGFPFCPLLLTPVAWGLVGAIA YAGLLGTIELKLDLVLLGAVAAVSSF LPFLWKAWAGWGSKRPLATLFP GPVLLLLLFR LAVFFSDSFVVAEAR ATPFLLGSFILLV VQLHWEGQLLP PKLLTMPRLGTSATTNPPRHNGAY ALRLGIGLLLCTRLAGLFHRCPEETP VCHSSPWLSPLASMVGGRKLNW YGACVAALVALLAAVRLWRRYG NLKSPEPPMLFVRWGLPLMALGTA AYWALASGADEAPPRLRVLVSGAS MVLPRAVAGLAASGLALLLWKPV T VLVKAGAGAPRTRTVLTPFSGPPTS QADLDYVVPQIYRHMQE EFRGRLE RTKSQGPLTVAAYQLGSVYSAAMV TALTLAFPLLLHAERISLVFLLLF LQSFLLLHLLAAGIPVTPGKYLSSD SLKDNSDSQGLRKRQPPGNEADA RVRPEEEEEPLMEMRLRDAPQH FYAALLQLGLKYLFI LGIQLACALAAS ILRRHLMVWKVFAPKFIFEAVGFIV SSVGLLLGIALVMRVDGAVLLSSAS TERHCQQTTRGRKPTLVSVLVLDSE QRKDGRLRSALVSSYRFLET PSAGAE LFRPASATMSRQTTSVGSSCLDLW REKNDR LVRQAKVAQNSGLTLRRQ QLAQDALEGLRGLLHSLQGLPAAV PVLPLELTVTCNFILRASLAQGFTE DQAQDIQ RSLERVLETQEQQGPRLE QGLRELWDSVLRASCLLP ELLSALH

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						RLVGLQAALWLSADRLGDLALLLE TLNGSQSGASKDLLLLLKTWSPPAE ELDAPLTLQDAQGLKDVLLTAFAY RQGLQELITGNPDKALSSLHEAASG LCPRPVLVQVYTALGSCHRKMGNP QRALLYLVAALKEGSAWGPPLLEA SRLYQQLGDTTAELESLELLVEALN VPCSSKAPQFLIEVELLLPPDLASP LHCQTQSQTKHILASRCLQTGRAGD AAHYLDLLALLLDSSEPRVGPCMP EVFLEAAVALIQAGRAQDALTLCEE LLSRTSSLLPKMSRLWEDARKGTKE LPYCPLWVSATHLLOGQAWVQLG AQKVAISEFSRCLELLFRATPEEKEQ GAAFNCEQGCKSDAALQQLRAAAL ISRGLEWVASGQDTKALQDFLLSV QMCPVSAKRLRPSFESSLPPLPLPL PPRGSGASVVRPTPRCRPRPARLAP LERTSGPGQVFRPTPPGRRPGALGR QSAVRPTTRRKPLVPGESRPREPEA PAGPEEDIKVQRLGNLPKITIKQWH NWNSDPMGLTIEFLLLTLLSKGDD LSTAILKQKNRPNRLIVDEAINEDNS VVSLSQPKMDELQLFRGDTVLLKG KKRREAVCIVLSDDTCSDEKIRMNR VVRNNLRVRLGDVISIQPCPDVKYG KRIHVLPIDDTVEGITGNLFEVYLKP YFLEAYRPIRKGDIFLVRGGMRAVE FKVVETDPSPYCIVAPDTVHCEGEP IKREDEEESLNEVGYYDDIGGCRKQL AQIKEMVELPLRHPALFKAIGVKPP RGILLYGPPGTGKTLIARAVANETG AFFFLINGPEIMSKLAGESESNLKA FEEAEKNAPAIIFIDELDAIAPKREKT HGEVERRIVSQLLTLMDGLKQRAH VIVMAATNRPNSIDPALRRFGRFDR EVDIGIPDATGRLEILQHTKNMKLA DDVDLEQVANETHGHVGADLAAL CSEAALQAIRKKMDLIDLEDETIDA EVMNSLAVTMDDFRVRTTPVPQW ALSQSNPSALRETVVEVPQVTWEDI GGLEDVKRELQELVQYPVEHPDKF LKFGMTPSKGVLFYGPFGCGKTL AKAIANECQANFISIKGPELLTMWF GESEANVREIFDKARQAAPCVLFFD ELDSIAKARGGNIGDGGGAADRVIN QILTEMMDGMSTKKNVFIIGATNRPDI IDPAILRPGRLDQLIYIPLPEKSRVA ILKANLRKSPVAKAGARSWADV LGVPGLKMTNGFSGS*P*QEILPACF AKLAIRESNREVKIKAKNREEGKT NPIKPMGRYE*WIDPVPEIRDSLL KEAQSFCAFLFSDNDRKYEMFA QTLSQ/ESRGFGSFRFSGNQGAGP SQGSGGGTGGSVYTEDNDDDLYG
5098	10595	A	5409	96	299	
5099	10596	A	5410	174	324	
5100	10597	A	5411	74	242	

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5101	10598	A	5412	129	899	AAPGLGRGGGAAAGGGAVCPGTE RPCAMAYAYLFKYIIIGRTTGVG*N PCPNALQFTD/KRGFQPSAMTLTIGV EFGA\RMITIDGKQIKL\QIWDTAGQ ESFRS\ITRSYYRGAAGALLVYDITR\ *DTFNH\LTWLEDARQHSNSNMV IMLIG\NKSD\LESRREVKKE/EKGEA FA\REHGLIFMETS AKTGFQCRKEG ILFNTAKEILLKKFPKGVFLTFN*W RANGH\IKLGPQPAAYPIATHAGQS G\GQQAGGGCC
5102	10599	A	5413	1	408	MQLKRANPGPRRAPVRETVMLLLC WGVPPGRPYKVDTESALLYQGPHN TLFGYSVVLHSHGANR\WGAPTAN WLANASVINPGAIRCRIGKNPGQT CEQLQLGSPNGEPCGKTCLEERDNQ WLGVTLSRQPGENG
5103	10600	C	5414	1	1026	MGLGIYLDQYTRQKGQDPVAELKQ LIPLVVSL SAPNLEPLLKKKTNP TFLKSLSGGLNLFNFPFVETVTEE VKVHPRNNTGGYNPEEEDETA NCFPWNVDGDLMEVASEVHIRRVQ KKEYVEENKIPRNPYKGC EGPLQE NYKPLL NKIKEDTNKWNIPCSWIG RTDTVKMAILPKHDRVAEQRVVGA LVKQRASQCPRCRGGRSGPPGTAT ASPSGRRPFGAVIAPRFP SHALSSW YAGCNAEKSEVNAPGTQGMRFIS AASYKDWVQVLQKQDVSRNMGTK ARM MPLGSSGGCHTIRTEVTQDSE GQLAAVTTTGYTVVGLEPPKVSD*
5104	10601	A	5415	1	681	
5105	10602	A	5416	1	779	MNNGRNYRCQNLVDKGVGENRGP ADNRMLVAHQCSREEKLKEPDEQV TPAVCQQDSLAMERLGRSPTAEK VPETTTTRFWAPGVEAPGDDAERRR REASGPATRHSP LPTAGITAPKAGS AKVQLSILKPSKLDKCSHKTSHTKS SYHYFLHYPV SSTVQPVAAAATPSY ALIGSSLWPVNERGRQESRTCIIDQ SAWHVGRAEIRKLLPYCSTQGGLK YSDVTSGMVKDPPDVL/DRQKCLD ALAALRHAKWSSEIRF
5106	10603	A	5417	1	1274	MEMRRYEEDMYWRRMEEEQHHW DDRRRMPDGGYPHGPPLGLLGV RPGMPPQPQGPAPLRPDSSDDRYV MTKHATITYPTEELQAVQKIVSITER ALKLVSDSLSEHEKNKNKEGDDKK EGGKDRALKGVLRVGVFAKGLLLR GDRNVNLVLLCSEKPSKTLLSRIAE NLPKQLAFISPEKYDIKCAVSEAAII LNSCVEPKMQVTITLTSPIREENMR EGDVTSGMVKDPPDVLDRQKCLDA LAALRHAKWFQARANGLQSCVHIIR ILRDLCQRVP/TWSDFPSWAMELLV EKAISSAS\SPQSPGDALARRVFECIS SGVILK\GSPG\LLDPCEKDPFDTLG QQ*PD\QQR\EDITSSAQFALRLLAFA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RQIHKVLGMDPLPQMS\QRFN\IHNH QDR\RRDSGDVDGFEAEGKKDKKD YDNF
5107	10604	A	5418	144	522	VDLLRAAGRQWQGPLRPRPSGRR* SARRA/LGKTTYCTDPAKFISVLWT YLATMLHVELPHMNLLSTMDLIEH YGKLAFLNDYYTEVLDLS*LLDHL AS/VPFLTAYRQVTEKLVQLIEDYIL RCFIHP
5108	10605	A	5419	1	2437	MAVPGEAEEEEATVYLVVSGIPSVLR SAHLRSYFSQFREERGGGFLCFHYR HRPERAPPQAAPNSALIPTDPAEAG QLLSQTSATDVRPLSTRDSTPIQTRT CCCVISVRGLAQARLIRMYSGRR WLDHGTWLPGRCLIRRLRLPTEAS GLGSFFPKTRKELQSWKAENEAFTL ADLKQLPELNPPVLMPRGNVGTPL RVFLELIRACRLPPRIITQLQLQFPKT GSSRRYGNVPFEYEDSETVEQEELV YTAEGEEIPQGTYLADIPASPCGEPE EEVGKEEEEEESHSEDDDRGEEWE RHEALHEDVTGQERTTEQLFEEIE LKWEKGGSGLVFYTDAQFWQEEE GDFDEQTADDWDVDMSVYYDRDG GDKDARDSVQMRLEQRLRDGQED GSVIERQVGTFERHTKGIGRKVMER QGWAEQGQLGCRCSGVPEALDSDG QHPRCKRGLGYHGEKLQPFQQLKR PRRNLGLISTIYDEPLPDQTESLL RRQPPTSMKFRDMAFAVIGPPGSG KTTYCLGMSEFLRALGRRVAVVNL DPANEGLPYECADVGLVGLGDV MDALRLGPNGGLLYCMEYLEANL DWLRAKLDPLRGHYFLFDCPGQVE LCTHHGALRSIFSQMAQWDLRLTA VHLVDSHYCTDPAKFISVLCTSLAT MLHVELPHINLLSKMDLIEHYGKLA FNLADYYTEVLDLSYLL*PPGLLTLS SATTRPASIEEA/MCKLIEDYNLVSF IPLNIQDKESIQRVLQAVDKANGYC FGAQEQRSLEAMMSAAMGADFHS STLGIQEKYLAPSNQSVEQEAMQL
5109	10606	A	5420	2	78	
5110	10607	A	5421	94	253	
5111	10608	A	5422	2	318	
5112	10609	A	5423	460	672	
5113	10610	A	5424	357	795	
5114	10611	A	5425	310	478	
5115	10612	A	5426	1	399	
5116	10613	A	5427	2	390	
5117	10614	A	5428	3	392	GGKIIVGDATEKDASKKSDSNPLTE ILKCPTKVLLRNVMVGAGEVDEDL EVETKEECEK\YGKVGKCV\IFEIPG APDDEAVRIFLEFERVESAIKAVVD LNGRYFGGRVVKACFYNLDFRVL DLAEQV
5118	10615	A	5429	837	1005	

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5119	10616	A	5430	174	247	
5120	10617	A	5431	1	360	
5121	10618	A	5432	1	382	
5122	10619	A	5433	338	442	
5123	10620	A	5434	1	140	
5124	10621	A	5435	3	339	PINFESVGPTYRGSSCLAVVVPEFLG MSVAFVPDWLRGKAEVNQETIQRL LE*NDQLIRCI\LEYQNKARGNECVQ YQHVLRNL\YLATIADAQSQPALS KAMGIIFQKQ
5125	10622	A	5437	157	371	
5126	10623	A	5438	150	284	
5127	10624	A	5439	84	901	ARKSVRMASRMTRRDPLTNKVAL VASTDGIGFAIARRLAQDRAHVVV SSRKQQNVQ\AVATL\QGEGLSVT GTVCHVGKAEDRGAAWWPPAVKL HGGIDILVSNAAVNPFFGSIMDVTE EV\WDKTLD\NVKGPKP*MTKAVV PEMEKRGGGS\VVIVSSIAAFSPSPG FSPYNVSKTALLGLAQTLPIELAPR NIRV\NCLAPG\LIKTSF\SRMLWMD KEKEESMKETLR\IRRLGEPEDCAGI VSFLCEDASYITGETVVVG\GGTPS RL
5128	10625	A	5440	2	468	
5129	10626	A	5441	63	219	
5130	10627	A	5442	3	558	
5131	10628	A	5443	7	909	DQCEVCRNSEVRPAACPGHSGSPA QGPPRPFRMKA\VLTLAVLFLTGSQ ARHFWQQDEPPQSPWDRVKDLAT VYVDVLKDSGRDYVSQFEGSALGK QLNLKLLDNWDSVTSTF\SKLREQL GPVTQEFWDNLEKETEGLRQEMSK DLEEVKAKVQPYL\DDFQKKW\QEE MELYRQKVEPLRAELQEGARQKLH ELQEKLSPLGEEMRDRARA\HVDAL RTHLAPYSGELRQRLGAR\LGALRE NGGARMGQYHA\QATEHLSTLSEK AKPAEDLRQGLLPVLESFKVSFLS ALEEYTKKLNTQ
5132	10629	A	5444	3	195	
5133	10630	A	5445	189	263	PPGSHLGHPANAPSH*GPYPGLHS
5134	10631	A	5446	1905	2052	
5135	10632	A	5447	1903	2050	
5136	10633	A	5448	1	115	
5137	10634	A	5449	1	402	GKTSKLEFSIYLAPHSTTAAIEPYN SILTTHTTLEHYDWFMA\YNGAIYDI CRRNLDIGRTTYTNLNTLIGQIESSIT ASLRFDGALNGDLT*FQTNLVYPYPR IHFLATYAPVISA\EKAYHEQLSVA EITNAC
5138	10635	B	5450	81	319	XVVEPYNSILTTHTTLEHSDCAFMV DNEAIYDICRRNLDIRPTYTNLNL IGQIVSSITASLRFDGALNVDLTFEQ TNL*
5139	10636	A	5451	1	422	GKKSLEFSIYPAPQVSTAVVEPYN SILTTHTTLEHSDCAFMVDNEAIYDI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						CRRNLDIERATYTNLNRIGQIVSSIT ASLRFDGALNVDLTEFQTNLVPYPR MHLPLGTYAPVICA EK/AYHETA FV QKTTCLG*PSQQMW
5140	10637	A	5452	771	1640	ALQLHPHPHPHPWSTLIVPFMVDN EAIYDICRRNLDIERPTYTNLNRVIR A/QMGPSITASLRFDGALNVDLTEF QTNPGAPTPIHLP/LWPTYAPVHLL AGGKPYHGTAFL*AGGFTNGLVLE ARPTQMGGNVDPW\HG VNYMGLL AWLYRGDVGF PKIDNGWPLPTIKN QAQHSFVDW/CGPTGLSRFGHSTY QPSTVVPGL ETWAKV\QRAV\CML\ SNTTAIAEVA*ARLDHKFDLMYAKR AFVHWYVVGEGMKEGEFSEAREDM AALEKDYEEVGVD SVEGE GEEGE EY
5141	10638	A	5453	89	435	
5142	10639	A	5454	2	287	TNEIEPEEN*HTKARNFRFRVTAINN TPRNIRE D/GDHL LHHWIAL LADCP TAHMYEDVALIKDHTLDNSLIRELQ TLQEFNITLETALVKGIDI
5143	10640	B	5455	218	3940	MSGGGGGGGGSAPSRFADYFVICGL DTETGLEPDELSALCQYIQASKARD GASPFISSTTEGENFEQTPLRRTFKS KVLARYPENVEWNPFDQDAVGML CMPKGLAFKTQADPREPQFHAFIIT REDGSRTFGFALT FYEEVTSKQICSA MQTLYHMHNAEYDVLHAPPADDR DQSSMEDGEDTPVTKLQRFNSYDIS RDTLYVSKCICLITPMSFMKACRSV LQQLHQA VTSPPPPPLESYIYNVL YEVPLPPPGRSLKFSGVYGPIICQRP STNELPLDFPVKEVFELLGVENVF QLFTCALLEFQILLYSQHYQRLMTV AETITALMFPPQWQHVVYPILPASL LHFLDAPVPYLMGLHSNGLDDRSK LELPQEANLCFVDIDNHFIELPEDLP QFPNKLEFVQEVSEILMAFGIPPEGN LHCSESASKLRRLASELVSDKRNG NIAGSPLHSYELLKENETIARLQALV KRTGVSLEKLEVREDPSSNKDLKV QCDEEELRIYQLNIQIREVFANRFTQ MFADYEVFVIQPSQDKESWFTNRE QMQNFDKASFLSDQPEPYLPFLSRF LETQMFASFIDNKIMCHDDDDKDP VLRVFD SRVDKIRLLNVRTPTLRTS MYQKCTTVDEAEKAIELRLAKIDHT AIHPHLLDMKIGQGKYEPGFFPKLQ SDVLSTGPASNKWKRNAPAQWRR KDRQKQHTEHLRLDNDQREKYIQE ARTMGSTIRQPKLSNLSPSVIAQTN WKFVEGLLKECRNKTKRMLVEKM GREAVELGHGEVNITGVEENTLIAS LCDLLERIWSHGLQVKQGSALWS HLLHYQDNRQRKLTSGSLSTSGILL DSERRKSDASSLMPPLRISLIQDMR HIQNIGEIKTDVGKARAWVRLSME

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KKLLSRHLKQLSDHELTKKLYKR YAFLRCDDEKEQFLYHLLSFNAVD YFCFTNVFTTILIPYHILIVPSKKLGG SMFTANPWICISGELGETQIMQIPRN VLEMTFECQNLGKLTTVQIGHDNS GLYAKWLVEYVMVRNEITGHTYKF PCGRWLKGGMDDGSLERILVGELL TSQPEVDERPCRTPLQQSPSVIRRL VTISPNNKPKLNTGQIQESIGEAVNG IVKHFFHKPEKERGSLTLLCGECGL VSALEQAFQHGFKSPRLFKNVFIWD FLEKAQTYEYETLEKNEVVPEENWH TRARNFCRFVTAINNTPRNIGQGWQ VSDAGVLGEPEITSYTTGICPAG*
5144	10641	A	5456	238	406	
5145	10642	A	5457	2	204	
5146	10643	A	5458	1	431	
5147	10644	A	5459	1	225	
5148	10645	A	5460	3	321	
5149	10646	A	5461	1	1257	MSHRKFSAPRHGSLGFLPRKRSSRH RGKVKSFPPKDDPSKPVHLTAFLGY KAGMTHIVREVDRPGSKVNNKEVV EAVTIVETPPMVVVGIVGYVETPRG LRTFKTVFAEHISDECKRRFYKNWH KSKKKAFTKYCKKWQDEDGKKQL EKDFSSMKKYCQVIRVIAHTQMRL LPLRQKK\AHLMGDQVERGALWPE KADWARER\LEQQVPVNQVFIGQD EMIDVIG\VTQGQKAYKGVTSRWH TQESCPRKDPTEGLRK\ACIRAW\H PARVAFSVARA\GQ\KGYHHRTEIN K\KIYKIGQGYLIKGG\KLIKNNAST\ DYDL\SLDKSINPSGWAFFVHLW*K* PNDFVML\KG\CVVGTKK\RVLTLR KSFAGCRRKRRGFGEELTLSSIDTTS KF\GHGRFQTMEEKKAFMG\PLKKD RIAKEEGA
5150	10647	A	5462	114	456	
5151	10648	A	5463	3	76	
5152	10649	A	5464	2	951	CWNSGEVRWPLPPPPPRFVARRKM ADLEEQLSDEEKVRIFLKFHAPP EINEGFNDVRLLLNNDNLLREGAA HAFAYNLDQFTPLKIEG\YEDQVLI TEHGRLGEMGKFLDPKNRICFKF* SL*GRRATDPKDPCAEVVENAVESWR TSVETALRAYVKEHYPEWESGTVY GQKNRWDSQTHIACIESHQFQAKNF WNGRWRSEWKFTITPSTTQVVG\IL KIQVHYEDGNVQLVSHKDIQDSL TVSNEVQTAKEFIKIVEAAENEYQT AISENYQTMSDTTFKALRRQLPVTR TKIDWNKILSYKIGKEMQNA
5153	10650	A	5465	3	553	
5154	10651	B	5466	26	384	MHHEALSEALPGDNGFNVKNVSV KDVRNGNVAGDSKNDPPMEAAAGF TAQVIILNHPGQISAGYALYWIAIVD MVPKPMCVESFSDYPPLGRFAVR

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						DMRQTVAVGVKAVDKKAAGLAS*
5155	10652	A	5467	1	1254	
5156	10653	A	5468	1	1386	
5157	10654	A	5469	33	1653	KLPLKAKMGKEKTHINIVVIGHVDS GKSTTTGHLIYKCGGIDKRTIEKFEK EAAEMGKGSFKYAWVLDKLAER ERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQAD\CAVLIVAA GVGEFEAG\ISKNGQTREHALLAYT LGVKQ\LIV\GVNKMDSTEPPYSQK RYEEIVKEVSTYIKKIGYY\PTDLAF EPISGWNDDMLEPSANMPWFKG WKVTRKDG\NAS\GTTLLEAL\DCVL PPTRPT\DKPLR\LPLQ\DVYKIGGIG\ TVPVGRVETGVLKPGMGVTFAPS QRLQREVKICPKMHHEAFE*SSFLG DNVGFNVKNVSCQGCSVRGNV*H GDSKNDPPMEA/SLGFTAQVINLNH PGPNKAPG*CPWYWDCHTAHAC KVCLSLKEKI*F/DRSW*KSLEDGP*I LGSLGDAGHWLIWVPGQAPCVFEK LLKTIPPALGRFA\VRDNEDRQLCGW VSIKSSWTKAAGSWAKVTKISAQ KSSERLKNWIPNTCHPTLYQVWEE RSQELFGSIGHLSLSSKRLVNDNNA S
5158	10655	A	5470	2	4966	
5159	10656	A	5471	2	4821	RWPRRARLLRRGRGGGGVESLPHF GAPVPRARLQLTARRGHAGLRARM REAAAALVPPPAFAVTPAAAMEEPP PPPPPPPPPEPETESEPECCLAARQE GTLGDSACKSPESDLEDFSDETNTE NLYGTSPSTPRQMKRMSTKHQRN NVGRPASRNLKEKMNAQNPPHK DTGKTVENVEEYSYKQEKKIRAAL RTTERDHKKNVQCSFMLDSVGGSL PKKSIPDVDLNKPYLSLGCSNAKLP VSVPMPIARPARQTSRTDCPADRLK FFETLRLLLKLTSVSKKKDREQRGQ ENTSGFWLNRNELIWLELQAWHA GRINDQDFFLYTARQAIPDIINEILT FKVDYGSFAFVRDRAGFNGTSVEG QCKATPGTKIVGYSTHHEHLQRQR VSFEQVKRIMELLEYIEALYPSLQAL QKDYEKYAAKDFQDRVQALCLWL NITKDLNQKLRIJMGTVLGIKNLSDI GWPVFEIPSPRPSKGNEPEYEGDDT EGELKELESSTDESEEEQISDPVPEI RQPIDNSFDIQSRDCISKKLERLESE DDSLGWGAPDWSTEAGFSRHCLTSI YRPFVDKALKQMGLRKLILRLHKL MDGSLQRARIALVKNDRPVEFSEFP DPMWGS DYVQLSRTPPSSEKCSA VSWEELKAMDLPSEPAFLVLCRVL LNVIHECKLRLEQRPAGEPSLLSIK QLVRECKEVLKGGLLMKQYYQFM LQEVLEDLEKPCDNIDAFEEDLHKM LMVYFDYMRSWIQMLQQLPQASHS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LKNLLEEEWNFTKEITHYIRGGEAQ AGKLFCDIAGML/LKSTGSFLEFGLQ ESCAEFWTSADDSSASDEIIRSVIEIS RALKELFHEARERASKALGFAKML RKDLEIAAEFRLSAPVRDLLDVLS KQYVKVQIPGLENLQMFVPDTLAE EKSIIQLLNAAAGKDCSKDSDDVL IDAYLLLTKHGDRARDSEDSWGTW EAQPVKVVVPQVETVDTLRSMQVDN LLLVVMQSAHLTIQRKAFQQSIEGL MTLCQEQTSSQPVIKALQQLKND ALELCNRISNAIDRVDHMFTEFDA EVDESESVTLQYYREAMIQYFN GFEYHKEVVRLMSGEFRQKIGDKYI SFARKWMNYVLTKCESGRGTRPR WATQGFDFLQAIEPAFISALPEDDFL SLQALMNECIGHVIGKPHSPVTGLY LAIHRNSPRPMKVPRCHSDPPNPHLI IPTPEGFRGSSVPENDRLASIAAELQ FRSLSRHSSPTEERDEPAYPRGDSSG STRRSWELRTLISQSKDTASKLGPIE AIQKSVRLFEEKRYREMRRKNIIGQ VCDTPKSYDNVMHVGLRKVTFKW QRGNKIGEGQYGVYTCISVDTGEL MAMKEIRFQPNHKTIKETADELKI FEGIKHPNLVRYFGVELHREEMYIF MEYCDEGTLEEVSRGLGLEHVIRLY SKQITIANVLHEHGIVHRDIKANIF LTSSGLIKLGDGFCSVKLKNNAAQTM PGEVNSTLGTAAYMAPEVITRAKG EGHGRAADIWSLGCVVIEMVTGKR PWHEYEHNFQIMYKVGGMGHKPPIP ERLSPEGKDFLSHCLESDPKMRWT ASQLLDHSFVKVCTDEE
5160	10657	A	5472	3	425	
5161	10658	A	5473	1	234	
5162	10659	A	5474	3	260	
5163	10660	A	5475	3255	3467	LNKNLGLIFFFFFFFFETASRSVTR LEYSGLAHCELRLPGSRHSPVSA TWEAEAGELPEPRRQRLR
5164	10661	A	5476	1	4497	
5165	10662	A	5477	2	891	
5166	10663	A	5478	1	9786	
5167	10664	A	5479	27	13959	VPFSVAAAEPAQPARAARPRGRS PGAAPPQLAMDPPRPALLALLALPA LLLLLAGARAEEMLENVSLVCPK DATRFKHLRKYTYNYEAESSGVP GTADRSRATRINCKVELEVPLCSFI LKTSQCILKEVYGFNPEGKALLKKT KNSEFAAAMSRYELKLAIEGKQV FLYPEKDEPTYILNIKRGIIISALLVPP ETEEAKQVFLDVTYGNCSHTFTV KTRKGNVATEISTERDLGQCDRFKP IRTGISPLALIKGMTRPLSTLISSQS CQYTLDAKRKHVAEAIKEQHLFL PFSYKNKYGMVAQVTQTLKLEDTP KINSRFFGEGTKKMGLAFESTKSTS PPKQAEAVLKTQVQLKLTISEQNI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QRANLFNKLVTLELRGLSDEAVTSLL PQLIEVSSPITLQALVQCGQPCSTH ILQWLKRVHANPLLDVVITYLVALI PEPSAQLREIFNMARDQSRATLY ALSHAVNNYHKTNPTGTQELLDIA NYLMEQIQDDCTGDEDYTYLILRVI GNMGGTMEQLTPELKSSILKCVQST KPSLMIQKAAIQALRKMEPKDKDQ EVLLQTFLLDDASPGDKRLAAYLML MRSPSQADINKIVQILPWEQNEQVK NFVASHIANILNSEELDIQDLKKLVK EVLKESQLPTVMDFRKFSRNYQLY KSVSIPSLDPASAKIEGNLIFDPNNY LPKESMLKTTLTAFGFASADLIEIGL EGKGFEPTEALFGKQGFPPDSVNK ALYWVNGQVPDGVSKVLVDHFGY TKDDKHEQDMVNGIMLSVEKLIKD LKSKEVPEARAYLRILGEELGFASL HDLQLLGKLLLMGARTLQGIPQMI GEVIRKGSKNDFFLHYIFMENAFEL PTGAGLQLQISSSGVIAPGAKAGVK LEVANMQAELVAKPSVSVEFVTNM GIIIPDFARSGVQMNTNFFHESGLEA HVALKPGKCLKFIIPSPKRPVKLLSGG NTLHLVSTTKTEVIPPLIENRQSWSV CKQVFPGLNYCTSGAYSNASSTDASA SYYPLTGDTRLELELRPTGEIEQYSV SATYELQREDRALVDTLKFVTQAE GAKQTEATMTFKYNRQSMTLSEV QIPDFDVLGTLRVNDESTEGKTS YRLTLDIQNKKITEVALMGHLSCDT KEERKIKGVISIPRLQAEARSEILAH WSPAKLLQMDSSATAYGSTVSKR VAWHYDEEKIEFEWNTGTNVDTKK MTSNFPVDLSDYPKSLHMYANRLL DHRVPQTDMTFRHVGSKLIVAMSS WLQKASGSLPYTQTLQDHLNSLKE FNLQNMGLPDFHIPENFLKSDGRV KYTLNKNLSLKIEIPLPFGGKSSRDLK MLETVRTPALHFKSVGFHLPSTREFQ VPTFTIPKLYQLQVPLLGVLDLSTN VYSNLYNWSASYSGGNTSTDHFSL RARYHMKADSVDLLSYNVQSGS ETTYDHKNFTLSCDGLSRHKFLDS NIKFSHVEKLGNPNVSKGLLIFDASS SWGPOMASVHLDSSKKKQHLFVKE VKIDGQFRVSSFYAKGTYGLSCQRD PNTGRLNGESNLRFNSSYLQGTNQI TGRYEDGTLSLTSTSDLQSGIHKNTA SLKYENYELTKSDTNGKYKNFAT SNKMDMTFSKQNALLRSEYQADYE SLRFFSLLSGSLNSHGLELNADILGT DKINSGAHKATLRIGQDGISTSATT NLKCSLLVLENELNAELGLSGASM KLTNNGRFREHNAKFSLDGKAALT ELSLGSAYQAMILGVDSKNIFNFKV SQEGLKLSNDMMGSYAEMKFDHT NSLNIAGLSLDFSSKLDNIYSSDKFY

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; v=possible nucleotide insertion)
						KQTVNLQLQPYSLVTTLNSDLKYN ALDLTNNGKLRLEPLKLHVAGNLK GAYQNNKIKHIYAISAAALSASYKA DTVAKVQGVFESHRLNTDIAGLAS AIDMSTNYNSDSLHFSNVFRSVMAP FTMTIDAHTNGNGKLALWGEHTGQ LYSKFLLKAEPLAFTFSDYKGSTS HHLVSRKSISAALEHKVSALLTPAE QTGTWKLKTQFNNNEYSQDLDAY NTKDKIGVELTGRTLADLTLLDSPI KVPLLLSEPINIIDALEMRDAVEKPO EFTIVAFVKYDKNQDVHSINLPFFET LQEYFERNRQTHVLENVQRNLKH INIDQFVRKYRAALGKLPQQANDY LNSFNWERQVSHAKEKLTALTCKY RITENDIQIALDDAKINFNEKLSQLQ TYMIQFDQYIKDSYDLHDLKIAIANI IDEIIEKLKSLDEHYHIRVNLVKTIH DLHLFIENIDFNKSGSSASWIQNV TKYQIRIQIEKLQQLKRHIQNIQ HLAGKLKQIEAIDVRVLLDQLGTT ISFERINDVLEHVKHVFVNLIGDFEV AEKINAFRAKVHELIERVEVDQQIQ VLMDKLVELAHQYKLKETIQKLSN VLQQVKIKDYFEKLGVFIDDAVKK LNELSFKTFIEDVNKFLDMLIKKLKS FDYHQFVDETNDKIREVTQRLNGEI QALELPQKAEALKLFLEETKATVA VYLESLODKITLINWLQEALSSAS LAHMKAKFRETLEDTRDRMYQMDI QQELQRYLSLVGQVYSTLVYISD WWTLAAKNLTDFAEQYSIQDWAK RMKALVEQGFTVPEIKTILGTMPAF EVSLQALQKATFQTPDFIVPLTDLRI PSVQINFKDLKNIKIPSRFSTPEFTIL NTFHIPSFTIDFVEMKVKIIRTIDQML NSELQWPVDIYLRDLKVEDIPLARI TLPDFRLPEIAIPEFIPTLNLNDFQVP DLHIPEFQLPHISHTIEVPTFGKLYSI LKIQSPLFTLDANADIGNGTTSANE AGIAASITAKGESKLEVLNFDQAN AQLSNPKINPLALKESVKFSSKYLR TEHGSEMLFFGNAIEGKSNTVASLH TEKNTLELSNGVIVKINNQLTLDN TKYFHKLNIPKLDSSQADLRNEIKT LLKAGHIAWTSSGKGSWKWACPRF SDEGTHESQISFTIEGPLTSFGLSNKI NSKHLRVNQNLVYESGSLNFSKLEI QSQVDSQHVGHSVLTAKGMALFGE GKAEFTGRHDAHLNGKVIGTLKNS LFFSAQPFEITASTNNEGNLKVRFPL RLTGKIDFLNNYALFLSPAQQASW QVSARFNQYKYNQNFSAAGNNENIM EAHVGINEANLDFLNIPLTIPEMRL PYTHITPPLKDFSLWEKTGLKEFLK TTKQSFDSLVSQAQYKKNKHRHSIT NPLAVLCEFISQSIKSFDRHFENRN NALDFVTKSYNETKIKFDKYKAES

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HDELPRTFQIPGYTPVVNVEVSPF TIEMSAFGYVFPKAVSMPSFSILGSD VRVPSYTLILPSLELPVLHVPRNLKL SLPDFKELCTISHIFIPAMGNITYDFS FKSSVITLNTNAELFNQSDIVAHLLS SSSSVIDALQYKLEGTTRLTRKRGL KLATALSLSNKFVEGSHNSTVSLTT KNMEVSVATTTKAQIPILRMNFKQE LNGNTKSKPTVSSSMEFKYDFNSSM LYSTAKGAVDHKLSLESLSYFSIES STKGDVKGSVLSREYSGTIASEANT YLNSKSTRSSVKLQGTSKIDDIWNL EVKENFAGEATLQRIYSLWEHSTKN HLQLEGLFFTNGEHTSKATLELSPW QMSALVQVHASQPSSFHDFPDLGQ EVALNANTKNQKIRWKNEVRIHSG SFQSQVELSNDQEKALDIAGSLEG HLRFLKNILPVYDKSLWDFLKLDV TTSIGRRQHRLRVSTAFVYTKNPNGY SFSIPVKVLADKFIIPGLKLNLDNSV LVMPTFHVPTDLQVPSCKLDFREI QIYKKLRTSSFALNPLTPEVKFPEV DVLTKYSQPEDSLIPFEITVPESQLT VSQFTLPKSVSDGIAALDNLAVANK IADFELPTIIVPEQTIEIPSIKFSVPAGI AIPSFQALTARFEVDSVPVYNATWSA SLKNKADYVETVLDSTCSSTVQFLE YELNVLGTHKIEDGTLASKTKGTFA HRDFSAYEEDGKYEGLQEWEGKA HLNIKSPAFTDLHLRYQKDKKGIST SAASPAVGTVGMDMDEDDDFSKW NFYYSPOSSPDKCLTIFKTEL RVRES DEETQIKVNWEEEAASGLTSLKDN VPKATGVLVDYVKNKYHWEHTGLT LREVSSKLRRNLQDHAEWVYQGAI REIDDIDERFQKGASGTTGTQEWK DKAQNLQELLTQEGQASFGGLKD NVFDGLVRVTQEFHMKVKHLIDSLI DFLNFPRFQFPGKPGIYTREELCTMF IREVGTVLSQVYSKVHNGSEILFSYF QDLVITLPFELRKHKLIDVISMYREL LKDLSKEAQEVFKAIQSLKTTEVLR NLQDLLQFIFQLIEDNIKQLKEMKFT YLINYIQDEINTIFNDYIPYVFKLLKE NLCLNLHKFNEFIQNELQEASQELQ QIHQYIMALREEYFGPSGVGWTVK YYEGEEKIVSLIKNLLVALKDFHSE YIVSASNFTSQLSSQVEQFLHRNIQ EYLSILTPDGKGKEKIAELSATAQ EIIKSQAIAATKKIISDYHQFFRYKLQ DFSDQLSDYYEK\FIAESKRLNDLSI QN\YHTFLDYTSREFNWKKLAIQPQ SLNPYMKLAPGELYHPLIFLKEIFN LFFFSNLFNFSHRHRKNCKLPILIKPY SEPALQ
5168	10665	A	5480	2	316	
5169	10666	A	5481	2	401	
5170	10667	A	5482	126	415	

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5171	10668	A	5483	3	499	
5172	10669	A	5484	1	241	
5173	10670	A	5485	12	308	
5174	10671	B	5486	394	565	MSAEERLRSSGVLSQKVIAHSLGFD KHGNRLGRGKGYDDAYLKRCLQH QEVKPYTLALAFKEQICLQVPVNEN DMK*
5175	10672	B	5487	674	807	MSAEERLRSSGVLSQKVIAHSEYQK SKRISIFLSMQDEIETEEIKDIFQRGK ICFLPSVRVPEQSHGYGLGFDKHGN RLGRGKGYDDAYLKRCLQHQEVK PYTLALAFKEQICLQVPVNENDIK*
5176	10673	A	5488	113	339	
5177	10674	A	5490	2	388	FLFFFFEMESRSVAQAGVQWCDLG SLQPPPPGLSDSPALASSVSWITDV RHHLWLIFVFLVETGFRHVGQASLK LPTSGDLPTLASQSAGITGVSHYAW LIFVFLVETEFHHVGQAGLELLAPS DPPA
5178	10675	C	5491	197	415	MLLYVGLEPHHHTHMLSLWPPRLMF PSVFFFFFFFFFLRQGLALLPRLECS GAILAHCNLHLLGSGDSLASF*
5179	10676	A	5492	768	1081	KGVLFFFFFFKTESHSVAQAGVQW CTLGSLQPP/PSRGSSDSPASASRVA GIRGVHHHARLIFVFLVETGFHYVG QAGLELPTSGDSPASASQSAGVTGV SHQCPA
5180	10677	A	5494	305	477	
5181	10678	A	5495	1	903	
5182	10679	A	5496	111	295	KPATSVPVIVCVCSAKPELPLCPAT YTEHHAGQPHWWYHAAR/DLVSW K*QISQRGEINPH
5183	10680	A	5497	1	505	
5184	10681	A	5498	3	345	
5185	10682	A	5499	1	1416	
5186	10683	A	5500	618	707	
5187	10684	C	5501	1729	2511	MDIASTNTSNKSDTNMEQVPATND TIKRLESKLLKNQAKQQSESGRLSL GASRGSSVESLPTSEGRMSADMS EIEARIAATTGNGQPRRSIQDLTVT GTEPGQVSSRSSPSVRMITTSPTS EKPTRSHPWTPDDSTDNTGSDNSIP MAYLTLDHQLQPLAPCPNSKESMA VFEQHCKMAQEYMKVQTEIALLLQ RKQELVAELDQDEKDQNTSRLVQ EHKKLLDENKSLSTYYQQCKQLE VIRSQQQKRQGT*
5188	10685	A	5502	1	3489	
5189	10686	A	5503	1	246	
5190	10687	A	5504	40	124	NVPQFTAKAPCKHEKCLNTNSPDLF EAC*DNIDQTAVSLTAPKTGKRK*R NKVQLS**PQFTAKAPCKHEKCLNT NSPDLFEAC
5191	10688	A	5505	156	1001	GIQQFGQYCLNMLQINQLLSKIKLA NPKEKTAMYLVLNELARFNRVQPQY KLLD*RGPAHSMFMSVQLSLGEQT WESEGSSIKKAQQA VGNKALTESTL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PKPI*KPPKSNVNNNPGCITPTVELN GLAMKRGRACHPQAIRSKAIPK**S *LQLSSHV*SEVS\FPIPKIFYVQLTV GNNEFFGEGKTRQAARHNAAMKA LQALQNEPI/LRKISSGMVNQERIW MMTK/HANKSEISLVFEIALKRNMMP VSFEVIKESGPPHMKSFVTRVSVGE FSAEGEGNSKK
5192	10689	A	5506	175	411	
5193	10690	A	5507	198	381	
5194	10691	A	5508	137	346	
5195	10692	A	5510	3	136	
5196	10693	A	5511	2	673	
5197	10694	A	5512	1	257	
5198	10695	A	5513	1	712	PRKT/PPAPHVDGDRKELPRTKLLPP API/STD*SQHADRGTEP/GPIRPSIEP GPPVQFGTSDKDSDLRLVVGDSLIA EKELPASVTEAIPVSRDWQLLGSGA ASAEPQSKNLD SGHCVPEHSSSGQR LYPEVFGSAGPSSSQISGGAMDFH LAFSGGQGRHLEKGPPDGQRSLGPE GTRSLGCPHPAEGVPLAPYPRGLYI DYKY/MKGERGGRGVGLGLPHFP SSPFPWSPVPGAVC
5199	10696	A	5514	2	322	
5200	10697	A	5515	1	6470	MSDRSGPTAKGKDGKKYSSLNLF TYKGKSLEIQKPA/VAPRHGLQSLG KVAIARR/MRPPANLPSLKAENKGN DPNVSLVPKDG TGWASKQEQSDPK SSDASTAQPPESQPLPASQTPASNQ KRPPAAPENTPLVPSGVKSWAQAS VTHGAHGDGGRASSLLSRFSREEFP TLQAAGDQDKAAKERESAEQSSGP GPSLRPQNSTTW RDGGGRGPDELE GPDSKLHHGHDPRGGLQPSGPPQFP PYRGMMPFMYPPYLPFPPPYGPQG PYRYPTPDGPSRFPRVAGPRGSGPP MRLVEPVGRPSILKEDNLKEFDQLD QENDDGWAGAHEEV DYTEKLKFS DEEDGRDSDEEGAEGHRDSQSASG EERPPEADGKKGNPSEPTPKTA WAETSRPETEPGPPAPKPLPPGDY PDRGGPPCKPPAPEDEDEAWRQRR KQSSSEISLAVERARRRREEEERM QEERRAACAEKLRLEKFGAPDK RLKAEPAPPAAPSTAPPPAVPKE LPAPPAPPASAPTETEPEEPAQAP PAQSTPTPGVAAATLVSGGGSTSS TSSGSFEASPVPEQLPSKEGPEPPEE VPPPTTPPVKVEPKGDGIGPTRQPP SQGLGYPKYQKSLPRFQRQQEQ LLKQQQQHQWQQHQQSAPPTVP PSPQPVTLGAVPAPQAPPPPKALY PGALGRPPPMPPMNFDRWMMIPP YVDPRLQGRPPLEFYPPGVHPSGL VPRERSDSLGLSSEFDRHAPAMLR ERGTPVDPKLA WVG DVFTATPAE

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						PRPLTSPLRQAADEDDKGMRSCTPP VPPPPPYLASYPGFENGAPGPPISR FPLEEPGRPLPWPPGSDEVAKIQTP PPKKEPPKEETAQLTGPEAGRKLPA SRSGAGPPPPRRESRTETRWGPRPG SSRRGIPPEEPGAPRRAGPIKKPPPP TKVEELPPKPLEQGDETPKPPKPDPL KITKGLGGPKETPPNGNLSPAPRL RRDYSYERVGPTSCRRGRGRGEYFA RGRGFRGTYGGRGRGG/RSEFRSYR EFRGDDGRGGGTGGPNHPPAPRGR HASETRSEGSEYEEIPKRCRQRGSET GSETHESDLAPSDKEAPTPKEGTLT Q/VPLAPPPPGAPP/SP/APARFTC/RG GRRVFTPR/GVPSRRGRGGGR/PPPQ VCPGWSPPAKSLAPKKPPTGPLPPS KEPLKEKLIPGLSPVARGGSNGGS NVGMEDGERPRRRRHGRAQQQDK PPRFRRLKQERENAARGSEGKPSLT LPASAPGPPEALTTVTVAPAPPRAA AKSPDLNQNDSQANEWETASESS DFTSERRGDKEAPPVLLTPKAVGT PGGGGGGA VPGISAMSRGDLSQRA KDLSKRSFSSQRPGMERQNRPPGPG GKAGSSGSSSGGGGGGPGGRTGPG RGDKRSWSPKNRSRPPEERPPGLP LPPPPSSSA VFRLDQVIHNSPAGIQ QALQLSSRQGSVTAPGGHPRHKP GPPQAPQGSPRPPTRYEPQRVNSG LSSDPHFEEPGPMVRGVGGTPRDSA GVSPFPKRRERPPRKPELLQESLP PPHSSGFLGSKPEGPGQAESRDG TEALTPHIWNLHTATSRKSYRPTS MEPWMEPLSPFEDVAGTEMSQSDS GVDLSGDSQVSSGPCSQRSSPDGGL KGAAEGPPKPPGGSSPLNAVCEGP PGSEPPRRPPAPHDGRKELPREQP LPPGPIGTERSQRTDRGTEPGIRPS HRPGPPVQFGTSDKDSLRLVVGDS LKAEKELTASVTEAIPVSRDWELLP SAAASAEPQSKNLDSGHCVPEPSSS GQRLYPEVFYGSAGPSSSQISGGA MDSQLHPNNGG/FRGTPSLHPYRS QPLYLPPGPAPPSALLSGVALKGQF LDFSTMQATELGKLPAGGVLYPPPS FLYSPAFCPSPLPDTSLQVRQDLP PSDFYSTPLQGGQSGFLPSGAPAQ QMLLPMVDSQLPV/VNFGSLPPAPP PAPPPLSLLPVGPALQPPSFVVRPQS SPSTGVLAP*LARFPVYFGRTELHP VNIKPFDRDFQKLSSNLGGPGSSRTP PTGRPPSSLRSFSGLNSRLQSQRLS NLTSGVFARNQAASTFYQAGLPHPD ALRWIPKPWERTG/RPPR/DGPSRR/ AEEP/SGRGDKEP/GLPPPR
5201	10698	A	5516	2	119	
5202	10699	A	5517	1	325	FFFFF*DRVSLLLPKLECNGTISAHC NLRLPGSSDSPASASSSFFTTHVAPLP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QLRHY*IFYDGTRSLYAG*YSQNLLI YSAPRQPQYHFKDMNKILDSIQRSY TKI
5203	10700	A	5518	228	481	QFFRNTIFF*DRVSLLLPKLECN SAISAHHNLCPLGSSDSPASASRVAGITG TCHHTRLL\FVFLVETGFYHVSQSG LELLTSGD
5204	10701	A	5519	175	431	LIVKMPFLK*SWKIF*MSK**VMLIH *GFVFLFVCFF*DRVSLLLPRLECN GPISAHNRNLHLPDSSDSPASAYIKGF VRQLSHEE
5205	10702	A	5520	257	453	TKGGGYTQRTAIQFILFIYLFY*DG VSLLLPRL*NGAISAHCNHLPGSS DSQKKTCKNFCTQ
5206	10703	A	5521	277	1230	ISFHLSTFGAPSFFFFEFMEFSLLLPR LECNGAISAHRNLRLPGSSDSPASAS PVGWDYRHHVHPRSANFVFFFSRDG VSPCWSGLVSNRPQMIPSRPPKV LDTGLATMPGLCLANFCGRNRVSL MCPWSPELKQSTCLSLPKCWDYR RAAVPGLFILFFLRHRCPTLTQDEV QWCDHSSLQPSTPEIKHPPASASQSS WDQRHAPLHLANFYFY*FFETES\ HSVTRLECSGAILAHCNLCPLGSSY SPAPAS*VAGTTGAH/RRLANFFVFL VEMGFHHVRQVDARSDDLVI CLR PPKVLGLQDVSHHRPAYF
5207	10704	A	5522	1	467	FFFLF*EGVSLLLPRLCSGAISA/HC NLHLPGSSDSPASASQEDGITGVRY HAWLIL/VFLVEIGFHHVGQADLKP *PQVIHPPLFFFLRQSFALVAQAGV QWCDLSSLQTPPPRVQGILLAQPE YL VAGFTGMRHHTRLFFFFAFLVET GFHPC
5208	10705	A	5523	293	681	QGTILIGLCPFDITPAIVDILLAFWHV R/CPRPTVSCFCKKVLLV*NFFFFF FFETESVTRLECSGVILAHCNL RLPGSSDSHASASRVAETTGVRRHA WPIFVFLVETRFHHVGQAGLELLTS GD
5209	10706	A	5524	274	321	
5210	10707	A	5525	2	733	
5211	10708	A	5527	1	3555	MHYVLNSSSMETFFVGEQNYEGSSR LCVCKRTREADDPSARDSVCEGVR ARFNICGINQIVLKCPWGCENPAQ MGCPPVGKADRCGLLAN SATCEKG MFCHADLVGITPTVPFSPHPRCKTTA SAKLACQQDQVLDLDRQSLSSIDKNPS ERGQSLSNPTDDSWKGRPYANQK LFASLLIKCVVQLELIQTIDNIVFYPA TSKKEDAEHMAAQQDTLDADIHI ETEDQGMKYMSSQHLFKLLDCLQ ESHFSKAFNSNYEQRTVLWRAGF KGKSKPNLLKQETSSLACCLRILFR MYVDENRRDSWEEIQRLLTV CSE ALAYFITVNSESHREAWTSLLLLLL TKTLKINDEKFKAHASMYYPYLCEI

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						MQFDLIPELRAVLRKFFLRIGVVYKI WIPEEPSQARCRILPGFECEAERRQ ERVVPATVRGWGSLLRFCIPTSSYN KCLLNMYCVPDIAMELS DANLQT LTEYLKKTLD PDPAIRRPAEKFLESV EGNQNYPLLLLTLEKSQDNVIKVC ASVTFKNYIKRNWRIVEDEPNKICE ADRVAIKANIVHMLSSPEQIQKQL SDAISIIGREDFPQK WPDLLTEMVN RFQSGDFH VINGVLR TAHS LF KRYR HEFKSNELWTEIKLVDAFALPLTN LFKICD NAALYAQKYDEEFQRYLPR FVTAIW NLLVTTGQEVKYDLLVSN AIQFLASVCERPHYKNLFEDQNTLT SICEKVIVPNMEFRAADEEAFEDNS EEYIRRDLEGSDIDTRRRACDLVR GLCKFFEGPVTGIFSGYVNSMLQEY AKNPSVNWKHKDAIYLVTSLASK AQTQKHGITQANELVNLTEFFVNHIL LPDLKSANAIMRSFSLQEAIIPIPT LITQLTQKLLAVSKNPSKPHFNHYM FEAICLSIRITCKANPAAVVNFEAL FLVFTEILQNDV/PSESVDQYRKQIFI LLFQRLQNSKTTKFIKSK*NHLDVL QK**KK\MFGMVLEKIIPIEQKVS NVEKKICAVGITKLLTECPMMDTE YTKLWTPLLQSLIGLFELPEDDTIPD EEHFIDIEDTPGYQTAFSQAFAAGK KEHDPVGQMVNNPKIHLAQSLHKL STACPRSCGSSPVEDGVCIGAPRSP TASVCFPSLVGSINGPAPAPPPPTVR TTSSGWHCGGACARKARRGPSGRS ALSRLDRSGPS
5212	10709	A	5528	1	4611	
5213	10710	A	5529	58	3051	CQLRSAAGVPSSVSVSPRDIAMEL SDANLQTLTEYLKKTLD PDPAIRRPA AEKFLSV EGNQNYPLLLLTLEKS QDNVIKVCASVTFKNYIKRN\WRIV EDEPNKICEADRVAIKANIVHMLSL SPEQIQ\KQLSDAISIGREDFPQ\KW PDLALTEM\VNRFQSGDFH VINGVLR TAHS LF KRYRHEFK\SNELWTEIK LVDAFALPLTYLFKATIELCSTH ANDASALRILFSSLILISKLFYSLNFQ DLPEFFAEDNMETWMNNFHTLLTLD NKLLQTDDEEEAGLLELLKSQICDN AALYAQKYDEEFQRYLPRFVTAIW NLLVTTGQEVKYDLLVSNAIQFLAS VCERPHYKNLFEDQNTLTSICEKVI VPNMEFRAADEEAFEDNSEEYIRRD LEGSDIDTRRRACDLVRGLCKFFE GPVTGIFSGYVNSMLQEYAKNPSV NWKHKDAIYLVTSLASKAQTQKH GITQANELVNLTEFFVNHILPDLKSA NVNEFPVLKADGIKYMIFRNQVPK EHLLVSIPLLINHLQAGSIVVHTYAA HALERLFTMRGPNNATLFTA AEIAP FVEILLTNLFKALTLP GSSENEYIMK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AIMRSFSLLEAIIPYIPTLITQLTQK LLAVSKNPSKPHFNHYMFEAICLSIR ITCKANPAAVVNFEEALFLVFTEILQ NDVQEFIPYVFQVMSLLETHKNDI PSSYMALFPHLLQPVLWERTGNIPA LVRLQAFLEGRSNTIASAAADKIP GLLGVFQKLIASKANDHQGFYLLNS IIEHMPPEVDQYRKQIFILLFQRLQ NSKTTKFIKSFLVFNLICYKYGALA LQEIFDGIQPKMFGMVLEKIIPEIQK VSGNVEKKICAVGITNLLTECPPMM DTEYTKLWTPLLQSLIGLFELPEDD TIPDEEHFIDIEDTPGYQTAFSLAF AGKKEHDPVGMVNNPKIHLAQSL HMLSTACPRVPSMVSTSLNAEAL QYLQGYLQAASVTLL
5214	10711	A	5530	1	396	
5215	10712	A	5531	1	1095	
5216	10713	A	5532	1	1077	
5217	10714	A	5533	1	986	
5218	10715	B	5534	214	975	MEVKTKARELRDECTSLSSRFQLE ERVLVMENQMNQMKQEEKFREKRI KRNEQSLQEIWDYVKRPNLRVIGVP ESDGENGTKLENTLQDIIQENFPNL ARKANIQIETQRMPPQRYSSRRATP RHIIVRFTKVEMKETMLRAAREKG RVTHKGKPIRLTADLSAETLQAKRE WGPFIENILKEKNFQPRISYPAKLSFIS EGEIKSFTDKQMLRDFVTTTPALKE LLKEALNMERNNQYQHCKNMPNC KDHPG*
5219	10716	A	5535	3	1135	
5220	10717	A	5536	1	1023	
5221	10718	A	5537	2	2747	LHLWGQGTDKQKQDSSNLCRLKCPC LTALKRAVVLPAWSRSENGQTAS SKGKLTTRKDIYTENPSVHHHHQRP KVDKTTKMGKKQNRKTGNSKKQS ASPPPKERSASPPPKERSSSPATEQS WREN/DLDFDELRAEGFKRSNYSE LWEDIQTKGKEVENFEKNLEECITRI TNEKCLKELMELKTKARELCEEC RSLRSRCDQLEERVVSAMEDEVKMN EMNEMKREGKFREKRIKRNEQSLQ EIWDYVKRPNLRLTGVPESDGENG TKLENTLQDIIQENFPNLARQANVQI QEIQRTPQRYSSRRATPRHIIVRFTK VEMKEKILRAAREKGRVTLKGKPIR LTADLSAETLQARREWGPIFENILKE KNFQPRISCPAKLSFISEGEIKYFTDK QMLRDFVTTKPALQELLKEALNME RNNRSPSSSPATEQSWMENDFDEL EEGFRSNYSELREDIQTGKKEVEN FEKNLEECITRITNEKCLKELMELK TKARELREECRSLRSRCDQLEERVS AMEDEMENEMKREGKFREKRIKRNE QSLQEIWDYVKRPNLRLIGVPESDV ENGTKLENTLQDIIQENFPNLARQA NVQIQEIQRTPHRFSSRRATTRNLIV

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						RFTKVEMKEKMLRAAREKGRVTH KGGPIRLTADLLAETLQARREWGPI FNILKEKNFQPRISYPAKLSFISEGEI KYFTEKQMLRDFVTTSPALEELLKE ALNMERNNRTRQKVNKDIQELNS ALHQADLIDISRTLHPKSTEYTFSSA PHHTYSKIDHIVGSKALLSKCKRTEI ITKCLSDHSAIKLELRIKLTQNCCTT TWKLNLLNDYWVQNEKMAEIK MFFENNENKDTTYQNLWDTFKA VCRGKFIALNAHKRQKRSKTDLTLS QLKELEKEEKHIQKLAEGKK
5222	10719	A	5538	99	432	
5223	10720	A	5539	100	732	
5224	10721	A	5540	242	1300	NPRRSGHSLEAKLRDSSYSELLRDIL QKHEAVHMEALDELYEALAETLM AKESTQGHRSYLLPSGGSVTLSEST AIISHGTTGLVTWDATLYLAEWAIE NPAAFTRNTVLELGSGAGLTGLAIC KDVPPPGIHLQRTCHSRVLEQLRGN VPSNGLSLEADITAKLDSRVTVAQ LDWDVATVHQLSAFQPDVVIADV LYCPEAIMSLVGVLRRLAACREDQ RAPEVYVAFTRVNPETCQLFTTELA PSTCEGVLSLSHLTDKDIRTHRGQA TLELLQTAARPPGSRASTIHPSLPMP RASAPAPPEHSPSWQPCQMHPQQ PLPAHRDTPNPVPHVGPVNYRA NKQAST
5225	10722	A	5541	3	167	
5226	10723	A	5542	2	378	
5227	10724	A	5543	3	359	
5228	10725	A	5544	15	347	
5229	10726	B	5545	141	371	DFGYFYGSSYVAAPDSSRTPGLSR RDGLLVAKLDLNLCCQVNDVWNF KMTGRYEMYARELAEAVKSNYSPT IVKE*
5230	10727	A	5546	1	1154	MAGAEWKSLEECLEKHLPLPDLQE VKRVLYGKELRKLDLPREAFEAAS REDFELQGYAFEAAEEQLRRPRIVH VGLVQNRIPANAPVAEQVSALHR RIKAIVEVAAMCGVNIICFQEAWTM PFAFCTREKLPWTEFAESAEDGPTT RFCQKLAKNHDMVVVSPILERDSE HGDVLWNTAVVISNSGAVLGKTRK NHIPRVGDFNESTYYMEGNLGHVP FQTQFGRIAVNICYGRHHPLNWL MYSINGAEIIFNPSTIGALSSESLWPIE ARNVAAIANHCFTCAINRVGTEHFP NEFTSGDGKKAHQDFGYFYGSSYV AAPDSSRTPGLSRSDGLLVAKLDL NLCCQVNDVWKFKITGRYEMYAR ELAEAVKSNYSPTIVKE
5231	10728	A	5547	424	604	
5232	10729	A	5548	52	318	
5233	10730	A	5549	3	148	
5234	10731	A	5550	258	458	

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5235	10732	A	5551	1	217	
5236	10733	A	5552	246	361	
5237	10734	C	5553	69	254	MDHLYNXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXEIQFXXXXERERNKN PFPAGDDIISRGVGQ*
5238	10735	A	5554	32	169	NPVPPYPLCPALVFFLLIYLLIY*PS PLL RMSAPAGKGFLFLSL
5239	10736	A	5555	417	490	
5240	10737	A	5556	2	121	
5241	10738	A	5557	69	398	
5242	10739	A	5558	2	732	GRVPSQCGWIRMRSRSCREDQKPG MDDQRDLISNNEQLSMLGRRPGAP ESKCSRGCPHSAFSLVTLVVQA INAYFLYH*HGRLDKLTVTPQNLQ LENLRMKLPKPPKPVSKMRMATP LL\MQALPMGALPQGPQMNAKYG NMTEDHVMHLLQNADPLKVYPPL KGSFPENLRHLKNTMETIDWKVFES WMHHWLLFEMSRHSLEQKPTDAPP KESLELEDPSGLGVTKQDLGPVPM
5243	10740	A	5559	2	359	
5244	10741	A	5560	2444	2755	DYYYFFEMESCSVAQAGVQWRDL GSLQPPPPSSRDSSASASRVAGTTG MHH/HNQLSFVFLVKMGFHHVQQA DFELLTSSDLPVSASQSAGITGVSHR ARPLSS
5245	10742	A	5561	1724	1941	AHLLYEWIFFFFFFFFEMESHVAQA GVLWRDLSSLQAPPPGSQSDSPAS ASWVAGITGACHHARHEWNFKC
5246	10743	A	5562	2	362	
5247	10744	A	5563	138	236	
5248	10745	A	5564	1	278	
5249	10746	A	5565	80	591	RGCKREGLSMSSLIRRVISTAKAPG AIGPPTVQAVLVDRTHLHFRDQIG HGPLPSWTS LCPGGVAGRSLNKL KNMGEIPESLPGCDF\TNVVKTTCS GLDINDLQLLFNEILQTVFSRSNFPA RAAYPSWLLLPQKGSRIEIEA\VAIQ GPLTTAFILSGDPCCVVWDC
5250	10747	A	5566	141	340	
5251	10748	A	5567	209	386	
5252	10749	A	5568	1	346	
5253	10750	A	5569	160	391	
5254	10751	A	5570	101	332	
5255	10752	A	5571	500	752	
5256	10753	A	5572	2	82	
5257	10754	A	5573	3	165	
5258	10755	A	5574	1	219	
5259	10756	A	5575	1	327	
5260	10757	A	5576	2	160	
5261	10758	A	5577	1	189	QQLRHPDLHLQRRSQAQQHQGGQ DS*AQMLCRVPTVPSTTCGRVSLP LPPKTQGHPHDLDP
5262	10759	A	5578	2	224	
5263	10760	A	5579	1	1392	
5264	10761	A	5580	1	1272	PGCGRPRAFSNLNIADIEEKRGTSHF VRQTPSPSPNNL*YLIYRRYRQFHA

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						LQSKLEERFGPDSKSSALACTLPTLP GRRPLPSCCCRAAVRIPALNAYMK VPVGLATLARGRALPPWDPLQSGG CLWSLSTQSQSPVSPDLCAWSLVR* PRQALGARVLDVRIFFYQSPYDSEQ VPQALRRLRPTRKV*VTSPWAST WPEPAAPRAEVTAPTLARLSHCNF KAGDVIFLLSRINKDWLEVSSEVRM EVRLKVVFVKILKDFPEEDDPTNWL CYYYEDTISTIKSVAWEGGACPAFL PSLRPLPLTSPSHGSLSHKAPSGSQ MSHNAVTSRQPGWPGQPHSPFPH PTLKDLLELTR*GAGNGAGELDTLD AEGDLVRLSDEEDVALMVRQARGL PSQKRLFPWKLHITQKDNRYVYNT MP
5265	10762	A	5581	437	728	
5266	10763	A	5582	570	1648	TQPGTGWARLSTCSLGPSTMAVA QQLRAESDFEQLPDDVAISANIADIE EKRGFTSHFVFVIEVKTKGGSKYLI YRRYRQFHALQSKLEERFGPDSKSS ALACTLPTLPAKVYVGVKQEIEM RIPALNAYMKSLSLPVWVLMDED VRIFFYQSPYDSEQVPQALRRLRP TRKVKSVSPQNSVDRMAAPRAEA LFDFTGNSKLELNFKAGDVIFLLSRI NKDWLEGTVRGATGIFLSFVKILK DFPEEDDPTNWLRCYYYEDTISTIK DIAVEEDLSSTPLLKDLLELTRREFQ REDIALNYRDAEGDLVRLSDEEDV ALMVRQARGLPSQKRLFPWKLHIT QKDNRYVYNTMP
5267	10764	A	5583	1705	2233	
5268	10765	A	5584	1	354	
5269	10766	A	5585	270	390	
5270	10767	A	5586	3	132	
5271	10768	A	5587	234	362	
5272	10769	A	5588	1	402	
5273	10770	A	5589	2	509	
5274	10771	A	5590	3	1607	SPRPGIPRCFHLVISTEHRRVMTEFG LSWVFLVAIFKGVQCEVQLVESGG DLVQPGGSLRLSCAASGFTFSSYAM HWVRQAPGKGLKYVSGISSNGRRT YYANSVKGRFTISRDN SKNTLYLQ MGSRAEDMAVYYCARGGDHIVP AAVAPFHMDVWGQGTTVTVSSASP TSPKVFPLSLCSTQPDGNVVIACLP PGLLPAGATQCDLERKRTGRDRQK LPTQPGCLRGPVHHEQPADPAGHT VPSRQVRDMPREALHESQPGCDCA LPSSLNSTYPISLNSTYPISLMLPPPT VTAPTGPSKDLFLGSKATFTCTLPG LRDASGVTFWDALKVGKSAVQGG P*RRDLGCGYSSVSSVLPGCAEAH GTHGEGPSLWHCWYPESKDPA*PP TLFKIRGNTFPGPRFHLL\PPPSEGAG PWNELVT\TCLGIGLSAPRMLLVC

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						WVAGGHRSLREKYLTWASROKP SQGTTTFAVTSILRVAAEDWKKGD TFSCMVGHEALPLAFTQKTIDRLAG KPTHVNVSVVMAEVDGTCY
5275	10772	A	5592	2	315	
5276	10773	A	5593	245	455	
5277	10774	A	5594	1	2863	MIFPAESSCALPOEGSAGPGSPGSAP PSRKRWSSEESNQTATGTSRWGD VSKKAPRHLSVPCTRPREARQEA DSTSRLSAESGETDQDAGDVGPDI PDSYYGLLGTLPCEALSHICSLPSE VLRHVFAFLPVEDLYWNLSLVCHL WREIISDPLFIPWKKLYHRYLMNEE QAVSKVDGILSNCGIEKESDLCVLN LIRYTATTKCSPSVDPERVLWSLRD HPLLPEAEACVRQHLPDLYAAAGG VNIWALVAADVLLSSSVNDIQRLLF CLRRPSTVTMPDVTETLYCIAVLL YAMREKGINISNSKKTITLTHEQQLI LNHKMEPLQVVKIMAFAGTGKTST LVKYAEKWSQSRFLYVTFNKSIAK QAERVFPNSVICKTFHSMAYGHIGR KYQSKKKLNLFKLTPFMVNSVLA GKGGFIRAKLVCKTLENFFASADEE LTIDHVPIWCKNSQQRVMVEQSE KLNGVLEASRLWDMRKLGECTEE AHQMTHDGYLKLWLSKPSLASFD AIFVDEAQDCTPAIMNIVLSQPCGKI FVGDPHQQIYTFRGAVNALFTVPHT HVFYLTQSFRFGVEIAYVGATILDV CKRVRKKTLVGGNHQSGIRGDAKG QVALLSRTNANVFDEAVRVTEGEF PSRIHLIGPEEERRKREYPPGLGALE GRTQVTGTRKKQAQSESGTRFPPEK GELVLLSSHDEGENLVKDKFIRRW VHKEGFGFKRYVTAEDKELEAKI AVVEKYNIRIPELVQRIEKCHIEDLD FAEYILGTVHKAKGLEFDTVHVLD DFVKVPCARHNLQPLALR\VEPFS\ EDEVNLLYVAVTRAKKRLIMTKS LENILTLAGEYFLQAE\TSNVLKTG VVR\CCVG\QC\NNAIPVDTVLTMMK LAPITY*ATGK\ENKGGYLCHSCAEQ RIGPLAFLTASPEQVRAMERTVENI VLPRHEALLFLVF
5278	10775	A	5595	3	613	
5279	10776	A	5596	2	1419	PPLLSSPFVAAPRARATAGAF TLS ASAMQEIAHLQAGQCGNQIGAKFW EVISDEHGIDPTGTYHGSDQLQLERI NVYYNEATG\GNYVPRAVLVDLEP GTMDSVRSGPFGQIFRPDNFVFGQS GAGNNWAKGHYTEGAELVDAVLD VVRKEAESCDCLQGFQLTHSLGGG TGSGMGTLISKIREFPDRIMNTFS VVPSPKCQD TVVEPYNATLSVHQL VENTDETYCIDNEALYDICFRTLKL TTPTYGDLNHLVSA TMSGVTTCLRF PGQLNADLRKLAVNMVPPRLHFF

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						MPAFAPLTSRGSQQYRGLTVPELTQ QMFDANKMMAACDPRHGRLTVA AVFRGRMSMKEVDEQMLSQSKN SSYFVEWIPNNVKTA VCDIPRGLK MAVTFIGNSTAIQELFKRISEQFTAM FRRKAFLHWYTGE GMDMEFTEAE SNMNDLVSEYQQYQDATAEQGEFE EEAEEVA
5280	10777	A	5603	1	384	
5281	10778	A	5604	185	700	
5282	10779	A	5605	1	414	
5283	10780	A	5606	3	138	
5284	10781	A	5607	1	433	NNPDFKAGV/MALPTL/LQIQRHDD YL VMLKAIRILVQERLTQDAVAKA NQTKGLPVALDKHILGFDTGDAV LNEAAQILRL LHIEELRELQTKINEA IVAVQAIHFWHVWKSCHILGGGS PENWVCSRDLPLLIAFFFNKV
5285	10782	A	5608	1	459	
5286	10783	A	5609	118	375	VAVVQIIFLPVFIAEKYKDLVPDNSK TADNATKNAEPLINLDVNNPDFKA GVMALANLLQIQRHDDYLVMLK\A IRILVQERLTQD
5287	10784	A	5610	344	513	
5288	10785	A	5611	3	116	
5289	10786	A	5612	3	869	HEVFSRPRPGEPNREAGTMFRRRLT VLDYHNPAGFNCKDETEFRNFIVW LEDQKIRHYKIEDRG\NLRNIHSSDW PK\FFEKYLRDVNCPFKIQDRQEAI DWLLGF A VRPEYGDNAEKYKDLV PDNSK\TADNAPKNAEPWINLDVN NPDFK\AGVMALG*PAFRFQRHDD\ FLVNA*RQFRIWVQE\RLTQDA\VA KAKSNKKRALPVALAQTHILGFDYT GDASSLMKLEILRIACTYEELRELT DQKSTKAIVAVQAIYC*SQRQDHRL GKSLEDEHFEDLQLSPLL
5290	10787	A	5613	298	403	
5291	10788	A	5614	3	611	
5292	10789	A	5615	192	340	
5293	10790	A	5616	187	361	
5294	10791	A	5617	187	385	
5295	10792	A	5618	2	340	
5296	10793	A	5619	1	702	EKYIQLVRQRALEGALGNTIYKSQ TAKGTPQETEGTSSGSKSNVRSGKR VPSGRMV/IHSHFPAEVT*E*TRVH WIWQS*CGESWKQVPFLCHSGS* RNALLCLRHDVDALLWQPHSSKQ DDMWEHIATFNALGYVQASKRDK KFFACAPNYSYAALCECLRRVFIYR QPAPMSTVLYNKKGRQA\VGQVAK QQVASLETNDPNLGIQATNERLFV LTTKNLFLIKVNTEN
5297	10794	A	5620	3	357	
5298	10795	A	5621	1	1926	
5299	10796	A	5622	1	362	LQTSDEETGFSCLF EYVCAATSFVL VCIINNWSCKAD*DTRWTFRIKIGR

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						T/SVVDLLYWRDINITGVVFGATLFL LLSLTVFSIVSVTAYIALALLSVTISF TIYKGVSHAIPKSDEGHPF
5300	10797	A	5623	247	533	KSFPGWQTYFSCGWVGCGLGRGS QNASPPASPLPQLPPG*RRSWPLRG TACRSWSALSGWAAGLYHPPRMPP LMWEAGAGSPGELRGTRIRER
5301	10798	A	5624	128	667	
5302	10799	A	5625	12	3756	VPRLSRPSQSSPTPTTARGSETRP RRRRQQLQHHLHPPAMEDLDQSPL VSSSDSPRPQPAFKYQFVREPEDEE EEEEEEEEDEDEDLEEVLERKPA AGLSAAPVPTAPAAGAPLMDFGND FVPPAPRGPLPAAPPVAPERQPSWD PSPVSSTVPAPSPLSAAAVSPSKLPE DDEPPARPPPPASVSPQAEPVWTP PAPAPAAPSTPAAPKRRGSSGSVD ETLFALPAASEPVIRSSAENMDLKE QPGNTISAGQEDFPSVLLETAASLPS LSPLSAAASFKEHEYLGNLSTVLPTE GTLQENVSEASKEVSEKAKTLLIDR DLTEFSELEYSEMGSFSVSPKAESA VIVANPREEIIVKNKDEEEKLVSNNI LHNQQLPTALTKLVKEDEVVSSEK AKDSFNEKRVAVEAPMREEYADFK PFERVWEVKDSKEDSDMLAAGGKI ESNLESKVDKKCFADSLEQTNHEK DSESSNDDTSFPSTPEGIKDRSGAYI TCAPFNPAATESIATNIFLLGDPTSE NKTDEKKIEEKKAIQVTEKNTSTKT SNPFLVAAQDSETDYVTTDNLTKV TEEVVANMPEGLTPDLVQEACESEL NEVTGKIA YETKMDLVQTSEVMQ ESLYPAAQLCPSFESEATPSPVLPD IVMEAPLNSAVPSAGASVIQSSSPL EASSVNYESIKHEPENPPPYEEAMS VSLKKVSGIKEEIKEPENINAALQET EAPYISACDLIKETKLSAEPAPDFSD YSEMAKVEQVPDHSSELVEDSSPDS EPVDLFSDDSDVPQKQDETVMVLV KESLTETSFESMIEYENKEKLSALPP EGGKPYLESFKLSLDNTKDTLLPDE VSTLSKKEKIPLQMEELSTAVYSND DLFISKEAQIRETETFSDDSPIIIDEF PTLISSKTD SFSKLAREYTDLEVSHK SEIANAPDGAGSLPCTELPHDLSLK NIQPKVEEKISFSDDFSKNGSATSKV LLLPPDVSALATQAEIESIVKPKVLV KEAEKKLPSDTEKEDRSPSAIFSAEL SKTSVVDLLYWRDIKKTGVVFGA/ SAVFLLS\LTVF\SIVSVTAYIALAL LSVTISFRIYKGVIAIQKS\DEGHP FRAISGNL/ESCLYLRELGSGRYSNS\ ALGSMWNCTVKGNFRAPSFSSWM DLVDSL/RSFAVLMWVFTYVGCLG LMVLDTTGFWALNF/ISSSGSWLIYE RHQAQIDH\YGLGLANKNVKDAMA KIQAQIPGLKRKAE

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5303	10800	A	5626	2	436	RRQFEERQQEMEHVYELLENKMQLLQEESRLAKNEAARMAALVEAEKENCNLELSEKLKGVTKNWEDVPGDQVKPDQ\YTEALAQRDK*VPSVLF\RLSFAHSQGIQQLSCSLSRT/RQ*ELHYF*DFMGPPQKTFPSGLNFQWYPL
5304	10801	A	5627	3	309	
5305	10802	B	5628	454	645	MTCKKENFSLKLLIYFLEERMQQKYEASREDIYKRNTTELKVEVESLKRELQDKKQPSGLKPWA*
5306	10803	A	5629	1	294	
5307	10804	A	5630	14	228	
5308	10805	A	5631	201	350	
5309	10806	A	5632	262	626	PSARPHCFGLEAMHARSLPCWNCSRRLLILAFS/WGSE/CCTRKPRIIDVVYNASNNELVRTKTLVKNCIVLIDSTPYR\QWYESH\YALPLGRKKGAKLTPEEEEEILNKKRSKKIQKKYDERKENAKISSLLEEQQQGLLACIASRPKQCGRADGYVLEGKELEFYLRK\IKARRKQINPCFVFTHGNRGVYCFVPTFMLPEYMTVFS\AIFPCPAKLIWGGGLQPLALTSASYPETGSPHC
5310	10807	A	5633	3	452	
5311	10808	A	5634	26	477	NSTDSETHHGARLLPDKTNVKAAGW\KVGAGAHAG\EYGAELERMFLSFP\TKTYFPHFD\SHG\SAQVKG/HTGKKVADALTNAVANVDDMPNALSALS\DLHAHKL\RDVPVNFKLLSHCLAGGPWAAHLPRPSSTPGGATPSLEQSSWASC
5312	10809	A	5635	1	147	
5313	10810	A	5636	1	503	AAAAARAAGTAGPWRSARLPALPASSLGAAAMAASAKRKQEEKHLKMLRDMTGLPHNRKCFDCDQRGPTYVNMTVGSFVCTSCSGSLRG*NPPHRVKSISMTTFTQQEIEFLQKHGNEVCPIPEQAKVVASVHASISGSSASSTSSTPEVRPLKSLLGDSAPTLHLN
5314	10811	A	5637	272	360	
5315	10812	A	5638	1	1934	WRRRRRLSRLCRLVWPVSPRTTAPGPRRAQYSQAAAAGSGAGGARRRRAAAAARAAGTAGPRRSAARLPALPASSLGAAAMAASAKRKQEEKHLKMLRDMTGLPHNRKCFDCDQRGPTYVNMTVGSFVCTSCSGSLRGLNPPHK/VGKSISMTTFTQQEIEFLQKHGNEVCKQIWLGLFDDRSAIPDFRDPOKVKEFLQEKYEKKRWYVPPEQAKVVASVHASISGSSASSTSTPEVKPLKSLLGDSAPTLHLNKGTPSQSPVVGSRQGGQKEKKQFDLLSDLGSDIFAAPAQSTATANFANFAHFNHAAQNSANADFANFADFQSSGSSNFQGGPTASHSPFPQTTGGSAAASVNANFAHFDNFPKSSSADFGTFNTSQSHQ TASAVSKVSTNKAGLQTADKYAALANLDN

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						IFSAGQGGDQGSFGTTGKAPVGSV VSVPSQSSASSDKYAALAE LDSVFS SAATSSNAYTSTSNASSNVFGTVPV VASAQTQPASSSVAPFGRTPSTNPF VAAAGPSVASSTNPFQTNARGATA ATFGTASMSMPTGFGTPAPYSLPTS FSGSFQQPAFPAQAAPFQQTAFSQQ PNGAGFAAFGQTKPVVTPFGQVAA AGVSSNPFMTGAPTQGFPTGSSSTN PFL
5316	10813	A	5639	1	307	
5317	10814	A	5640	957	3132	GEEELWQGCSAGLPWLPAEPLCK* RREKPRFCAAYQRPLCGHAEKQAR *PLGPWCSRKKKGAEEEKPKRRR QEKQAACPFYNHEQMGLLRDEALA EVKDMEQLLALGKEARACPYGSR LAIPAAQLVVLPHYQMLLHAATRQA AGIRLQDQVVIIDEAHNLIDTITGMH SVEVSGSQLCQAHSQQLQYVERYG KRLKAKNLMYLKQILYLLEKFVAV LGGNIKQNPNTQSLSTGTTELKTIN DFLFQSQIDNINLFKVCVPSAPQMK HGHCRNLNPKLVTQISNSDCPRVQRY CEKSMISRKLFGFTERYGAVFSSRE QPKLAGFQQFLQSLQPRTEALAAP ADESQASTLRPASPLMHIQGFALAAL TTANQDGRVILSRQGSLSQSTLKFL LLNPAVHFAQVVKECRAVVIAGGT MQPVSDFRQQLACAGVEAERVVE FSCGHVIPPDNILPLVICSGISNQPLE FTFQKRELPMQMMDEVGRILCNLCG VVPGGVVCFFPSYEYLRQVHAHWE KGGLLGRLAARKKIFQEPKSAHQV EQVLLAYSRCIACGQERGQVTGA LLLSVVGKMSSEGINFSDNLGRCV VMVGMPPFNIRSAELQEKMAYLDQ TLPRAPGQAPPKALVENLCMKAV NQSIGRAIRHQKDFASVLLDQRYA RPPVLAKLPWIRARVEVKATFGPA IAAVQKFLQVYGTSLPLNHL SKLQD TFYPNTS NYAKGR
5318	10815	A	5641	1	1668	
5319	10816	A	5642	947	2782	GEEELWQGCSAGLPWLPAEPLCK* RREKPRFCAAYQRPLCGHAEKQAR\ KKKGAEEEKPKRRRQEKQAACPFY NHEQMGLLRDEALAEVKDMEQLL ALGKEARACPYGSR LAIPAAQLV VLPYQMLLHAATRQAAGIRLQDQV VIIDEAHNLIDTITGMHSVEVSGSQL CQAHSQQLQYVERYGKRLKAKNL MYLKQILYLLEKFVAVLGGNIKQNP NTQSLSTGTTELKTINDFLFQSQIDN INLFKVQRYCEKSMISRKLFGFTER YGAVFSSREQPKLAGFQQFLQSLQPR RTTEALAAPADESQASTLRPASPLM HIQGFALAALTTANQDGRVILSRQGS LSQSTLKFLLLNPAVHFAQVVKECR AVVIAGGT MQPVSDFRQQLACAG

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						VEAERVVEF/SCGHVIPPDNILPLVICSGISNQPLEFTFQKRELPQMIFQEPKSAHQVEQVLLAYSRCIQACGQERGQVTGALLSVVGGKMSEGINFSDNLGRCVVMVGMPFPNIRSAELQEKMAYLDQTLPRAPGQAPPKGALVENLCMKAVNQSIGRAIRHQKDFASVVLDDQRYARPPVLAKLPWIRARVEVKATFGPAIAAVQKFHREKSASS
5320	10817	A	5643	1143	3233	GEEEPWQGCAGLPWLPAEPLCK* RREKPRFCAAYQRPLRGHAELQAR\KKGAEEEKPKRRRQEKQAACPFYNHEQMGLLRDEALAEVKDMEQLLALGKEARACPYRSLAIPAAQLV VLSYQMLLHAATRQAAGIRLQDQV VIIDEAHNLIDTITGMHSVEVSGSIQ LCQAHSQLLQYMERYGKRLKAKN LMYLKQILYLLEKFVAVLGGNIKQ NPNTQSLSQGTGTELKTINDFLFQSQI DNINLFKVQRYCEKSMISRKLFGFT ERYGAVFSSREQPKLAGFQQFLQSL QPRTEALAAPADESQASVPQASP LMHIEGFLAALTANQDGRVILSRQ GSLSQSTLKFLLLNPAVHFAQVVKE CRAVVIAGGTMQPVSDFRQQLLAC AGVEAERVVEFSCVFGPSLALTGH VIPPDNILPLVICSGISNQPLEFTFQK RELPQMMDDEVGRILCNLCGVVPGG VVCFFPSYEYLRQVHAHWEKGGLL GRLAARKKIFQEPKSAHQVEQVLL AYSRCIQACGQERGQVTGALLSV VGGKMSEGINFSDNLGRCVVMVG MPFPNIRSAELQEKMAYLDQTLPRAPGQAPPKGALVENLCMKAVNQSIGRAIRHQKDFASIVLLDQRYARPPVLAKLPWIRARVEVKATFGPAIAAVQKVSPTEFFLRASPPRDHISHCLLSAQFHREKSASS
5321	10818	A	5644	3	744	
5322	10819	A	5645	40	126	
5323	10820	C	5646	187	366	MDERDSHCPYLLSSETTAKGTGLAESAGKEDPVELDSSLEARVRRRPPSTSMPLTSAPC*
5324	10821	A	5647	1	382	TADCAKPVPLAVVSLDSRYGQWESSIIHA\VTN*ASSSSSSSSSSVSFR\VYPRFIEFIHFDIQSTGQ/RITSR*HPPR/DLRDALF*LNSLIPLVRTSSKSAARRR\GEAPRGTA VPGADPAGGTRPR
5325	10822	A	5648	3	684	QGPRAALGALFPCWAPGKYVHGVRAKHPRATARAPRGSP/LPPHRVSEKTIRVVVFHRRPAGPADPAPGPSRGHRGGAG/EPPTYSTPLMSLHRARLESSTGSSFPADSAKPVPLAVVSLDSR*GQWESSIIHA\VTN*ASSSSSSSSSSVSFR\VYPRFIEFLHFDIQSTGQ/RITSRQHPPR/DLRDALF*LNSRIPLVRTSSKSAARRR\GEAPRGTAAPGADPAGGP

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5326	10823	A	5649	2	331	
5327	10824	A	5650	3	340	
5328	10825	A	5651	1	94	
5329	10826	A	5652	2	496	ASMGCSPLLSLLSLLVGAWLKLGH*TAGHAGGAGKGDGALRPGGREPEAPLPASGMRLQPPAGEVALGAQGASPPCAFNFLWNLSIQAQLRRVRGQGCSWRWLVLAQAIEELLGDPALVPTRRQPVGRAAPAAPASSLCCADPAGREVTQVVVVQVVVNSSS
5330	10827	A	5653	3	997	
5331	10828	A	5654	3	131	
5332	10829	A	5655	112	289	
5333	10830	A	5656	35	5228	LDPLGRMVMGIFANCIFCLKVKYLPQQQKKKLQTDIKENGKFSFSLNPQCTHIILDNADVLSQYQLNSIQKNHVHIANPDFIWKSIREKRLLDVKNYDPYKPLDITPPPDQKASSEVKTEGLCPDSATEEEDTVELTEFGMQNVEIPLHPQDFEVAKYNTLEKVGMEGGQEA VVVELQCSRDSRDCPFLISSHFLDDGMETRQRQFAIKKTSEDASEYFENYIEELKKQGFLREHFTPEATQLASEQLQALLLEEVMNSSSTLSQEVSDLVEMIWAEALGHLEHMLLKPVNRISLNDVSKAEGILLLVKAALKNGETAELQLQKMMTEFYRLIPHKGTMPKEVNLGLLAKKADLCQLRDMVNVCEITNLSKPNPPSLAKYRALRCKIEHVEQNT EEFLRVRKEVLQNHHSKSPVDVLQIFRVGRVNETTEFLSKLGNVRPLLHGSPVQNIIVGILCRGLLPKVVEDRGVQRTDVGNLGSIGYFSDSLSTSIKYSHPGETDGTRELLICDVALGKCMDLHEKDFSLTEAPPGYDSVHGVSTASVTDFEDDEFVYKTNQVKMKYIHKFSMPGDQIKDFHPSDHTELEEYRPEFSNFSKVEDYQLPDAKTSSSTKAGLQDASGNLVPLEDVHIKGRIDTVAQVIVFQTYTNKSHVPIEAKYIFPLDDKA AVCGFEAFINGKHVGEIKEKEEAQQEYLEAVTQGHGAYLMSQDAPDVF TVSVGNLPPKAKVLIKITYITELSILGTVGVFFMPATVAPWQQDKALNENLQDTVEKICIKEIGTKQSFSLTMSIEMPYVIEFIFSDTHELKQKRTDCKAVISTMEGSSLDSSGFSHLIGLSAAYLPRMWVEKHPEKESEACMLVFQPDLDVLDPLANESEVILCLDCSSSMEGVTFLQAKEIALHALSLVGEKQKVNIIQFGTGYKELFSYPKHITSNTAAAEFIMSATPTMGNTDFWKTLRYLSLLYPARGSRNILLVSDGHLQDESLTLQLVKRSRPHTRLAFACGIGSTANRHVLRILSQCGAGVFEYFNAKSKHSWRKQIEDQMTRLCSPSCHSVSVKWQQLNPD APEALQAPAQVPSLFRNDRLLVYGFIPHCTQATLICALIQEKEFCTMVSTTE

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						LQKTTGTMIHKLAARALIRDYEDGI LHENETSHEMKKQTLKSLIILKSKE NSLITQFTSFVAVEKRDENESFPDI PKVSELIKEDVDFLPYMSWQGEF QEAVRNQSLLASSEWPELRLSKRK HRKIPFSKRKMELSQPEVSEDFEED ALGVLPFTSNLERGRVEKLLDLS WTESCKPTATEPLFKKVSPWETSTS SFFPILAPAVGSYLTPTTRAHSPASL SFASYRQVASFGSAAPRQFDASQF SQGPVPGTCADWIPQSASCTGPPQ NPPSAPYCGIVFSGSSLSSAQSAPLQ HPGGFTTRPSAGTFPELDSPLHFSL PTDPDPIRGFGSYHPSAYSPFHFQPS AASLTANLRLPMASALPEALCSQSR TTPVDLCLLEESVGSLEGRCPVFAT QSSDTESEDELSEVLQDSCFLQIKCDT KDDSI PCFLEVKEEDEIVCTQHWQD AVPWTELLSLQTEDGFWKLTPELG LILNLNTNGLHSFLKQKGIQSLGVK GRECLLDLIATMLVLQFIRTRLEKE GIVFKSLMKMDDPSISRNPWAFEAI KQASEWVRRTEGQYPSICPRLELGN DWDSATKQLLGLQPISTVSPLHRVL HYSQG
5334	10831	A	5657	10	82	
5335	10832	C	5658	189	396	MVHPAGPLASQXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXELWLHHLSSSS *
5336	10833	C	5659	54	485	MXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXRPEDFATYQC QNYISPLTFGGGTKVEIXRTVAAPS VFIFPPSX*
5337	10834	A	5660	5	417	
5338	10835	A	5661	3	398	
5339	10836	C	5662	12	451	MXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXFSSYYCQ QSYSVPTFGPGTKVDIKRTVAAPS VFIFPPSDEQ*
5340	10837	A	5663	3	679	AWWNSETPAQLLFLLLWLPTYSG EIVLTQAPGTLSPGERATLSCRAS QTIGSTYLA WYQQRPGQAPRFLIYG ASSRATGIPDSSSSSSSSSSSSSSSS SSSSSSSSSQYYTSPLTFGGGTKV EIRRTVAAPSVFIFPPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYLSST LTLKADYEKHKVYA\CEVTHQG
5341	10838	B	5664	94	321	XDRVITTCQATQDIGNYLNWYQHK PGKAPNLLIYDASNLETGVPSRFSG RSGGTHFTFTISSLPEDIATYYCQQ

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						YX*
5342	10839	A	5665	3	764	AWLESISPTMRVPAQLLGLLLWIP GSVADIMMTQTPLSLSVSPGQSASIS CKSSQSLHSDGKTHVYWLQKPG QSPQLLIYEVSSRFSGVPDRFSGSGS GTDFTLKITRVEAEDVGVIYCCQY NSYLLFTFGPGTKVDIKRTVAAPSV FIFPPASDEQLKSGTASVVCLLNNFL FPVRRAKVQWEGGINALQSGNSQEC VTEQDSKSGTYSLSSTLTVSKADY EKHKVYACEVTHQGLSSPVTKSFN RGEN
5343	10840	A	5666	1	534	RRPRREPWKQSRFSSSCYS/ELPDT TGEIVLTQSPGTLSPGERATLSCR ASQSVSNYYLAWYQQKPGQAPRL IYDTSSRATGIPDRFSGSASGTDFTL TISRLEPEDFAVIYCCQYGSSPPMY TFGQGTKEIKRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKV QW
5344	10841	A	5667	184	621	LHECISVLPISDTTGEIVLTQSPATL SLSPGERATLSCRASQSVNNYYLA WYQQKPGQPPRLIYDASNRITGIP ARFSGSGSGTEFTFHSAACSLKDF CSLFTVQQLINWASDSPLGQGTSL GD/IKRTVAAPSVFIFPPSDE
5345	10842	A	5668	156	364	
5346	10843	A	5669	2	2143	SSDGSWWTGFWREWRQAGRSVN SWDNPKQEVRASSKDKSRGSIQEA MRMQSSAKLLCSAWTLAYSIAVRT LSSDSEGQPLVIHRQTGSGEDLQQ TPTDLQLRVLTIIRKTNKQKGPHQ NPISSRRQETKIRAEKKIETQKPFK KINESRSWFFKINKIDRLARLIKK KIEKNQIDAIKNDKGNITNPTETQ TIREYYKHLANKLEHLEMDKFL DIYTLPRLNQEEVESVNRPTGSEIE AIINSLPTKKSPGPDRTAELYQRYK EELVPFLKLQFQIEKEGILPNSFYEA SIILISKPRDRTTKENFRPISLMNID AKILNKILANQIQHIKKLIHHHQV GFIPGMQGWFNILKSINVIHHNRTK DKNHMIISIEAEKAFDKIQPFMLKT LNKLGIDGTYLTYLKIIRAIYDKPTA NIILNGQKLEAFPFKTGTRQGCPLSP LLFNIVLEALARAIRQEKEIKGIQLG KEDVKLSLFADDMIVYLENPIVSAQ NLLKLISNFSEVSGYKINVQKSQAFL YTNNRQTESQIMSELPFTIASKRIKY LGIQLTRDVKDLFKENYKPLLNEIK EDTNKWKNIPCSWIGRINIVKMAIL PKTLNQKFSYWFRVKNHYIHQRTEP LKETEFNTIATLYNGASP/RTAPKST GTNGHQASGLPRF*RIAFCSALVKS KRKLYQGYLPGQTDRREEGVSWCP GGP
5347	10844	A	5670	1	2781	
5348	10845	A	5671	1	2988	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
5349	10846	A	5672	1	3516	
5350	10847	A	5673	1	2850	
5351	10848	A	5674	1	2850	
5352	10849	A	5675	1	3087	
5353	10850	A	5676	1	3111	
5354	10851	A	5677	1	2742	
5355	10852	A	5678	1	3474	
5356	10853	B	5679	1	3264	MGDFNTPLSTLDRSMRQKVNKDTQ ELNSALHQADLIDYRTLHPKSTEYT FFSAPHHTYSKTDHIVGSKALLSKC KRTEHTNCLSDHSAIKLELRIKNLTQ NRSTTWKLNQLLNDYWAHNEMK AEIKMFFETNENKDTTYQNLWDTF KAVCRGKFIALNAHKRKQERSKIDT LTSQLEKEKQEQTHSKASRRQEIT KIRAELEKETQKILQKINESRSWFF ERINKIDRPLARLIKKKREKNQIDAI KNDKGDITDPTEIQNTIREYYKHL YTNKLENLEEMDKFLDTYTLPRLN QEEVESLNRPTGPEIVAIINSLPTKK SPGPDGFTAKFYQRYKEELVPFLK LFQSIEKEGILPNSFYEASIIIPKPGR DTTKKENFRPISLMNIDAKILNKILA KRIQQHIKKLIHHDQVGFIPGMQGW FNIHKSINVIQHINRPKDKNHMISID AEKAFDKIQPFMLKTLNKLGDGT YFKIISAIYDKPTANIILNGQKVEAFP LKTGTRQGCPSPLLFNIVLEVLR AIRQEKEIKGIQLGKEEVKLSLFADD MIVYLENPIVSAQNLLKLISNFSKVS GYKINVQKSQAFLYTNNRQTESQIM SELPFTIASKRIKYLGIQLTRDVKDL FKENYKPLLKEIKEDTNKWKNIPCS WVGRINIVKMAILPKVIYRFNAIPIK LPMFTFFTELEKTTLKFIWNALITKSI LSQKNKAGGITLPDFKLYYKATVT KTAWYWYQNRDIDQWNRTEPSEIT PHIYNLIFDKPEKNKQWGKDSLLN KWCWENWLAICRKLKLDPFLTPYT KINSRWIKDLNVRPKTIKLEENLGI TIQDIGMGKDFMSKTPKAMATKAK IDKWDLIKLSFCTAKQTTIRVNRQ PTKWEKIFATYSSDKGLISRIYNELK QIYKKKTNNPIKKWAKDMNRHFSK EDIYAAKHKMKCSSSLAIREMQIK TTRYHLTPVRMAIHKSGNNRTW EYNILCSLVPLLCSSLWLHLTDHHL KEDRTKHLTASDNLEKTELSRWKE RALLYEHRVLRPAIDSQHSAPRRI QGHLVCGSDLTGFMDDVAVIDVS PF*
5357	10854	A	5680	1	3780	
5358	10855	A	5681	1	3290	MGELITPLSTLDRSTRQKVNKDTQE LNSALHQGLIDYRTLHPKSTEYTF FSAPHHTYSKIDHILGSKALLSKCKR TEIITNYLSDHSAIKLELRIKNLTQN RSTTWKLNLLNDYWIHNEKAE

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						IKMFFETNENKDDTTYQNLWDAFKA VCRGKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFFERI NKIDRPLARLIKKKREKNQIDTIKND KGDIATNPTEIQTIREYYKHLYAN KLENLEEMDKFLDTYTLPRNLQEE VESLNRPIGAEIVAINSLPTKKSPG PDGFTAESYQRYKEELVPFLLKLQF SIEKEGILPNSFYEASIIIPKPGRDTT KKENFRLISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFIPGMQGWFN RKSINVIQHINRAKDKNHMISIDAE KAFDKIQPFMLKTLNKLIGDGYF KIIRAIYDKPTANIIENGQKLEAFPLK TGTRQGCPLSPLLFNIVLEVLAIR QEKEIKGIQSGKEEVKLSLFADDMI VYLENPIVSDQNLLKLISNFSKVSGY KINVQKSQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLTRDVKDLFK ENYKPLLKEIKEDTNKWKNI PCSW VGRISIVKMAILPKVIYRFSAPIKLP MTFFTELEKTTLKFIWNQKRARIAK AILSQKNKAGGITLPDFKLYYKATV TKTARYWYQNRDIDQWNRTEPSEI TPHIYNYLIFDKPEKNKQWGKDSL NKWCWENWLAICRKLKLDPFLTPY TKINSRWIKDLNIRPKTIKTLEENLG STIQDIGMGKDFMSKTPKAMATKD KIDIWDLIKLKSFACTAKETTIRVNGQ PTKWEKIFATYSSDKGLISRICNELK QIYKKKTNNPIKKWAKDMNRHFSK EDIYAAKHKMKCSSSLAIRQMQUIK TTMRYHLTP/VKFRSTSHQSP*REAR GPGPLANAGSPGLRQIPETCHLKHP LGMLLSHHSALSATHNPTPCKLQS SVMFTTSAAMLSDPWGLRKGLGRE MFSCKTTEGNQLEAGAAEQSLYAL PKPSDLQT
5359	10856	A	5682	1	3780	
5360	10857	A	5683	1	2877	
5361	10858	A	5684	1	3126	
5362	10859	A	5685	3	3244	
5363	10860	A	5686	1540	3288	SSSLHPWDARLVQYTQINKCNPAY KQSQRQKPHYQQLEAFPLKTGTRQ QPFMLKT/LYSIVLEVLAIRQKKE IKGIQLGKEEVKLSLFADDMIVYLE NPIVSAQNLLKLISNFSKVSGYKINV QKSQAFLYTKNRQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKENYK PLLKEIKEDTNKWKNI PCSWVGRIN IVKMAILPKVIYRFNAIPIKLPMTFFT ELEKTTLKFIWNQKRARIAKSILSQK NKVGGITLPDFKLYYKATVTKTAW YWYQNRVIDQWNRKEPSEITPHY NYLIFDKPEKNKQWGKDSL FNKWC WENWLAICRKLKLDPFLTPYTKINS RWIKDLNVRPKTIKTLEENLGITIQD

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						IGMGKDFMSKTPKAMATKAKIDK WDLIKLSFCTAKETTIRVNRQPTT WEKIFTTYSSDKGLISRIYNELKQIY KKKTNNPIKKWVKDMNRHFSKEDI YAAKKHMKKCSSSLAIREMQIKTT MRYHLTPVRMAIHKSGNNRCWRG CGEIGTLLHCWWDCCKLVQPLWKS VRFLRDLELEIPFDPAIPLLG IYPND YKSCCYKDTCT
5364	10861	A	5687	1182	3406	YQSLAETQPKKENFRPISLMNIDAKI LNKILAKRIQQHIKKLIHHDQVGFIP GMQGWFNIRKSINVTQHINRAKDK NHMIISIDAEKAFDKIQPFMLKTLN KLGIDGTYFKIIRAIYDNPTANIILNG QKLEAFPLKTGTRQGCPSPLLFNIV LEVLARAIQEKEIKGIQLGKEEVK LSLFADNMIVYLENPIVSAQNLLKLI SNFSKVSGYKINVQKSQAFLYTNNR QTESQIMSQLPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDTNK WKNIPCSGVEGRINIVKMAILP/KELE KTKLFIWNQKRAHIAKSILNQKNK AGGITLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSEITQHIYSYLI FDKPEKNQWKGDSLFWKWCWEN WLAICRKLKLDPFLTPYTKINSRWI KDLNVRPKTIKLEENLGITIQDIGM GKDFMSKTPKAMATKDKIDKWDL VKLKSFCTAKETTIRVNRQPTKWEK IFATYSSDKGLISRIYNELKQIYKKK TNNPIKKWAKDMNRHFSKEDIYAA KKHMKKCSSSLAIREMQIKTTMRY HLTPVRMAIHKSGNNRCWRGCGE TGTLHHCWWDCCKLAQPLWKS VWR FLRDLELEIPFDPAIPLLG IYPNDYKS CCYKDTCTRMFIAALFTIAKTWNQP KCPTIIDWIKKMWHIYTMEYYAAIK NDEFVSFVG TWMKLEIILSKLSQE KTTHRIFSLIGGN
5365	10862	A	5688	1	7578	
5366	10863	A	5689	16775	19999	KMIKGISPPIPQKYKTTIREYYKHL ANKLENLEEMDKFLDTYTLPRNLQ EEVESLNRSITGSEIEAINSLPTKKSP GPDGFTAIFYQRYKEELVPFLKLF QSIEKEGILPNSFYESSILIPKGRDT TKKENFRPISPISLMNIDAKILNKILA KRIQQHIKKLMHHDQVGFIPGMQG WFNIRKSINVIQHINRAKDKNHMIIS IDAEKAFDKIQPFMLKTLNKLID GTYFKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPSPLLFNIVLEVL ARAIQEKEIKGIQLGKEEVKLSLFA DDMIVYVENPIVSAQNLLKLISNFS KVSGYKINVQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNKWK NIPCSWVGRINTVKMAILPKVIYRF NAIPIKLPMFFTELEKTTLKF IWNQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KRARIAKSILRQKNKAGGITLPDFK LYYKATVTKTAWYWYQNRDIDQW NRTEPSEITPHIYNYLIFHKPEKNKQ W GKDSL FNKWCWENWLAICRKLK LDPFLTPYTKINSRWIKDLNVRPKTI K TLEENLGITIQDIGMCKDFMSKTP KAMATKDKIDKWDLIKLSFCTAK ETTITVNRQPTKWEKIFATYSSDKG LISRIYNELKQIYK\KKTNNPIKKWA RDMNRHFSKEDIYAAKHKMKCCSS SLAIREMQIKTTMRYHLTPVRMAII KKS GNNRSWYFEKINKIDRLRLARI KKKREKNQIDAIKNDKG DITTDPTET QTTTREYYKHL YANKLENLEEMDK FLDTYNLPRLKQEEVESLNRPIRGSE IVAIINSLPTKKSPGPDGFTAIFYHR YKEELVPLLLKLFQSIEKEVILPNSF YEASILIPKPDRDTAKKENFRPISLM NIDAKILNKILANRIQQHIKLIHHD QVGFI PGMQGWFNIRKSVNVIQHIN RTKDKNHMIISIDA EK SFDKIQQHF MLKTLNKL GIDG SYLKIIRATYDKP TANIILNGQKLEAFPLKTGTRHGCP LSPLL FNIVLEV LARAI RQEKEIKGIQ LGKEEVKLSLFIDDMIVYLENPIISA QNLLKLISNFSSLRIQNQCTKITSILV HQ
5367	10864	A	5690	78	308	
5368	10865	A	5691	1	611	GASLGGFLAQKFAEYTHKSPRVHSL ILCNSFSDTSIFNQWTANSFWLMP AFMLKKIVLGNFSSGPVDPMMADA IDFMVDRLESLGQSELASRLTLNCQ NSYVEPHKIRDIPVTIMDVFDQSAL STEAKEEMVQA\YPNA\RRRAHLKTG GNFPYLCRSAEGN\LMVQIHLQFH GTKYAAIDPSMVSAEELEVQKGS LISQEEQ
5369	10866	A	5692	3	301	
5370	10867	A	5693	75	361	
5371	10868	A	5694	3	356	
5372	10869	A	5695	1	583	SPLAAKSPPSLHLE/AFKNITSSSPE RHIFGEDRVVSEQPQVGTLEERNV VEALTGSAASRLRGGTSSRRLSSTP LPKAKRSLESEMYLEGLGRSHIASP SPCPDRMPLPSPTESRHSSSIPP\SSP PEQKVGLYRRQTELQDKSEFSDVD KLA FKDN EEFESSFECVDQKQIEEQ KEEKIREQQVKERRQR
5373	10870	A	5696	306	4412	RLMMAQSNMFTVADVLSQDELRLK KLYQTFKDRGILDTLKTQLRNQLIH ELMHPVLSGELQPRSSIVEGSSLLIG ASNSLVADHLQRCGYEYSLSVFFPE SGLAKEKVFTMQDLLQLIKINPTSSL YKSLVSGSDKENQKGF LMHFLKEL AEYHQAKESCNMETQTSSSTFN RDS LAEKLQLIDDQFADAYPQRIKFESL EIKLNEYKREIEEQLRAEMCQKLF FKDT EIAKIKMEAKKKYEKELTMF

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						QNDFEKACQAKSEALVLEKSTLE RIHKHQEIETKEIYAQRQLLLKDMD LLRGREAEKQKQVEAFELNQLQE EKHKSITEALRRQEQNIKSFEETYDR KLKNELNLFHRLHGVCLALGILI*L WQVLEFGGSSPQECFYFLLPKGQL VTAGKKG*NCENVPGIANPDIMLL AVGSQDCA*SLSTKVLTLVGGGQM VQVDWK*PSDYHLGLSLLCAV*I*F TPLLFSVETN*KVIAFSK*PYDNTT LHFV*LSFGTQFIGSRKGFTGHFMFR GYIPGFSIEDFEVYKLSCLAPSGAPV P*ISSCTDNSLSRKMPPEELIFSHSDS\ RYQLELKDDYIIRTNRLIEDERKNK EKAVHLQEELIAINSKKEELNQSVN RVKELELELESVKAQSLAITKQNHM LNEKVKEMSDYSLLKEEKLELLAQ NKLLKQQLSESRNENLRLNRLAQP APELAVFQKELRKAIEAIVVEHEEF ESCRQALHKQLQDEIEHSAQLKAQI LGYKASVKSLLTQVADLKLQKQT QTALENEVYCNPKQSVIDRSVNGLI NGNVVPCNGEISGDFLNNPFKQENV LARMVASRITNYPTAWVEGSSPDS DLEFVANTKARVKELQQAERLEK AFRSYHRRVIKNSAKSPLAAKSPPS LHLLEAFKNITSSSPERHIFGEDRVV SEQPQVGTLKEERNDVVEALTGSE ASRLRGGTSSRRLSSTPLPKAKRSL ECEMYLEGLGRSHIASPSPCPDRMP LPSPTESRHSLSIPPVSSPPEQKVGLY RRQTELQDKSEFSDVDKLAFKDNE EFESSFEFNSFNENTLTSKYVAKW LCWELHRILLGKGAPSYFGFSSRAP VSCPHTALPFFVLVLLLRTHGTIVPH AAAGNMPRQLEMGGLSGAGDMSH VDAAAAAVPLSYQHPSVDQKQIEE QKEEEKIREQQVKERRQREERRQSN LQEVLERERRELEKLYQERKMIEES LKIKIKKELEMENELEMSNQEIKDK SAHSENPLEKYMKIIQQEQDQESAD KVPVPWAGQSVGGGHPGLPWLNFL GRESVFSIEDKKSSKMMVQEGSLVD TLQSSDKVERHCIDPLWRTQQQGTI LEAETGPSPDIEPASAFDLRLPSL
5374	10871	A	5697	3	721	
5375	10872	A	5698	3	265	
5376	10873	A	5699	2	216	
5377	10874	A	5700	3	268	
5378	10875	A	5701	2	465	
5379	10876	A	5702	1	196	
5380	10877	A	5703	2	213	
5381	10878	A	5704	1	438	LQTWGPKQVC/SFFRRGGFEERVLL KNIRENGITGALLPCLDESFRFENLGV SSLGERKKLLSYIQLRVQIHVDTMK\ VGYLAGCLVHALGEKQPELQISERD VLCVQIAGLCHDLGHGPFSSHMFDFG RFIPLARPEVKWTVCIHTVNSQ

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5382	10879	A	5705	2	1925	
5383	10880	A	5706	330	590	
5384	10881	A	5707	3	139	
5385	10882	A	5708	2	126	
5386	10883	A	5709	1	157	
5387	10884	A	5710	85	489	EKPLRWDSHLSCMLCWQAGFEAEQ KVSGSSRKLAI SHALLEMLTPPPAG AMIPPPPSLPGPPRPGMMP\APHMG G\PPMMPMMGPPPPGMMPVGPAPG MRPPMGGHMPMMPGPPVTRPPARP MMVPTRPGMTRPDR
5388	10885	A	5711	235	874	VVRRSGFLFCLFVLFSSMNSASVD GHLSGCRLFLFLSPLFRFYCDYCDT/ YLSPHDSPSVRQTHCSGK\KHIENV KDYQK\WMEK\QSQSL\DKTTA\A FQQGKIPPTPFSAPPP\AGA\MIPPPK \SFPGPPSLV*MPKHPHMGGPPFW M\PMMPGPSFLLGDGWPVGPASGEL R\PMG\GHYCLIAWGPMDVGPS CPFH*WCPLGPGMTRPDR
5389	10886	A	5712	2	406	FRSPADPPVHCDKE*VLEVQREDED YHDSAKEKDEEDDSITRLL\FELEA YLSHNDYDGIKLLQQLFLKAPVN TAE\TNFLIQNHIGSVIKHTDVS*D SIDDMDDEDEAFGISLLNLPDRKGT QCGEQIQE
5390	10887	A	5713	3	379	AVERGVPHFPDSPVQRDEEEKEVD TEDDDDDSDQEKDDDNALDEEV NIEF\AAYSLSYNDYDGIKLLPQLFI AAPVNTAKLPDLLIQNHIGSAIKQ TDVSEDSNDDMDEEEASYSIDRLYN
5391	10888	B	5714	65	188	MWGFRIPADALIQRDEEEKEVLNE DEDDDDSDKEKDEEDRX*
5392	10889	A	5715	3	365	
5393	10890	A	5716	3	356	
5394	10891	A	5717	1	168	
5395	10892	A	5718	281	422	
5396	10893	A	5719	1	107	
5397	10894	A	5720	3	291	
5398	10895	A	5721	1	1260	WRTAAFWAFTVFLGDIILLTDVVIH EDQWIGETVLQSTFSSQLNLGSYS SIQPEEYSSVCEVVLQDLLAYVSS KHSYLRDLPPRQPQRVNSIDFV\EL EHLQPDVLVHGSKELLDFITL TEG S/VYSYRGQKQ\KKVMLTV\DQAQG QHYALVLWGSWGQPGYPQLQRKK GYIWEFKYLFVQCNYTLENLELHTT PWSSCECLFDDDIRAITFKAKFQKS APSFVKISDLATHLEDKCSGVVLK AQISELAFITASQKIALNAHSSLKSI FSSLPNIVYTGCAKCGLEETDENRI YKQCFSCLPFTMKKIYYRPALMTAI DGRHDVCIRVESKLIKILLNISADC LNRVIVPSSEITYGMVVADLFHSL AVSAEPCVLKIQSLFVLDENSYPLQ QDFSLLDFYPDIVKHGANARL
5399	10896	A	5722	122	390	TFCVRSGLLDFAFPEPWRWGEKWK

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						NWPESLEVWVLVLAVPLTHCDLGI LCCEDISQVLHVSQQI*PTRPGKR*L LGCAEVVLSSASPG
5400	10897	A	5723	605	902	
5401	10898	A	5724	116	470	
5402	10899	A	5725	1	9786	
5403	10900	A	5726	10996	13825	MLTLRTRRS DGKMKSGFILGLSRAR SSFPMTKKRATPGHCRDPLEGLHRF LKNILPVYDKSLWDFLKL DVTTSIG RRQHLRVSTAFVYTKNPNNGYSFSIP VKVLADKFITPGLKLNLSNVLM PTFHVPFTDLQVPCKLDFREIQIYK KLRTSSFALNLP LPEVKFPEVDVLT KYSQPEDSLIPFFEITVPESQLTVSQF TLPKSVSDGIAALDNLNAVANKIADF ELPTIIVPEQTIEIPSIKFSVPAGIVIPS FQALTARFEVDSPVYNATWSASLK NKADYVETSLDSTCSSTVQFLEYEL NVLGTHKIEDGTLASKTKGTLAHR DFSAEYEDGKFEGLEWEGKAHL NIKSPAFTDLHLRYQKDKKGISTSA ASPAVGTVGMDMDEDDDFSKWNF YYSPQSSPDKKLTIFKTEL RVRESDE ETQIKVNWEEEAASGLTSLKDNVP KATGVLYDYVNKYHWEHTGLTLR EVSSKLRRNLQNNAEWVYQGAIRQ IDDDVRFQKAASGTTGT YQEWKD KAQNL YQELLTQEGQASFQGLKDN VFDGLVRVTQKFHMKVKHLIDSLID FLNFRPFQFPKGPGIYTREELCTMFI REVGTVLSQVYSKVHNGSEILFSYF QDLVITLPFELRKHKLIDVISMYREL LKDLSKEAQEVFKAIQSLKTTEVLR NLQDLLQFIFQLIEDNIKQLKEMKFT YLINYIQDEINTIFNDYIPYVFKLLKE NLCLNLHKFNEFIQNELQEASQELQ QIHQYIMALREEYFDPSIVGWTVKY YELEEKIVSLIKNLLVALKDFHSEYI VSASNFTSQLSSQVEQLHRNIQEY LSILTDPDGKGKEKIAELSATAQEII KSQAIATKKIISDYHQFQRYKLQDF SDQLSDYYEKFIAESKRLIDLSIQNY HTFLIYITELLKKLQSTTVMNPYMK LAPGELTIIL
5404	10901	A	5727	3	182	
5405	10902	A	5728	2	221	
5406	10903	A	5729	577	722	
5407	10904	A	5730	3	176	
5408	10905	A	5731	1	496	LLGVAPSRAFQEEILR/DRASFHE/RP NLFALKHPTSKAECTAEKCYRVTK GRGIFPSGSPFKSVTLEDGKTFIPGQ GNNAYVFP GVALGVIAGGIRHIPDEI FLLTAEQIAQEVFEQHLSQGRLYPP LSTIRDVSLRIAIVLDYAYKHNLD YTWPKEAMNVQTV
5409	10906	A	5732	228	448	
5410	10907	A	5733	3	1877	EGEDRGLPRTMGAALGTGTRLAPW

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						PGRACGALPRWTPPTAPAQGCHSKP GPARPVPLKKRGYDVTRNPHLNKG MAFTLEERLQLGIHGLIPPCFLSQDV QLLRIMRYERQQSDLDKYIILMTL QDRNEKLFYRVLTSDVEKFMPIVYT PTVGLACQHYGLTFRRPRGLFITIHD KGHLATMLNSWPEDNIKAVVVTGD ERILGLGDLGCYGMGIPVGKLALYT ACGGVNPQQCLPVLLDVGTTNEEL LRDPLYIGLKHQRVHGKAYDDLLD EFMQAVTDKFGINLIQFEDFANAN AFRLLNKYRNKYCMFNDDIQGTAS VAVAGILAAALRITNNKLSNHVFVFQ GAGEAAMGIAHLLVMALEKEGVPK AEATRKIWMVDSKGLIVKGRSHLN HEKEMFAQDHPESNSLDEVVRLVK PTAIGVAAIAEA\FTEQILRNMAF RRAPIIFALSNNPPRKAECTA\EKCYR VTEGPRGFFASG\SPF*GVLIWEMGK TFIPGGRGNNA\YVFPGVATGVIA\ GGIRHIP\DEIFLLDSRAKLPQEVSEQ HL\SQGRLYPPLSTIRDVSLRIAIVL DYAYKHNL\SYYPEPKDKEAFCKI PGSYTPDYDSFYT/VDSYIWAQGKA MNVQTV
5411	10908	A	5734	14	304	
5412	10909	A	5735	3	413	
5413	10910	A	5736	2	328	
5414	10911	A	5737	3	472	VTEFAKTCVADESAENCDSLHTLF GDKLCTVATLRETYGEMADCCAK QEPERNECFLOHKDDNPRLVPR EVDVMCTAFHDNEETFLKKYLYEI ARRHPYFYAPELLFFAK/RLDELRD EGKASSAKQRLKASLQKFGERAF KA\VARLSQRFP
5415	10912	A	5738	1	2975	MKWVTFISLLFLFSSAYSRGVFRRT PLGPASSLPQSFLKCLEQVRKIQGD GAALQEKLCATYKLCHPEELVLLG HSLGIPWAPLSSCPSQALQLAGCLS QLHSGFLYQGLLQALEGISPELGPT LDTLQLDVADFATTIWQQMEELGM APALQPTQGAMPAFASAFQRRAGG VLVASHLQSFLEVSYRVLRLHAQPG GGGDAHKSEVAHRFKDLGEENFKA LVLIAFAQYLQQCPFEDHVKL VNEV TEFAKTCVADESA*/ENCDSLHTLF GDKLCTVATLRETYGEMADCCAK QEPERNECFLOHKDDNPRLVPR EVDVMCTAFHDNEETFLKKYLYEI AR\RHPTCIAPELLFFAK\RYKAAFT ECCQAADKAACL\LPKLDELARDEG KASSAKQRLKASLQKFGRKSF HGAVARL\SQEVFPKLEFCQEVSVQ *WTGL*PKFPHGNCCHGRSCFECC WMDR/RRDLWPKYILWKIQDFDLP S*TGRDCC\EKPLVWGKIPTCICRK WEN*WRLPGLDFAFH*ACLIFVWK VKGCFGQNYCLRAKDVPFGACFLY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						\DYARRAS*FTLFVPAEEDLPRTYET TLEECCAAADPHECYAKVFDEFKPL VEEPQNLIKQNCLEFEQLGEYKFQN ALLVRYTKKVPQVSTPTLVEVSRN LGKVGSKCKHPEAKRMPCAEDYL SVVLNHLCLVLEKTPVSDTVTKCC TESFVNTPPCFSALEVDETYVPKHF NAETFTFHAHISTLSQKERQIKKQT ALVDLVKHKPKATKEQLKAVMDD FAAFVEKCKKADDKETCFAEEGKK LVAASQAALGLTPLGPASSLPQSFL LKCLEQVRKIQGDGAALQEKL CAT YKLCHPEELVLLGHSGLIPWAPLSS CPSQALQLAGCLSQLHSGFLYQGL LQALEGISPELGPTLDTLQLDVADF ATTIWQQMEELGMAPALQPTQGA MPAFASAFQRRAGGVLVASHLQSF LEVSYRVLRLHLAQP
5416	10913	A	5739	132	918	
5417	10914	A	5740	59	335	
5418	10915	A	5741	219	642	KGWFLGAFHKL\KTMKHL LLLTGMG C/VF*VKSQGVNDNEEGFFSARGHR PLDKKREEAPSLRPAPPPISGRWAI RASSQPKQLATSKGK*ERKSPWIA KVVFSRLDPDLGVVCCSLQGCSVC QGGFFLTTRGKGPQELVV
5419	10916	A	5742	1	359	
5420	10917	A	5743	1	322	
5421	10918	A	5744	2	862	FVDGKLHGRGSTDDKGPVAGWINA LEAYQKTGQEIPVNVRFCLGEMEE SGSEGLDELIFARKDTFFKDVDYVC ISDNYWLGGKKPCITYGLRGICYFFI EVECSNLDLHSGVYGGSVHEAMTD LILLMEEHKL YDDIDFDIEFAKDV GAQILLHSHKSHLHLDLLPVVVRLL GQALFHTAHFPDNIPSSSKDILMHR WRYPSSLHGLEGA FSGSGAKTVIP RKVVGKFSIRLVPNMTPEVVGEQA CGAGTRESMSSLGYPSRAEDDSGLS ALPSQPQPFILYAT
5422	10919	A	5745	455	601	SLAICGSCPFLLKFTTITGVFLSSL*YD PSKPALTGRMILSQFVLLNKK
5423	10920	A	5746	25	458	
5424	10921	A	5747	3	396	
5425	10922	A	5748	2	797	AGPAALGGAGLCRAADAGLCSAGC GFVKVVKNKAYFKRYQVKFRRRR KGKT\DYARKR\LVIQDNKYNTP KYRMIVRVTRNDIICQIAYA\RIEGD MIVCAA*CTPNLPKYGV\KVGLTNY AAA\CT\GLLL\ARRL\LNRF\MDN \YEGQ\VEVTG\DEYNVESIDWSAQ GAF\TCY\LDAGLAR\TTTG\NKVFG\ ALKGMLWMGGLSIPHSSKRFLGLSI PHSTK*ILGYDSENKEFNAEVRKHI MGQKFADDLHCLIEEDENASKK
5426	10923	A	5749	172	333	
5427	10924	A	5750	2	282	SLSREVQRQMHLVFFSKNKLKAGY

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						LMSVESSE/CFLEEVG/SQALVAGSY MPPSTVLQQIDS/VANADINAACKF VS/GQKSMAAGGNLGHHTPLVDEL
5428	10925	A	5751	813	998	
5429	10926	A	5752	1	1418	MKLLTRAGSFSRFYSLKVAPKVKA TAAPAGAPPQPQDLEFTKLPNGLVI ASLENYSPVSRIGLFIKAGSRYEDFS NLGTTHTLLRLTSSLTTKGASSFKITR GIEAVGGKLSVTATRENMAYTVEC LRGDVDILMEFLNVTTAPEFRWE VADLQPOLKIDKAVAFQNPQTHVIE NLHAAAQNALANPLYCPDYRIGK VTSEELHYFVQNHFTSARMALIGLG VSHPVLKQVAEQFLNMRGGLGLSG AKANYRGGEIREQNGDSLVAHAFV AESAVAGSAEANAFAVSLQHGRVL GHHVKSQQQPPAHLHQ\AVAKA\T QQPFDVSAFNASYSDS\GLFGI\YTIS QGHQLAGDCIK\AA\YNQVKTI\AQG NLSNTDV\QAAQEPS*KAGIP*WSV ESSE\CFLEEVVRPRALVAGSYMPP VHSSFQI/DSPKRGWGGAKMPDII NGGKRSFVSGPEVQWAASLENLGT LHLFV
5430	10927	A	5753	150	355	
5431	10928	A	5754	2	388	FLFFFFEMESRSVAQAGVQWCDLG SLQPPPP\GLSDPALASSVSWITDV RHHLWLIFVFLVETGFRHVGQASLK LPTSGDLPTLASQSAGITGVSHYAW LIFVFLVETEFHHVGGQAGLELLAPS DPPA
5432	10929	C	5755	197	415	MLLYVGLEPHHTHMLSLWPPRLMF PSVFFFFFFFFFLRQGLALLPRLECS GAILAHCNLHLLGSGDSLASF*
5433	10930	A	5756	764	1079	KGVLFFFFFFKTES\HSVAQAGV\QW CTLGSLLQPP/PSRGSSDSPASASRVA GIRGVHHHARLIFVFLVETGFHYVG QAGLELPTSGDSPASASQSAGVTGV SHQCPA
5434	10931	A	5757	213	383	
5435	10932	A	5758	1	981	
5436	10933	A	5759	124	354	
5437	10934	A	5760	2	646	CGGIHGNHTFKMALNQFSDMSFAEI KHKYLWSEPQNCSATKSNYLRTGT PYPPSVDWRKKGNFVSPVKNQGAC GSCWTFSTTGALESIAIATGKMLS LAEQQLVDCAQDFNNHGCQGGLPS QAFEYILYNKGIMGEDTYPY\QGGK GYCK\FQPGKAIGFVKDVANITIYD EEAMVEAVALYNPVSAFEVTDQDF MMYRTGIYSSTSCHKTPDK
5438	10935	A	5761	1	218	
5439	10936	A	5762	272	364	
5440	10937	A	5763	1	1956	
5441	10938	A	5764	105	533	
5442	10939	A	5765	292	568	
5443	10940	A	5766	1	279	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
5444	10941	A	5767	3	352	
5445	10942	A	5768	375	485	TPGLK*FSHLDLLNCWDYRCETVH LAElAQVSEKQI
5446	10943	A	5769	3	221	
5447	10944	A	5770	793	1039	SFSFTFKMLSGRRETFFFGGRFFWF VVVFFFFLAGRGSFALVAQAGVQ WRDLRSLQPPRGFRFFCLSLPGA CGPRYLGG
5448	10945	C	5771	33	334	MSDSGKSSPVAHSILWIWGRSDA YRDKQHILWPKRADCTESYPRVPA GGELPTYFLPPENKGLRIHELNSDD YSTEEEAQTPDCSITDFTRRHTLSYL V*
5449	10946	A	5772	194	593	
5450	10947	A	5773	1	877	
5451	10948	A	5774	2	352	
5452	10949	A	5775	3	726	EQEVDPKEFNAETTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCKKADD EMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLKQNCCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLKRVGSKCKKHPEA KRMPCAEDYLSVVLNQLCVLH/EK TPVSDRVTKCCTESLVNRRPCFSAL EVDETYVPKEFNAETTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCKKADD EMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLKQNCCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLKRVGSKCKKHPEA KRMPCAEDYLSRGPEPVMCVA
5453	10950	A	5776	4274	5255	HTLFGDKLCTVATLRETYGEMADC CAKQEPERNECFQHKDDNPNLPR LVRPEVDVMCTAFHDNGETFLKK* VIRCL*FKIKKHGVTP*ANTL*KLP* QKYFQH*DLEVLL**FFKEVVFDTT KFYTAKNMIKDILKFJETGYNLSQK FKIDKFFNVFRYVYVMVVIIDFVLV SNILPKFNHLCTHTHTHTLTLFST YLKNDRDKTIMCKLSLIG*LLESLEF GGSGENVNYFCNIVCYRK/ADCF SFLKFRYLIEIARRHPYFYAPELLFF AKRYKAAFECCQAADKAACLLPK VLCTRIEKKSLLSNLILSILWDLGT LSV
5454	10951	A	5777	15	218	
5455	10952	A	5778	141	318	
5456	10953	A	5779	1	290	TMSLNRLQEFGTSLVTLDAIPHILPE GDELLEENQEGCFS*SFLFATNATL GPRLWSPWLASGLSLPEACASPKH AAQGPHPKPPRLQPPQHSVCQ

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5457	10954	A	5780	2	643	GTRLFEQLGEYKFQNALIRYTKKV PQVSTPTLVEVSRNLGKVGSKCK HPESKKECPVQEDYLSRGSWNQLL CVCIEKTPVKLTESPKC\CTESLG*T GRPLLFSALGKFDWKHYGFPRSF NCLKTFHLSMAGFMAHFFEEGRRT NSRKTNWHLFELVETQGPRQQRQ LKA\VMGGFAAFVEKCKADDKET CFAEEGKKLVAASQAALGL
5458	10955	A	5781	1	135	
5459	10956	A	5782	1	330	
5460	10957	A	5783	247	434	
5461	10958	A	5784	140	2569	SGSPVLDPSEPQPLAAMHVIKRDGR QERV MFDKITSRIQKLCYGLNMDF VDP AQITMKVIQGLYSGVTTVELDT LAAETAATLTTKHPDYAILAARIA\W SNLHKETKKVFSDV\MEDLYNYINP HNGKHSPMVAKSTLADIVLANKDRL NSAIHYDRDFS YNYFGFTLERSYLL KINGKVAERPQHMLMRVSVGIHKE DIDAAIETYNNLSERWFTHASPTLFN AGTNRPOLSSCFLLSMKDDSIIEGY DTLKQCALISK SAGGIGVAVSCIRA TGSYIAGTNGNSNGLVPMRLVYNN TARYVDQGGNKRPGAFIYLEPWH LDIFEFLDLKNTGKEEQRARDLFF ALWIPDLFMKR VETNQDWSLMCPN ECPGLDEVWGEEFEKLYASYEKQG RVRKVVKAAQQLWYAIIESQTETGTP YMLYKDSCNRKSNQQLGTIKCSN LCTEIVEYTSKDEVAVCNLASLALN MYVTSEHTYDFKKLAEVTKVVVRN LNKIIDINYYPVPEACLSNKRHRPIGI GVQGLADAFILMRYPFESAEQAQLN KQIFETIYYGALEASCDLAKEQGPY ETYEGSPVSKGILQYDMWNVPTD LWDWKVLKEKIAKYGIRNSLLIAP MPTASTAQILGNNEIEPYTSNIYTR RVLSGEFQIVNPHLLKDLTERGLWH EEMKNQIIACNGSIQSIPEIPDDLKQL YKTVWEISQKTVLKMAAERGAFIG QSQSLNIHIAEPNYGKLTSMHFGW KQGLKTGMYYLRTRPAANPIQFTL NKEKLDKEKVSKEEEKERNTAA MVCLENRDECLMCGS
5462	10959	A	5785	1	161	
5463	10960	A	5786	2	170	
5464	10961	C	5787	219	398	MSQESVILFYSGMSLFLFLFRVVT NFTFFPLAVICIRASHLLACPLPSLS LPHQPTH*
5465	10962	A	5788	2	472	
5466	10963	A	5789	3720	5308	PLLPFLSPPHLTEVEGQGRMVGTTEE TWSNCSGAFKPKCSPQPQICLV LAP TRELAQQVQQVADDY GKCSRLKST CIYGGAPKGPQIRDLERGVEICISTP GRLIDFLESGKTNLSRCTYLVLDET DKMLDMGSEPQIL*IGDPIRDRQTL

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						MWSATWPKEVRQLAEDFLRDYTOI NVGNLELSANHNILQIVDVCMESEK DHKLIQLMEEIMAEKENKTIIFVETK RRCDDLTRMRRDGWPAMCIHGD KSQPERDWVLNEFRSGKAPILIATD VASRGLDVEDVKFVINYDYPNSSD YVHRIGRTARSTNKGTAYTFFTPGN LKQARELIKVLEEANQAINPKLMQL VDHRGGGGGGGKGGRSRYRTTSSA NNPNLMYQDECDRLRGVKDGGGR RDSASYRDRSETDRAGYANGSGYG SPNSAFGAQAGQYTYGQTYGAAA YGTSSYTAQEYAGTYGASSTTSTG RSSQSSSQFSGIGRSGQQPQLMS QQFAQPPGATNMIGYMGQTAYQYP PPPPPPPSRK
5467	10964	A	5790	1	307	
5468	10965	A	5791	2821	5781	
5469	10966	A	5792	1	981	
5470	10967	A	5793	99	1023	NHKDGEKTEQKNGKL*KSECLSKN KAGGITLPDFKLYYKATVTKTAWY WYQNRDIDQWNRTEPSEIMPHIYN HLIFDKPDKNKKWGNDLSFNKWC WENWLAICRKLKLDPFLTPYTKINS RWIQDLNIRPKNIKTLEEILGNTIQDI GMGKDFKSKTPKAMAIAKAKIDKW DLIKLSFCTEKETTIRVNRQPTWE KIFAIYSSEKGLISRIYNELQQIYKKK TNNPIQKRVKDMNRHFSKEDIYAA K\KT*KNAHHHMKKCSSSPAIREIQI KTTMRYHLIPRMVVIKKSGNKGCV RGCGEIGTVLH
5471	10968	A	5794	3	1218	
5472	10969	B	5795	1	1098	MIDKGDITDPSEIQTIREYYNYLY TNKLENLEEMDKFLDTYTLPRLNQ EEVESLNRPTTGSEIEAIMNSLPTKK VQDQMDSQPNSTRVLEVLARAIQ EKEIKGIQLGKEEVKLSLFADDMIV YLENPIVSARNLLKLIGNFSKVSGY KINVQKSQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLKRDVKDLFK ENYKPLLKEIKEDTNKWKSIKSWV GRINIMKMAILPKVIYRFNAIPNKL MPFFTELEKTTLKFIWNQKRAHIAK SILSQKNKAGGITLPDFKLYYKATV TKTAWYWYQNRDIDQWNRTEPSEI MPHIYNHLIFDKPDKNKKWGKDSL FNKWCWENWQPYVES*
5473	10970	A	5796	1	1245	
5474	10971	A	5797	1	969	MIVYLENPIVSAQNLLKLIGNFSRVS GYKINVQKSQAFLYTNNRQTENQII SELPFTIASKRIKYLGIQLTRDVKDL FKENYKTLLKEIKEDTKWKNIPCS WVGRINIVKIAIPKVIYRFAIPIKL PMTFFTELEKTTLKFIWNQKRARIA KSILSQKNKAGGIMLPDFKLYYKAT VTKTAWYWYQNRDIDQWNRTEPS EIMLHIYKHLIFDKPDKNKQWGKDS

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						LFNKWCWENWLAICRKLKLDPFLT PYTKINSRWIKDLNVRPKTIKLEEN LGNTIQDIGTGKDFMSKTPKAMAT KAKIDKWD/LRFCTAK*TTIRV
5475	10972	B	5798	1	1383	MGDFNTPLSTLDRSKRQKVKKDIQ ELNSALHQVDLIDYRTPYPKSTEYT FFSAQHHTYSKTDHIVGSKELLSKC KRTEIITNCLSDHSAIKLELRKILTO NRSTTWKLNLLNDYWVHNEMK AEIKMFFETNENKDTTYQNLRLTLK AVCRGKFVALNAHQKQKISKIDTL TSQLEKEKQEQTHSKASRRQEITKI RAELKEIETQKTLQKINDSRSAIR QEKEIKGIQLGKEEVQSLFADDMI VHLENPIVSAQNLLKLIGNFSKVS YKINVKKSQAFLYTNNRQTESQIMS EFPFTIASKRIKYLGIQLTRDVKDLF KENYKTLLEIKEDTNKWKNIPCS WVGRINIVKMAILPKVIYRFNAISIK LPMTFFTELGKPTLKLWNQKRVRI AKSILSQKNKAGGIMLPDFKLYYKA TVTKTAWYWYQNRDIDQWNRTEP SEIMPHITTI*
5476	10973	A	5799	1	1272	MIISMDAEKAFDKIQCCFMLKTLNK LGIDGTYLKKIRAIYDKPTVNIILNG QKLEALPLKTGTRQGCPLSPLFNIV LQALARAIRQEKEIKGIQLGKEEVK LSLFADDMIVYLENPIVKAQNLLKL ISNFSKVSQYKISMQKSQAFLYTNN RQIESQIMSELPFTIASKRIKYLGIQL TRDVKDLFKENYKPLLNEIKEDKN KWKNIPCSWVGRINIVKMAILPKFI WRQKRAHIAKSILSQKNKAGGIKLP DFKLYYKATVTKTAWYWYQNRDI DQWNRTEPSEIMLHIHNYLIFDKPD KNKKWRKDSL FNKWCWENWLAK CRKLKLHPFLTPYTKINSRWIKDLH VRPKTIKLEENLGITQDKGMGKD FMSKTPEALATKANIDKSDLIKLS SCK\ETTIRVNRQPTWEKIFAIYSS
5477	10974	A	5800	1	1398	
5478	10975	A	5801	564	2444	LTNQKKSRTRWIHSRILPEVQGGAV LEVLAIRAEK\EVKGIQLGKEEV KLSLFADDMIVYLENPIISAQNLLKL IGNFSKVSQYKINVQKSQAFLYTNN RETESQIMSELPFTTASRIKYLGIQ LTRDVKELFKETYNPLLNEIKEDTT KWKNIPCSWVGRINIVKIAILPKVICI FNAIPIKLPMTFFTELEKTTLKFIRNQ KRARIAKSILSQKNKAGDVTLPDFK LYYKATVTKTVWYWYQNRDIDQW NRTEPSEIILHIYNHLIFDTPDKNKK WGKDSL FNKLCWENWLAICRKLKL DPFFTPYTKINSRWIKDLHVRPKTIK TLEENLGNTIQDIGIGKDFMTKTQK AMATNAEIHKWDLIKHKHFCTAKE TTIRVNRQPTKWENIFAIYSSDKRLI SRIYKELKHIYKRKTNNPINKWAKD

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						MNRHFSKEDIYAANRHMKKCSSSL AIREMQIKTTMRYHLTPVRMAIHKK SGNNRCWRGCGENHSQQTITRTKIQ TLHVLNHRWELNNENTWTQEGEH HTLGPVVGWGRGEGQQCISPYSMG KASIPHAVLVWVFFGLCQNAPLDW SLVSLWWCLLGFTNFFCKEPDCKY VRLFRPLGIVFATPPLPPPPSSSTS S
5479	10976	A	5802	1	2430	
5480	10977	A	5803	2022	4573	
5481	10978	A	5804	1169	3077	VHCRFWILALCQMSRLQKSPLLFNI VLEVLAKAIKQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQNLLIL QLISNFSKVSQYKINQKSQAFLYT NNRQTESQMRSELPFTVATKRIKYL GIQLTRDVKDLFKENYKLLLNEIKE DTNKWKNIPRSWVGGRINLVKMAI LPKVIYRFNAIPIKLPMFFTELEKTT LKFIWNQKRALIAKSSLSQKNKTGG ITLPDFKLYYKATVTKTSWYWYQN RDIDQWNRTEPSEIMPHIYNYLIFDK PDKNKK\WGKDSL FNK WFWENCL AICRKLKLDPFL\TNYTKINSRWIKD LNFRPKTIKTLEDNLGNTIQDIGMG KDFMSLP/KTPEAMATKAKIDKWD LIK\KLSFCTAKETTIRVNRQPTKWE KIFAIYSSDKGLISRIYNELKQIYKK KVTNNPIKKWAKDTNRHFSKEDIYA ANRHMRCSSSLVIREMQIKTTMR YHLTPVRTAIKKSGDNRCWRGCGE IGTLLHCWWDCCLVQPLWKS VWR FLRDLELEIPFPAIPLLG IYPKDYKS CCYKDTCTCMFIAALFTIAKTWNQP KCPTMIDWIKKMWHIYTM EYYAAI KNDEFVSFVGTWMKLEIILSKLSQE QKTKHCIFSLIGGN
5482	10979	A	5806	133	358	
5483	10980	A	5807	3	164	
5484	10981	A	5808	1573	1720	
5485	10982	A	5809	1573	1720	
5486	10983	A	5810	1	4860	
5487	10984	A	5811	2	2887	VRVIKSEDDVLVVCPTILTEDGMQA QHLGATLALYRLVKGQSVHQLLP TYRDVWLEWSDAEKKREELNKME TNKPRDLFIKLLNKLKQQQQQQQ QHSENKRENSDEPEESWENLVSDE DFSALSLESANVEDLEPVRNLFRL QSTPKYQKLLKERQQLPVFKHRDSI VETLKRHRVVVVAGETGSGKSTQV PHFLLEDLLLNEWEASKCNIVCTQP RRISAVSLANRVCDELGCENGPGAG RNSLCGYQIRMESRACESTRLLYCT TGVFA*GKLQEDGLSK*CVSMFIVD EVHERSVQSDFLIILKEILQKRSD LHLILMSATVDSEKFSTYFTHCPILR ISGRSYPVEVFHLEDIIEETGFVLEK

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						DSEYCQKFLEEEEEVTINVTSKAGGI KKYQEYIPVQTGAHADLNPFYQKY SSRTQHAILYMNPHKINLDLILELLA YLDKSPQFRNIEGAVLIFLPGLAHIQ QLYDLLSNDRRFYSERYKVIALHSI LSTQDQAAFTLPPPGVRKIVLATNI AETGITIPDVVFVIDTGRTKENKYHE SSQMSSLVETFVSKASALQRQGRA GRVRDGF CFRMYTRERFEGFMDYS VPEILRVPLEELCLHIMKCNLGSPED FLSKALDPPQLQVISNAMNLLRKIG ACELNEPKLTPLGQHLAALPVNVKI GKMLIFGAIFGCLDPVATLAAVMTE KSPFTTPIGRKDEADLAKSALAMAD SDHLTIYNAYLGWKKARQEGGYRS EITYCRRNFLNRTSLLTLEDVKQELI KLVKAAGFSSSTTSTSWEGNRASQT LSFQEIALLKAVLVAGLYDNVKGII YTKSVDVTEKLACIVETAQGKAQV HPSSVNRDLQTHGWLLYQEKIRYA RVYLRETTLITFPVLLFGGDIEVQH RERLLSIDGWIFYQAPVKIAVIFKQL RVLIDSVLRKKLENPKMSLENDKIL QITELIKTENN
5488	10985	A	5812	1	132	
5489	10986	A	5813	383	667	
5490	10987	A	5814	2444	2755	DYYYFFEMESCSVAQAGVQWRDL GSLQPPPPSSRDSSASASRVAGTTG MHH/HNQLSFVFLVKMGFHHVGQA DFELLTSSDLPVSASQSAGITGVSHR ARPLSS
5491	10988	A	5815	1724	1941	AHLLYEWIFFFFFFFFEMESHVAQA GVLWRDLSSLQAPPPGSQSDSPAS ASWVAGITGACHHARHEWNFKC
5492	10989	A	5817	37	2496	
5493	10990	A	5818	2	1814	
5494	10991	A	5819	1	394	
5495	10992	A	5820	2	1785	QLFACVPKTSPPATVISSVTSTCSSL PSVSSAPITSGQAPTTFLPASTSQAQ LSSQKMESFSAVPPTKEKVSTQDQP MANLCTPSSTANSCSSASNTPGAP ETHPSSSPTPTSSNTQEEAQSSVSD LSPMSMPFASNSEPAPLTLTSPRMV AADNQDTSNLPQLAVPAPRVSHRM QPRGSFYSMVPNATIHQDPQSIFVT NPVTLTPPQGPPAAVQLSSAVNIMN GSQMHNIPANKSLPPTFGPATLFNH FSSLFDSSQVPANQGWGDGPLSSRV ATDASFTVQSAFLGNSVLGHLENM HPDNSKAPGFRPPSQRVSTSPVGLP SIDPSG\SSPSSSAPL\ASFSGIPGNQ GFFLQGP\APVGGLLSFNQRHF/SFP HPW\TSASNSCDSPIPSVSSGSSSPLS ATS\APPTLG\QPKGSQCQSRIKGY LPPIGTERLARILQGGSV AQAPAGT SFVAPVGHSG\WSFGVNAVSEGL\ S GWSQSVMG\NHPMAFNFSFGPKAH FSQHQP MERDDSGMVAPSNIFHQP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MASGFVDFSKGLPISMYGGTIIPSH QLADVPGGPLFNLHNPDPANPM IKVIQNSTECTDAQQVKWA
5496	10993	A	5821	3	125	
5497	10994	A	5822	3448	3831	KNRFCSGVSSNSKSNNSCVVYIDR DIDHTYIHIHTNICIHLFFFFETES HALSPRLECNGVISAHCNLHPPGASS DSPASAAARVAGITGTCHHAQLIFFF FVFLVETGFHHAAQAGSQTPDLR*S TPLGFPKC*DYRR/AAIVPGIFLLH*I R*\KVPTLLTDMRNASEYDCDFSTN KIDKEETFS*NASLNLCLLST*PYEM VTHFKGY*ILPLFFFFFLRQSL/SSVT QAGVQWHNLGSLQPLPPGFKQFSC LSLPSSWDYRYQLPRLA/NF/FVFLV ETGFHHAAQAGSQTPDLR

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-5497, a mature protein coding portion of SEQ ID NO: 1-5497, an active domain of SEQ ID NO: 1-5497, and complementary sequences thereof.
- 5 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 10 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 15 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
- 20 7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively
25 associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
 - 30 (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
 - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-5497.
11. A composition comprising the polypeptide of claim 10 and a carrier.
- 35 12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
 - 5 b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with
 - 10 nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
 - b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
 - c) detecting said product and thereby the polynucleotide of claim 1 in the
 - 15 sample.
15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 20 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
 - b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
- 25 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
 - 30 b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-5497, a mature protein coding portion of SEQ ID NO: 1-5497, an active domain of SEQ ID NO: 1-5497, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-5497, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 5498-10994, the mature protein portion thereof, or the active domain thereof.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-5497.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
- 5 28 A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.